



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number 114289

TO: Lorraine Spector
Location: REM/4D55/4C70
Art Unit: 1647
Monday, February 23, 2004

Case Serial Number: 10/063671

From: Toby Port
Location: Biotech-Chem Library
Remsen 1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Spector,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a

Db	1921	ATCTGAGTTGGAGCTCTAAGCTCAGTGTCTCTCTCCACCTACACCCACACACAGCCCTTGTCGCA	1980
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Db	2101	GTTCCTCAAGTGTGAGGAGCCGCTCTTCTTATGAAAGCAATGATATGACATCTGTCCCT	2160
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DEFINITION	Sequence 49 from Patent WO0208284.		
ACCESSION	AX454464		
VERSION	AX454464.1	GI:21713856	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE			
AUTHORS	Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J., Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I., and Ye,W.		
TITLE	Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis		
JOURNAL	Patent: WO 0208284-A 49 31-JAN-2002, Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard, Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ; Hillan, Kenneth J. (US) ; Marsters, Scott A. (US) ; Pan, James (US) ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ; Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William I. (US)		

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DEFINITION	Sequence 225 from Patent WO0104311.		
VERSION	AX697644		
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SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens (human)		
REFERENCE	1. Ashkenazi, A.J., Botstein, D., Desnovers, L., Eaton, D.L., Ferrara, N., Flivner, E., Fong, S., Gao, W.Q., Gerber, H., Gertsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, C.J., Gunney, A.L., Hillan, K.J., Kijawski, I.J., Mathers, J.P., Pan, J., Pao, N.F., Roy, M.A., Stewart, T.A., Tuma, D., Williams, P.M., and Wood, W.I. Secreted and transmembrane polypeptides and nucleic acids encoding the same		
TITLE	Patent: WO 0104311-A 235 18-JAN-2001; Genentech Inc. (US)		
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Best Local Similarity	100.0%;	Pred. No. 0;	
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 Homo sapiens (human)
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 REFERENCE
 1 (bases 1 to 2586)
 Wood, W.I., Gurney, A.L., Goddard, A., Penica, D., Chen, J. and Yuan, J.
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 JOURNAL
 Patent: JP 2001516580-A 195 02-OCT-2001;
 GENENTECH INC
 OS Homo sapiens (human)
 PN JP 2001516580-A/195
 PD 02-OCT-2001
 PR 16-SEP-1998 JP 2000511867
 PR 17-SEP-1997 US 60/059112, 17-SEP-1997 US 60/059117 PR 60/059184 PR
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 17-SEP-1997 US 60/059119, 18-SEP-1997 US 60/059263 PR
 18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/062125 PR
 17-OCT-1997 US 60/062287, 17-OCT-1997 US 60/062285 PR
 21-OCT-1997 US 60/062486, 24-OCT-1997 US 60/062816 PR
 24-OCT-1997 US 60/062814, 24-OCT-1997 US 60/063127 PR
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 27-OCT-1997 US 60/063549, 28-OCT-1997 US 60/063542 PR
 28-OCT-1997 US 60/063550, 28-OCT-1997 US 60/063564 PR
 28-OCT-1997 US 60/063544, 28-OCT-1997 US 60/063564 PR
 29-OCT-1997 US 60/063734, 29-OCT-1997 US 60/063728 PR
 29-OCT-1997 US 60/063704, 29-OCT-1997 US 60/063735 PR
 29-OCT-1997 US 60/064215, 29-OCT-1997 US 60/063745 PR
 29-OCT-1997 US 60/064103, 31-OCT-1997 US 60/063870 PR
 31-OCT-1997 US 60/064248, 07-NOV-1997 US 60/064809 PR
 12-NOV-1997 US 60/065186, 17-NOV-1997 US 60/065846 PR
 18-NOV-1997 US 60/065693, 21-NOV-1997 US 60/066122 PR
 21-NOV-1997 US 60/066364, 24-NOV-1997 US 60/066772 PR
 24-NOV-1997 US 60/066466, 24-NOV-1997 US 60/066770 PR
 24-NOV-1997 US 60/066511, 24-NOV-1997 US 60/066453 PR
 25-NOV-1997 US 60/066840
 PI WILLIAM I WOOD, AUSTIN L GURNEY, AUDLEY GODDARD, DIANE PENICA, PI
 JEAN CHEN,

PI JEAN YUAN
PC C12N15/09, C07K14/47, C07K14/705, C07K16/18, C07K16/28, C07K19/00,
PC C12N1/19, C12N5/10, C12P21/02, C12P21/08, C12Q1/02, C12P21/08, PC
C12R1/31,
PC C12N15/00, C12N5/00
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BASE COUNT 631 a 679 c 703 g 573 t

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ORGANISM  Homo sapiens
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AUTHORS   Wood,M.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
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JOURNAL   Patent: JP 2002238586-A 195 27-AUG-2002;
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		Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and		
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1 Kobayashi, K., Ouchida, M., Tsuji, T., Hanafusa, H., Miyazaki, M.,
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Reduced expression of the REIC/Dkk-3 gene by
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Ouchida, M., Kobayashi, K., Tsuji, T., Namba, M. and Shimizu, K.
Direct Submission
Submitted (15-MAR-2001) Mamoru Ouchida, Okayama Medical School,
Medicine; Shikata-cho 2-5-1, Okayama, Okayama 700-8558, Japan
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 DEFINITION Cell proliferation inhibiting proteins, polynucleotides, antisensepolynucleotides to the polynucleotides, and cell proliferation inhibiting agents, cancer diagnostic agents, cancer therapeutic agents and compositions for gene therapy using same.

ACCESSION BD093627
 VERSION 1
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2632)
 AUTHORS Namba,M. and Tsuji,T.
 TITLE Cell proliferation inhibiting proteins, polynucleotides, antisensepolynucleotides to the polynucleotides, and cell proliferation inhibiting agents, cancer diagnostic agents, cancer therapeutic agents and compositions for gene therapy using same

JOURNAL Patent: WO 0138528-A 3 31-May-2001;
 HISAMITSU PHARMACEUTICAL CO INC,MASAYOSHI NAMBA,TOSHITAYA TSUJII
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 PC C12N15/12,C07K14/47,C12Q1/68,C12P21/02,A61K38/17,A61K31/711,
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VERSION	AX235333.1	GI:15593878		
KEYWORDS				
SOURCE				
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	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE				
AUTHORS	Heath, H.M., Parekh, R.B., Rohlf, C. and Patel, T.P.			
TITLE	Dp1-6, a therapeutic biomarker in neurological disorders			
JOURNAL	Patent: WO 0163295-A 1 30-AUG-2001;			
	Oxford Glycosciences (UK) Limited (GB)			

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 QY 2282 ACTTAGCAGCACTGAGAGACATTAATCAACAGCTGAGAAATCAAAACGAGAGGGCT 2341
 Db 2169 ACTTAGCAGCACTGAGAGACATTAATCAACAGCTGAGAAATCAAAACGAGAGGGCT 2228
 QY 2342 GTGTGAAAACATGTTGTAATATGCACTGCGAACAATGAACTTACGCTCCACAAT 2401
 Db 2229 GTGTGAAAACATGTTGTAATATGCACTGCGAACAATGAACTTACGCTCCACAAT 2288
 QY 2402 GATGTTTCAAGTGTCACTGAGTGTGCACTGATTTCACTCAGAGTCTTAAAGTTT 2461
 Db 2289 GATGTTTCAAGTGTCACTGAGTGTGCACTGATTTCACTCAGAGTCTTAAAGTTT 2348

QY 2462 AAAGTTGCAATGATTTGTAATGACATGCTTTCTTTGAAGTTTAAATTAATTAACAATA 2521
 Db 2349 AAAGTTGCAATGATTTGTAATGACATGCTTTCTTTGAAGTTTAAATTAATTAACAATA 2408
 QY 2522 AGTTGCAATTTGAATTAAGCAATAATCACTTCAACTGCAAAAAA 2581
 Db 2409 AGTTGCAATTTGAATTAAGCAATAATCACTTCAACTGCAAAAAA 2468
 QY 2582 AAAAA 2586
 Db 2469 AAAAA 2473

Search completed: February 19, 2004, 21:18:11
 Job time : 9417 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 20, 2004, 14:56:18 ; Search time 24 Seconds
(without alignments)
685,806 Million cell updates/sec

Title: US-10-063-671-8

Perfect score: 1880
Sequence: 1 MQRGLATLCLLLAAVPTA.....EMALGPAAAAALLGGEEL 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1880	100.0	350	1 DKK3_HUMAN	Q9UBP4 homo sapien
2	1589	84.5	349	1 DKK3_MOUSE	Q9QUN4 mus musculu
3	1017	54.1	350	1 DKK3_CHICK	Q98B39 gallus gall
4	214.5	11.4	224	1 DKK4_HUMAN	Q9UBD3 homo sapien
5	174.5	9.3	266	1 DKK1_HUMAN	Q94907 homo sapien
6	165.5	8.8	272	1 DKK1_MOUSE	Q94908 mus musculu
7	162	8.6	259	1 DKK2_HUMAN	Q94942 homo sapien
8	154	8.2	259	1 DKK2_MOUSE	Q94948 mus musculu
9	145	7.7	242	1 SGY1_HUMAN	Q94885 homo sapien
10	138	7.3	577	1 ITB6_CAVPO	P18563 cavia porce
11	131.5	7.0	676	1 PRIS_HUMAN	P07225 homo sapien
12	126	6.7	788	1 ITB6_HUMAN	P18564 homo sapien
13	126	6.7	1394	1 LTB3_HUMAN	P22064 homo sapien
14	126	6.7	1595	1 LTB3_MOUSE	Q14766 homo sapien
15	125.5	6.7	230	1 SGY1_MOUSE	Q94949 mus musculu
16	123.5	6.6	787	1 ITB6_MOUSE	Q94882 mus musculu
17	119	6.3	2318	1 NTC3_MOUSE	Q04174 drosophila
18	117	6.2	1712	1 LNA_DROME	Q01751 homo sapien
19	116	6.2	1172	1 LMB3_HUMAN	P10040 drosophila
20	116	6.2	2139	1 CRB_DROME	Q13751 homo sapien
21	115	6.1	1807	1 ITB4_RAT	Q04632 rattus norv
22	113	6.0	618	1 DLJ3_HUMAN	Q9NYJ7 homo sapien
23	113	6.0	3562	1 PGCV_CHICK	Q90953 gallus gall
24	112	6.0	1389	1 LTB3_MOUSE	Q86318 mus musculu
25	112	6.0	1713	1 LTB3_MOUSE	Q86319 mus musculu
26	110.5	5.9	864	1 LDBR_MOUSE	P33551 mus musculu
27	110.5	5.9	2214	1 SORL_HUMAN	P21783 h. sapien
28	110	5.9	2524	1 NOTC_XENLA	Q00741 papio cynoc
29	109.5	5.8	655	1 ITB5_PAPCY	Q00741 papio cynoc
30	109.5	5.8	1712	1 LTB1_RAT	Q00918 rattus norv
31	109.5	5.8	1822	1 ITB4_HUMAN	P16144 homo sapien
32	109	5.8	1168	1 LMB3_MOUSE	Q61087 mus musculu
33	109	5.8	2319	1 NTC3_PAT	Q94172 rattus norv

34	108.5	5.8	757	1 COMP_HUMAN	P49747 homo sapien
35	108.5	5.8	852	1 SRCH_RABIT	P16230 coryctolagus
36	108	5.7	1170	1 TSP1_HUMAN	P07996 homo sapien
37	107.5	5.7	799	1 ITB5_HUMAN	P18084 homo sapien
38	107	5.7	589	1 DLJ3_RAT	O88671 rattus norv
39	107	5.7	755	1 COMP_RAT	P35444 rattus norv
40	107	5.7	1693	1 SAS_DROME	Q04164 drosophila
41	106.5	5.7	3695	1 LNA5_HUMAN	O15230 homo sapien
42	106	5.6	227	1 AGT_ORYSA	P11219 oryza sativ
43	106	5.6	1221	1 PBL2_MOUSE	P37889 mus musculu
44	106	5.6	2471	1 NTC2_HUMAN	Q04721 homo sapien
45	105.5	5.6	96	1 BYR_BOMVA	Q9PW66 bombyx mori

ALIGNMENTS

RESULT 1	ID	DKK3_HUMAN	STANDARD;	PRT;	350 AA.
AC	Q9UBP4; Q9ULB7;				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	15-SEP-2003 (Rel. 42, Last annotation update)				
DE	Dickkopf related protein-3 precursor (DKK-3) (Dkk-3).				
GN	DKK3 OR REIC.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TRISUB-Fetal brain;				
RX	MEDLINE=20035735; PubMed=10570958;				
RA	Krupnik V.E., Sharp J.D., Jiang C., Robison K., Chickering T.W.,				
RA	Amaravadi L., Brown D.E., Guyot D., Mays G., Leiby K., Chang B.,				
RA	Drong T., Gooden A.D., Gearing D.P., Sokol S.Y., McCarty S.A.,				
RT	"Functional and structural diversity of the human Dickkopf gene				
RT	family.";				
RL	Gene 238:301-313(1999).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Tanaka S., Sugimachi K.,				
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20119095; PubMed=10652205;				
RA	Tsuji T., Miyazaki M., Sakaguchi M., Inoue Y., Namba M.,				
RT	"A REIC gene shows down-regulation in human immortalized cells and				
RT	human tumor-derived cell lines.";				
RL	Biochem. Biophys. Res. Commun. 268:20-24(2000).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RA	Tate G., Mitsuura T.,				
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=21673998; PubMed=11814687;				
RA	Kobayashi K., Ouchida M., Teuji T., Hanafusa H., Miyazaki M.,				
RA	Namba W., Shimizu N., Shimizu K.,				
RT	"Reduced expression of the REIC/Dkk-3 gene by promoter-				
RT	hypermethylation in human tumor cells.";				
RL	Gene 282:151-158(2002).				
RN	[6]				
RP	SEQUENCE FROM N.A.				
RC	TRISUB-Kidney;				
RX	MEDLINE=22388257; PubMed=12477932;				
RA	Strauberg R.L., Feinsold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Stetten G.M., Schuler G.D.,				
RA	Altschuler S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Shat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton W., Soares M.B., Bonaldi M.F., Casavant T.L., Schertz T.E.,				

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mallahy S.J., Riosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H., Rader S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vallat D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting J., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.N., Krzywinski M.I., Skalka U., Smalhus D.E., Schnerch J., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).

CC -1- FUNCTION: INHIBITOR OF WNT SIGNALING PATHWAY (POTENTIAL).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN HEART, BRAIN, AND SPINAL CORD.

CC -1- PTM: N-GLYCOSYLATED.

CC -1- SIMILARITY: BELONGS TO THE DICKKOPF FAMILY.

CC -----

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CC -----

DR EMBL; AF177396; AAF02676.1; -

DR EMBL; AB034421; BAA85488.1; -

DR EMBL; AB034203; BAA90548.1; -

DR EMBL; AB035182; BAA87044.2; -

DR EMBL; AB045205; BAA87044.2; JOINED.

DR EMBL; AB045206; BAA87044.2; JOINED.

DR EMBL; AB045207; BAA87044.2; JOINED.

DR EMBL; AB045208; BAA87044.2; JOINED.

DR EMBL; AB045209; BAA87044.2; JOINED.

DR EMBL; AB045210; BAA87044.2; JOINED.

DR EMBL; AB057591; BAA84360.1; -

DR EMBL; AB057804; BAA84361.1; -

DR EMBL; BC007660; AAH07660.1; -

DR Genbank; HGNC:2893; DKX3.

DR MIM; 605416; -

DR GO; GO:0005615; C:extracellular space; TAS.

DR GO; GO:0007345; P:embryogenesis and morphogenesis; TAS.

DR InterPro; IPR006796; dickkopf_N.

DR Pfam; PF04706; dickkopf_N_1.

KW Developmental protein; Signal; Wnt signaling pathway; Glycoprotein.

FT SIGNAL 1 16 POTENTIAL.

FT CHAIN 17 350 DICKKOPF RELATED PROTEIN-3.

FT DOMAIN 147 195 DKK-TYPE CYS-1.

FT DOMAIN 208 284 DKK-TYPE CYS-2.

FT DOMAIN 338 343 POLY-ALA.

FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 335 335 G -> R (IN REF. 4).

FT SEQUENCE 350 AA; 38291 MW; 72F504122B40AFBE CRC64;

Query Match 100.0%; Score 1880; DB 1; Length 350; Best Local Similarity 100.0%; Freq. No. 3.6e-128; Indels 0; Gaps 0; Matches 350; Conservative 0; Mismatches 0;

QY 1 MORGATLILLLAAVTPAPAPATSAVPKGPALSYPOEBATLNMFRVEELMED 60

DB 1 MORGATLILLLAAVTPAPAPATSAVPKGPALSYPOEBATLNMFRVEELMED 60

QY 61 TQHLRSVEMEMEBEAAKASSEVNLANLPSPSHNETNDTKYGNNTIHVEIHKITN 120

DB 61 TQHLRSVEMEMEBEAAKASSEVNLANLPSPSHNETNDTKYGNNTIHVEIHKITN 120

QY 121 NQTSQWFESETVITSVSDERGRSHCEIIDDCGSPMYCQFASRQYTCQCRQRMCTR 180

DB 121 NQTSQWFESETVITSVSDERGRSHCEIIDDCGSPMYCQFASRQYTCQCRQRMCTR 180

QY 181 DSECCGQLCWNGCTKATRGSGNGTICDNORDQDPLCCAFQRLGILFPVCTPLPVGEL 240

DB 181 DSECCGQLCWNGCTKATRGSGNGTICDNORDQDPLCCAFQRLGILFPVCTPLPVGEL 240

QY 241 CHDPASRLDLITWLEPDGALDRCPASGLLCQPHSHSLVYCKPTFVGSRDQDGEILL 300

DB 241 CHDPASRLDLITWLEPDGALDRCPASGLLCQPHSHSLVYCKPTFVGSRDQDGEILL 300

QY 301 PREVPDEYVGSFMEYVROELDERSTEMALGEPAALALGEEI 350

DB 301 PREVPDEYVGSFMEYVROELDERSTEMALGEPAALALGEEI 350

RESULT 2

ID DKK3_MOUSE STANDARD; PRT; 349 AA.

AC Q9QUN9;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE 15-SEP-2003 (Rel. 42, Last annotation update)

DE Dickkopf related protein-3 precursor (Dkk-3) (Dkkopf-3) (mdk-3).

GN DKK3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10090;

RP SEQUENCE FROM N.A.

RP MEDLINE=99425169; PubMed=10495270;

RX Monaghan P.A., Kioschis P., Wu W., Zuniga A., Bock D., Pousetka A., Dellus H., Niehus C.; "Dkkopf genes are co-ordinately expressed in mesodermal lineages." Mech. Dev. 87:45-56(1999).

RT "Dkkopf genes are co-ordinately expressed in mesodermal lineages."

RL "Functional and structural diversity of the human Dickkopf gene family.";

RT Gene 238:301-313(1999).

RN [3]

RP SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J; TISSUE=Liver;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I., Saito T., Okazaki H., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H., Kuenl P., Lewis S., Matsuo Y., Nkaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberees P., Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilting L., Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kontsuki S., Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

CC -1- FUNCTION: INHIBITOR OF WNT SIGNALING PATHWAY (POTENTIAL).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BRAIN, EYE, AND HEART.

[illegible]

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 19-28 AND 134-144.
 RX MEDLINE=20035735; PubMed=10570958;
 RA Krupnik V.E., Sharp J.D., Jiang C., Robison K., Chickering T.W.,
 Amaravadi L., Brown D.E., Guyot C., Mays G., Leiby K., Chang B.,
 Duong T., Goodenart A.D.J., Gearing D.P., Sokol S.Y., McCarthy S.A.,
 "Functional and structural diversity of the human Dickkopf gene
 family.";
 RT J. Biol. Chem. 274:19465-19472(1999).
 RL Gene 338:301-313(1999).
 RP SEQUENCE FROM N.A.
 RA Tate G., Mitsuya T.,
 "Human Dickkopf as well as DAN family members, Cerberus and Gremlin,
 are preferentially expressed in the epithelial malignant cell lines.";
 RT J. Biochem. Mol. Biol. Biophys. 3:239-242(1999).
 RL [3]
 RP SEQUENCE FROM N.A.
 RA Tate G., Suzuki T., Mitsuya T.,
 Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INHIBITOR OF WNT SIGNALING PATHWAY.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN CEREBELLUM, T-CELLS, ESOPHAGUS,
 AND LUNG.
 CC -1- PTM: APPARS NOT TO BE GLYCOSYLATED.
 CC -1- PTM: CAN ALSO BE PROTEOLYTICALLY PROCESSED BY A FURIN-LIKE
 PROTEASE.
 CC -1- SIMILARITY: BELONGS TO THE DICKKOPF FAMILY.
 CC
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 or send an email to license@ebi.ac.uk).
 CC
 DR EMBL; AF177397; AA02677.1; -
 DR EMBL; AB018005; BAA33475.1; -
 DR EMBL; AB018003; BAA33475.1; JOINED.
 DR EMBL; AB018004; BAA33475.1; JOINED.
 DR EMBL; AB017788; BAA33478.1; -
 DR HSSP; P25687; 11MT.
 DR GeneW; HGNC:2894; DKK4.
 DR MIM; 605417; -
 DR GO; GO:0030178; P:negative regulation of wnt receptor signal. .; NAS.
 DR InterPro; IPR006796; dickkopf_N.
 DR Pfam; PF04706; dickkopf_N; 1.
 KM Developmental protein; Signal; Wnt signaling pathway.
 FT SIGNAL 1 18
 FT CHAIN 19 224 DICKKOPF RELATED PROTEIN-4.
 FT CHAIN 134 224 DICKKOPF RELATED PROTEIN-4 SHORT FORM.
 FT DOMAIN 41 90 DKK-TYPE CYS-1.
 FT DOMAIN 145 218 DKK-TYPE CYS-2.
 FT CONFLICT 93 93 M -> L (IN REF. 3).
 SQ SEQUENCE 224 AA; 24875 MW; 45F8BEC476961357 CRC64;
 Query Match 11.4%; Score 214.5; DB 1; Length 224;
 Best Local Similarity 26.5%; Pred. No. 1.2e-08;
 Matches 57; Conservative 21; Mismatches 72; Indels 65; Gaps 7;
 QY 124 GQMVSEVITVSGEERG-RRSHECTIDECGSPMYC-QFASFOYTCQPCRGOMLCTRD 181
 DB 17 GALTVDNNIRASADLHGARKSGCCLSDPTDCNTRKFCQPPDEKPFCAICGLRRPCORD 76
 QY 132 SECCGDLCTWGHCTKM-----A 199
 DB 77 AMCCGGLTGVNDVCTTMDAPILERQLDDEODGTHAETGHPVOENQPKKPSIKSGG 136
 QY 200 TFGSNGTICNDQDQGLCAFGRLGLFPVCTPLPVEGELC---HDPASRLDLITWE 255

DB 137 RKGGEGECCLTFDGPFLCCA--RHFWTKCKEVLLGGYCSRGHDTAQAREI----- 190
 QY 256 LEPDGLRRCPCASGLLCP-----HSHSLVYVCK 285
 DB 191 -----FQRCDCGPGLLCRSQLTSNRQHLRLVQCQ 219
 RESULT 5
 ID DKK1 HUMAN STANDARD; PRT; 266 AA.
 AC 094907;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Dickkopf related protein-1 precursor (Dkk-1) (Dkkopf-1) (Dkk-1)
 DE (SK).
 GN DKK1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NX NCBI_TaxID=9606;
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 RP SEQUENCE FROM N.A.
 RC TISSUE=Leiomyosarcoma;
 RX MEDLINE=99315900; PubMed=10383463;
 RA Fedi P., Ballico A., Nleto Soria A.,
 Bottaro D.P., Kraus M.H., Aaronson S.A.,
 "Isolation and biochemical characterization of the human Dkk-1
 homologue, a novel inhibitor of mammalian wnt signaling.";
 RT J. Biol. Chem. 274:19465-19472(1999).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal kidney;
 RX MEDLINE=20035735; PubMed=10570958;
 RA Krupnik V.E., Sharp J.D., Jiang C., Robison K., Chickering T.W.,
 Amaravadi L., Brown D.E., Guyot C., Mays G., Leiby K., Chang B.,
 Duong T., Goodenart A.D.J., Gearing D.P., Sokol S.Y., McCarthy S.A.,
 "Functional and structural diversity of the human Dickkopf gene
 family.";
 RT J. Biol. Chem. 274:19465-19472(1999).
 RL [3]
 RP SEQUENCE FROM N.A.
 RA Tate G., Suzuki T., Mitsuya T.,
 Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 RL [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20422487; PubMed=10965128;
 RA Roessler E., Du Y., Glinika A., Dutra A., Niehrs C., Menne M.,
 "The genomic structure, chromosome location, and analysis of the human
 RT DKK1 head inducer gene as a candidate for holoprosencephaly.";
 RL Cytogenet. Cell Genet. 89:220-224(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Strausberg R.L., Feilgold E.A., Grouse L.H., Derge J.G.,
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 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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 Brown S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullishy S.J.,
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 Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
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 Fehey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallegange D.E.,
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

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RT      "Generation and initial analysis of more than 15,000 full-length
RL      human and mouse cDNA sequences."
CC      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC      -1- FUNCTION: INHIBITOR OF WNT SIGNALING PATHWAY.
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- TISSUE SPECIFICITY: PLACENTA.
CC      -1- SIMILARITY: BELONGS TO THE DICKKOPF FAMILY.
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC
DR      EMBL; AF127563; AA021087.1; -.
DR      EMBL; AF177394; AA02674.1; -.
DR      EMBL; AB020315; BAA34651.1; -.
DR      EMBL; AB020314; BAA34651.1; JOINED.
DR      EMBL; AF261158; AAG15544.1; -.
DR      EMBL; AF261157; AAG15544.1; JOINED.
DR      EMBL; BC001539; AA01539.1; -.
DR      Genew; HGNC:2891; DKF1.
DR      MIM; 605189; -.
DR      GO; GO:0008083; F: growth factor activity; TAS.
DR      GO; GO:0004871; F: signal transducer activity; TAS.
DR      InterPro; IPR006796; dickkopf_N.
DR      Pfam; PF04706; dickkopf_N.1.
DR      Developmental protein; Signal; Wnt signaling pathway; Glycoprotein.
FT      SIGNAL 1..19
FT      CHAIN 1..19
FT      DOMAIN 85..138
FT      DOMAIN 189..263
FT      CARBOHYD 256..256
SQ      SEQUENCE 266 AA; 28671 MW; 5E878B2CCE42365A CRC64;
Query Match 9.3%; Score 174.5; DB 1; Length 266;
Best Local Similarity 25.6%; Pred. No. 1;e-05;
Matches 50; Conservative 18; Mismatches 60; Indels 67; Gaps 8;
QY      145 HECIIEDDCGPMYCOF-----ASFOYCPQPCGQRLCTRDSCCGDQLCVWGHG--- 195
DB      83 YPCAEDCECGIDRYCASTRGADGAGV-ICLACKRKRCKCRHAMCCPGNYCCNKGICVSS 141
QY      196 -----TKV-ATRGSNGTICDNQDCCPELCC 220
DB      142 DQNHFRGEIETITESFGNDHSTLDGYSRPTTLSSKMYHTKGQGSVCLRSSSCASGLCC 201
QY      221 AFOGGLLPVCTPLPVEGELC---HDPASRLDLITWLEPFDGALDRCPASGLC----- 273
DB      202 A--RHFWSKTKPVLKEGVCTKRRKSGHLEI-----FQRCYCGEGLSCRIQK 249
QY      274 ---QPHSHSLVYCK 285
DB      250 DHQASNSRLHTCQ 264

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RESULT 6

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ID      DKF1_MOUSE STANDARD; PRT; 272 AA.
AC      054908;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Dickkopf related protein-1 precursor (Dkk-1) (Dkkopf-1) (mdk-1).
GN      DKK1.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxId=10090;
RN      [1]
RP      SEQUENCE FROM N.A.

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RX      MEDLINE=98111224; PubMed=9450748;
RA      Glinka A, Wu W, Delius H, Monaghan A.P., Blumenstock C., Niehrs C.;
RT      "Dickkopf-1 is a member of a new family of secreted proteins and
RT      functions in head induction."
RL      Nature 391:357-362(1998).
CC      -1- FUNCTION: INHIBITOR OF WNT SIGNALING PATHWAY.
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- SIMILARITY: BELONGS TO THE DICKKOPF FAMILY.
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CC      or send an email to license@isb-sib.ch).
CC
DR      EMBL; AF030433; AAC02426.1; -.
DR      HSSP; P25687; 1MT.
DR      MGD; MGI:1329040; DKF1.
DR      InterPro; IPR006796; dickkopf_N.
DR      Pfam; PF04706; dickkopf_N.1.
DR      Developmental protein; Signal; Wnt signaling pathway; Glycoprotein.
FT      SIGNAL 1..31
FT      CHAIN 1..31
FT      DOMAIN 86..141
FT      DOMAIN 195..269
FT      CARBOHYD 262..262
SQ      SEQUENCE 272 AA; 29268 MW; AB9FA35DFA57D3EE CRC64;
Query Match 8.8%; Score 165.5; DB 1; Length 272;
Best Local Similarity 22.3%; Pred. No. 4.9e-05;
Matches 59; Conservative 27; Mismatches 98; Indels 81; Gaps 9;
QY      87 LANPPSYHNEINTPTKYGNNTIHYHREIHKITNNQTSQWTFSETVITSVGDEGR--- 143
DB      21 LCLSLPLGASATLVLSVLSNAT---KNLPPGLGAGQPGSAGVAVAGVYEGGNKYQT 77
QY      144 -----SHEIIDEDCGPMYCOFAS-----FYTCQPCGQRLCTRDSCCGDQLCV 191
DB      78 LDNYQPYPCAEDCEGSDPEYCSSPSRGAAGVGVQVICTACRRRRRCMTTHAVCCPGNYCK 137
QY      192 WGHG-----TKMA-----TRGSGTICDN 210
DB      138 NGICMPSDHSHPREIEISITENLGNHNAAAGDYPRTTLTSKIYHTKGQEGSVCLR 197
QY      211 QRDCCPGIICAFQGLLPVCTPLPVEGELC---HDPASRLDLITWLEPFDGALDRCPG 267
DB      198 SSDCAAGLCCA--RHFWSKTKPVLKEGVCTKRRKSGHLEI-----FQRCYC 245
QY      268 ASGLLC-----QPHSHSLVYCK 285
DB      246 GGLACRIQKHQASNSRLHTCQ 270

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RESULT 7

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ID      DKF2_HUMAN STANDARD; PRT; 259 AA.
AC      Q9UBT2; Q9UIU3;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Dickkopf related protein-2 precursor (Dkk-2) (dickkopf-2) (mdk-2).
GN      DKK2.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxId=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RP      TISSUE=Fetal lung;
RX      MEDLINE=20035735; PubMed=10570958;
RA      Krupnik V.E., Sharp J.D., Jiang C., Robison K., Chickering T.W.,

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RA Amaravadi L., Brown D.E., Guyot D., Mays G., Leiby K., Chang B.,
 RA Duong T., Goodheart A.D.U., Gearing D.P., Sokol S.I., McCarthy S.A.,
 RT "Functional and structural diversity of the human Dickkopf gene
 family." J.
 RL Gene 238:301-313(1999) ..
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Tanaka S., Sugimachi K., Sugimachi K.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 75-259 FROM N.A.
 RA Tate G., Suzuki T., Mitsuya T.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INHIBITOR OF WNT SIGNALING PATHWAY (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, SKELETAL MUSCLE AND
 CC LUNG.
 CC -1- PFM: MAY BE PROTEOLYTICALLY PROCESSED BY A FURIN-LIKE PROTEASE.
 CC -1- SIMILARITY: BELONGS TO THE DICKKOPF FAMILY.
 CC -----
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 CC -----
 DR EMBL; AF177395; AAF02675.1; -
 DR EMBL; AB033308; BAA85465.1; -
 DR EMBL; AB035181; BAA87056.1; -
 DR EMBL; AB035180; BAA87056.1; JOINED.
 DR Genew; HGNC:2892; DK2.
 DR MIM; 605415; -
 DR GO; GO:0005645; C:extracellular space; TAS.
 DR InterPro; IPR006796; dickkopf_N.
 DR Pfam; PF04706; dickkopf_N.1.
 KW Developmental protein; Signal; Wnt signaling pathway; Glycoprotein.
 KM SIGNAL 1 33 POTENTIAL.
 FT CHAIN 1 33 DICKKOPF RELATED PROTEIN-2.
 FT DOMAIN 78 127 DKR-TYPE CYS-1.
 FT DOMAIN 183 256 DKR-TYPE CYS-2.
 FT CARBOHYD 52 52 N-LINKED (GLCNAC...) (POTENTIAL).
 FT SEQUENCE 259 AA; 28447 MW; 39DDA3FA8975EB87F CRC64;
 SQ
 Query Match 8.6%; Score 162; DB 1; Length 259;
 Best Local Similarity 24.0%; Pred. No. 8.3e-05;
 Matches 50; Conservative 24; Mismatches 60; Indels 74; Gaps 9;
 QY 137 GDEGR--RSHECIIDEDGSPMYC---QFASFOYTCPCRGQRMCTRDSECCGDDQ 189
 Db 65 GSKKKGSLGQAYPCSSDKEGVRGYSHPQSS--ACWVCRKKRCHRDGMCCEGTR 121
 QY 190 CVMGHC-----TKMA-TRGSNGT 206
 Db 122 CNGGICIPVTESILTPHLPALDGRHRDRNNGHNSHDLGMQNLGRPHKMGHGED 181
 QY 207 ICDNQRDCQPGLCAPFGRLFPVCTPLPYVEGELC--HDPASRLDLITWELPDDGALD 263
 Db 182 PCLRSSDIDIFGCCA--RHFWTKICKPVLHGEVCTQKRKKGSHGLEI-----FQ 229
 QY 264 RCPGASGLICP-----HSHSLVYVCK 285
 Db 230 RCDCAKGLSCRWKDATYSSKARLHVQ 257
 RESULT 8
 ID DK2 MOUSE STANDARD; PRT; 259 AA.
 AC Q9QY28;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Dickkopf related protein-2 precursor (Dkk-2) (Dkkopf-2) (mdk-2).
 GN DK2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99425169; PubMed=10495270;
 RA Monaghan P.A., Kioschis P., Wu W., Zuniga A., Bock D., Pousetka A.,
 RA Bellus H., Niens C.;
 RT "Dickkopf genes are co-ordinately expressed in mesodermal lineages".
 RL Mech. Dev. 87:45-56(1999).
 CC -1- FUNCTION: INHIBITOR OF WNT SIGNALING PATHWAY (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PFM: MAY BE PROTEOLYTICALLY PROCESSED BY A FURIN-LIKE PROTEASE.
 CC -1- SIMILARITY: BELONGS TO THE DICKKOPF FAMILY.
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 CC -----
 DR EMBL; AJ243963; CAB60110.1; -
 DR MGD; MGI:1890663; Dkk2.
 DR InterPro; IPR006796; dickkopf_N.
 DR Pfam; PF04706; dickkopf_N.1.
 KW Developmental protein; Signal; Wnt signaling pathway; Glycoprotein.
 KM SIGNAL 1 33 POTENTIAL.
 FT CHAIN 1 33 DICKKOPF RELATED PROTEIN-2.
 FT DOMAIN 78 127 DKR-TYPE CYS-1.
 FT DOMAIN 183 256 DKR-TYPE CYS-2.
 FT CARBOHYD 52 52 N-LINKED (GLCNAC...) (POTENTIAL).
 FT SEQUENCE 259 AA; 28416 MW; EAAB76F2D2C9780D CRC64;
 SQ
 Query Match 8.2%; Score 154; DB 1; Length 259;
 Best Local Similarity 23.6%; Pred. No. 0.00031;
 Matches 49; Conservative 24; Mismatches 61; Indels 74; Gaps 9;
 QY 137 GDEGR--RSHECIIDEDGSPMYC---QFASFOYTCPCRGQRMCTRDSECCGDDQ 189
 Db 65 GSKKKGSLGQAYPCSSDKEGVRGYSHPQSS--ACMLCRKKRCHRDGMCCEGTR 121
 QY 190 CVMGHC-----TKMA-TRGSNGT 206
 Db 122 CNGGICIPVTESILTPHLPALDGRHRDRNNGHNSHDLGMQNLGRPHKMGHGED 181
 QY 207 ICDNQRDCQPGLCAPFGRLFPVCTPLPYVEGELC--HDPASRLDLITWELPDDGALD 263
 Db 182 PCLRSSDIDIFGCCA--RHFWTKICKPVLHGEVCTQKRKKGSHGLEI-----FQ 229
 QY 264 RCPGASGLICP-----HSHSLVYVCK 285
 Db 230 RCDCAKGLSCRWKDATYSSKARLHVQ 257
 RESULT 9
 SG11 HUMAN
 ID SG11 HUMAN STANDARD; PRT; 242 AA.
 AC Q9UK85;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Soggy-1 protein precursor (SGY-1).
 GN SGY1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]

FT DISULFID 253 265 BY SIMILARITY.
 FT DISULFID 285 529 BY SIMILARITY.
 FT DISULFID 311 315 BY SIMILARITY.
 FT DISULFID 326 338 BY SIMILARITY.
 FT DISULFID 335 370 BY SIMILARITY.
 FT DISULFID 340 349 BY SIMILARITY.
 FT DISULFID 351 361 BY SIMILARITY.
 FT DISULFID 376 381 BY SIMILARITY.
 FT DISULFID 378 411 BY SIMILARITY.
 FT DISULFID 383 396 BY SIMILARITY.
 FT DISULFID 398 403 BY SIMILARITY.
 FT DISULFID 417 422 BY SIMILARITY.
 FT DISULFID 419 450 BY SIMILARITY.
 FT DISULFID 424 433 BY SIMILARITY.
 FT DISULFID 435 442 BY SIMILARITY.
 FT DISULFID 456 461 BY SIMILARITY.
 FT DISULFID 458 504 BY SIMILARITY.
 FT DISULFID 463 473 BY SIMILARITY.
 FT DISULFID 476 479 BY SIMILARITY.
 FT DISULFID 483 492 BY SIMILARITY.
 FT DISULFID 489 561 BY SIMILARITY.
 FT DISULFID 508 537 BY SIMILARITY.
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 245 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 322 322 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 434 434 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 555 555 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON_TER 577 577
 SQ SEQUENCE 577 AA; 62298 MW; B83B469C83EDCC9 CRC64;
 Query Match 7.3%; Score 138; DB 1; Length 577;
 Best Local Similarity 26.4%; Pred. No. 0.011;
 Matches 46; Conservative 22; Mismatches 66; Indels 40; Gaps 10;

QY 154 GPSNYCPAFQYTCPCRCQRMCTDSEC-CGDQCWVG-----HCYKATR--GSN 204
 DB 393 GP--YCCQDNF--SC--VRHGLGCGNGCCEGCRCGSGTWGECNCTSTDTCTISBD 446
 QY 205 GTTCNDNDCPCPLGCACAFORGLLEPVCTPLPVEGELCHDPASRLDLITWELSPDG---- 260
 DB 447 GTLCGSGGDCVCGKCVCTNPGASGPTCEPCPT-----CSDPCNKRSGTIECHLADQPEB 502
 QY 261 -ALDRCPQ-----SGLCQPHSHSLVYCKFTFGSGRPDQSEILL 300
 DB 503 ECVDKCKLAGVTTISKADFSKDSVSCSLQGEN---ECLITFLISTDNEKTI 553

RESULT 11
 PRS_HUMAN STANDARD; PRT; 676 AA.
 AC P07225; Q15518;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Vitamin K-dependent protein S precursor.
 GN PROS1 OR PROS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87092407; PubMed=3467362;
 RA Hoskins J., Norman D.K., Beckmann R.J., Long G.L.;
 RT "Cloning and characterization of human liver cDNA encoding a protein
 S precursor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:349-353(1987).
 RN [2]
 RP SEQUENCE FROM N.A.

RX MEDLINE=88005138; PubMed=2820795;
 RA Ploos van Amstel H.K., van der Zanden A.L., Reitsma P.H.,
 RA Bertina R.M.;
 RT "Human protein S cDNA encodes Phe-16 and Tyr 222 in consensus
 sequences for the post-translational processing.";
 RL FEBS Lett. 222:186-190(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91084444; PubMed=2148110;
 RA Schmidel D.K., Tatro A.V., Phelps L.G., Tomczak J.A., Long G.L.;
 RT "Organization of the human protein S genes.";
 RL Biochemistry 29:7845-7852(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Liver;
 RX MEDLINE=91084445; PubMed=2148111;
 RA Ploos van Amstel H.K., Reitsma P.H., der Logt C.P., Bertina R.M.;
 RT "Intron-exon organization of the active human protein S gene PS alpha
 and its pseudogene PS beta: duplication and silencing during primate
 evolution.";
 RL Biochemistry 29:7853-7861(1990).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Uterus;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bluetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., Mesman P.J., McKernan K.J., Malek J.A., Gnatovic P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay D.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield J.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schercher A., Schein J.E., Jones S.J.M., Matra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE OF 27-676 FROM N.A.
 RX MEDLINE=86313649; PubMed=2544113;
 RA Lundwall A., Dackowski W., Cohen E., Shaffer M., Mahr A., Dahlback B.,
 RA Stenflo J., Wydo R.;
 RT "Isolation and sequence of the cDNA for human protein S, a regulator
 of blood coagulation.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:6716-6720(1986).
 RN [7]
 RP VARIANT HEBERLEN PRO-501.
 RX MEDLINE=90335440; PubMed=2143091;
 RA Bertina R.M., Ploos van Amstel H.K., van Wijngaarden A.,
 RA Coenen J., Leemhuis M.P., Deutz-Terlouw P.P., van der Linden I.K.,
 RA Reitsma P.H.;
 RT "Heerlen polymorphism of protein S, an immunologic polymorphism due
 to dimorphism of residue 460.";
 RL Blood 76:538-548(1990).
 RN [8]
 RP VARIANT PROS DEFICIENCY SER-258.
 RA Cooper D.N.;
 RL Unpublished observations (SEP-1993).
 RN [9]
 RP VARIANT TOKUSHIMA GLUT-196.
 RX MEDLINE=94129009; PubMed=8298131;
 RA Haysashi T., Nishiohara U., Shigeakiyo T., Saito S., Suzuki K.;
 RT "Protein S Tokushima: abnormal molecule with a substitution of Glu
 for Lys-155 in the second epidermal growth factor-like domain of
 protein S.";

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=90307653; PubMed=2365683;
 RA Sheppard D., Rozzo C., Starr L., Quaranta V., Eyle D.J., Pytela R.;
 RT "Complete amino acid sequence of a novel integrin beta subunit (beta
 6) identified in epithelial cells using the polymerase chain
 reaction.";
 RL J. Biol. Chem. 265:11502-11507 (1990).
 RP REVISIONS TO 18-24; 158; 642 AND 719.
 RA Askins J.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE OF 116-197 FROM N.A.
 RX MEDLINE=93002753; PubMed=1382574;
 RA Jiang W.M., Jenkins D., Yuan Q., Leung E., Choo K.H., Watson J.D.,
 RA Kristensen G.W.;
 RT "The gene organization of the human beta 7 subunit, the common beta
 subunit of the leukocyte integrins HML-1 and LPM-1.";
 RL Int. Immunol. 4:1031-1040 (1992).
 CC -1- FUNCTION: INTEGRIN ALPHA-V/BETA-6 IS A RECEPTOR FOR FIBRONECTIN
 AND CYTOACTIN. IT RECOGNIZES THE SEQUENCE R-G-D IT ITS LIGANDS.
 CC -1- SUBUNIT: HEMEROPOLYMER OF AN ALPHA AND A BETA SUBUNIT. BETA-6
 ASSOCIATES WITH ALPHA-V.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
 CC -1- SIMILARITY: Contains 2 VMPA-like domains.
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FT REPEAT 544 582 III.
 FT REPEAT 583 619 IV.
 FT DISULFID 23 454 BY SIMILARITY.
 FT DISULFID 31 41 BY SIMILARITY.
 FT DISULFID 34 70 BY SIMILARITY.
 FT DISULFID 44 59 BY SIMILARITY.
 FT DISULFID 197 204 BY SIMILARITY.
 FT DISULFID 252 293 BY SIMILARITY.
 FT DISULFID 394 406 BY SIMILARITY.
 FT DISULFID 426 670 BY SIMILARITY.
 FT DISULFID 452 456 BY SIMILARITY.
 FT DISULFID 467 479 BY SIMILARITY.
 FT DISULFID 476 511 BY SIMILARITY.
 FT DISULFID 481 490 BY SIMILARITY.
 FT DISULFID 492 502 BY SIMILARITY.
 FT DISULFID 517 522 BY SIMILARITY.
 FT DISULFID 519 552 BY SIMILARITY.
 FT DISULFID 524 537 BY SIMILARITY.
 FT DISULFID 539 544 BY SIMILARITY.
 FT DISULFID 538 563 BY SIMILARITY.
 FT DISULFID 560 591 BY SIMILARITY.
 FT DISULFID 565 574 BY SIMILARITY.
 FT DISULFID 576 583 BY SIMILARITY.
 FT DISULFID 587 602 BY SIMILARITY.
 FT DISULFID 589 645 BY SIMILARITY.
 FT DISULFID 604 614 BY SIMILARITY.
 FT DISULFID 617 620 BY SIMILARITY.
 FT DISULFID 624 633 BY SIMILARITY.
 FT DISULFID 630 702 BY SIMILARITY.
 FT DISULFID 649 678 BY SIMILARITY.
 FT CARBOHYD 97 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 98 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 541 541 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 575 575 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 788 AA; 85935 MW; EDB7D533BE4C6C4D CRC64;

Query Match 6.7%; Score 126; DB 1; Length 788;
 Best Local Similarity 20.5%; Pred. No. 0.12;
 Matches 76; Conservative 45; Mismatches 130; Indels 120; Gaps 18;

42 QERATINEMFRE-----VEELMEDTQHKLR--SAVEEMBAE-EAAKASSE-VNLA-- 88
 332 QEEVHLVENYAKLIPGATVGLQKDSGNTLQILIAVEHLRSVELVYGDTEGINTLST 391
 DB 89 ---NLPSYHNETNTDTRVN-----NTIHVREIHKITNNQTG-----QWVFS-- 129
 DB 392 ALGNNGTLEFOHKCKSHMKVGDPAFVTVNIPHCERRSRHIIIPVGGDALELLVSPE 451
 QY 130 -----EIVTISVGBEERBSHECTIDE-----DCGPRSM----- 157
 DB 452 CNCDCKEVEVNSKCHHNGSFQCGVCACHPHNGPRCECGEDMLSTDSCKEAPDHPSC 511
 QY 158 -----YCOFASFQYTCPCPCGQMLCTRDSQC-CGDQLCW 192
 DB 512 SGNGDCVCGCGICHLSPYGNITGYPCQDNF--SC--VNHKGLCGSNGDDCCGECVCS 567
 QY 193 G-----HCTKATR--GSGNTICDNQRCQCGELCCAFRGILLFPCTLLPVEGELCHDP 244
 DB 568 GWTGEYCNCTTSIDSCVSDGVLCSSRGSCVCGKCTNPGASGPTCEKCPCT---CGSP 623
 QY 245 ASRLLDITWLELPDG-----ALDRPCASGLLCQPHSHSL-----VYVCKPTV 289
 DB 624 CNKRSGCTIBCHLSAQAQAEECVCKKLAGATISEEDRPSKDSVSCSLQGENECILITPL 683
 QY 290 GSRDQDGEILL 300
 DB 684 ITTDNEKGTII 694


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RESULT 13
LTRBS_HUMAN
ID LTRBS_HUMAN STANDARD; PRT; 1394 AA.
AC P22064; Q8TD95;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Latent transforming growth factor beta binding protein, isoform 1S
DE precursor (LTBP-1) (Transforming growth factor beta-1 binding protein
DE 1) (TGF-beta1-BP-1).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Fibroblast, and Platelet;
RX MEDLINE=90275601; PubMed=2350783;
RA Kanazaki T., Olofsson A., Moren A., Wernstedt C., Hellman U.,
RA Miyazono K., Claesson-Welsh L., Heldin C.-H.;
RT "TGF-beta 1 binding protein: a component of the large latent complex
RT of TGF-beta 1 with multiple repeat sequences."
RL Cell 61:1051-1061(1990).
RX [2]
RN SEQUENCE FROM N.A.
RA Kwak J.H., Shin K.Y., Kim S.I.;
RT "Major alternative spliced-form of LTBP1 mRNA in human glomerular
RT endothelial cell."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RX [3]
RN INTERACTION WITH FIBRILLIN.
RX PubMed=12429738;
RA Isogai Z., Ono R.N., Ushiro S., Keene D.R., Chen Y., Mazzei R.,
RA Charbonneau N.L., Reinhardt D.P., Rifkin D.B., Sakai L.Y.;
RT "Latent transforming growth factor beta-binding protein 1 interacts
RT with fibrillin and is a microfibril-associated protein."
RL J. Biol. Chem. 278:2750-2757(2003).
CC -! SUBUNIT: The large, latent complex of TGF-beta1 from platelets is
CC composed of the TGF-beta1 molecule noncovalently associated with a
CC disulfide-bonded complex of a dimer of the N-terminal propeptide
CC of the TGF-beta1 precursor and a third component denoted TGF-
CC beta1-BP. TGF-beta1-BP does not bind directly to active TGF-BETA1.
CC Binds to fibrillin.
CC -! SUBCELLULAR LOCATION: Secreted.
CC -! ALTERNATIVE PRODUCTS:
CC -! SUBALTERNATIVE SPLICING: Named isoforms=2;
CC Name=Short;
CC IsoId=P22064-1; Sequence=Displayed;
CC Name=Long;
CC IsoId=Q14766-1; Sequence=External;
CC -! PTM: CONTAINS HYDROXYLATED ASPARAGINE RESIDUES.
CC -! PTM: The N-terminus is blocked.
CC -! SIMILARITY: Contains 16 EGF-like domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M34057; AA61160.1; -
DR EMBL; AF489528; AA003124.1; -
DR PIR; A35626; A35626.
DR HSSP; P00750; 1TPG.
DR GlycoSuiteDB; P22064; -
DR Genew: HGNC:6714; LTBP1.
DR MIM; 150390;
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001881; EGF_Ca.
DR

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DR	InterPro: IPRO006209; EGF-like.
DR	InterPro: IPRO002212; Fibin1-aseoc.
DR	Pfam: PF00008; EGF; 15.
DR	Pfam: PF00693; TB; 4.
DR	SMART: SM00179; EGF_CA; 13.
DR	PROSITE: PS00010; ASX_HYDROXYLU; 13.
DR	PROSITE: PS00022; EGF_1; 2.
DR	PROSITE: PS01186; EGF_2; 11.
DR	PROSITE: PS01187; EGF_CA; 15.
KW	Growth factor binding Repeat; EGF-like domain; Hydroxylation; Signal
KW	Glycoprotein; Alternative splicing.
FT	CHAIN 1 20
FT	CHAIN 21 1394
FT	DOMAIN 300 340
FT	REPEAT 348 412
FT	DOMAIN 546 587
FT	DOMAIN 588 659
FT	DOMAIN 630 670
FT	DOMAIN 671 710
FT	DOMAIN 711 751
FT	DOMAIN 752 792
FT	DOMAIN 793 833
FT	DOMAIN 834 874
FT	DOMAIN 875 916
FT	DOMAIN 917 958
FT	DOMAIN 959 1001
FT	REPEAT 1017 1084
FT	DOMAIN 1097 1139
FT	REPEAT 1190 1262
FT	DOMAIN 1140 1180
FT	DOMAIN 1294 1334
FT	DOMAIN 1335 1379
FT	SITE 847 849
FT	DISULFID 304 315
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FT	DISULFID 550 562
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FT	DISULFID 573 586
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FT	DISULFID 681 695
FT	DISULFID 698 709
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FT	DISULFID 721 735
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FT	DISULFID 762 776
FT	DISULFID 778 791
FT	DISULFID 797 808
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FT	DISULFID 970 984
FT	DISULFID 986 1000
FT	DISULFID 1101 1114
FT	DISULFID 1109 1123
FT	DISULFID 1125 1138
FT	REPEAT A.
FT	REPEAT B.
FT	REPEAT C.
FT	REPEAT D.
FT	REPEAT E.
FT	REPEAT F.
FT	REPEAT G.
FT	REPEAT H.
FT	REPEAT I.
FT	REPEAT J.
FT	REPEAT K.
FT	REPEAT L.
FT	REPEAT M.
FT	REPEAT N.
FT	REPEAT O.
FT	REPEAT P.
FT	REPEAT Q.
FT	REPEAT R.
FT	REPEAT S.
FT	REPEAT T.
FT	REPEAT U.
FT	REPEAT V.
FT	REPEAT W.
FT	REPEAT X.
FT	REPEAT Y.
FT	REPEAT Z.
FT	REPEAT AA.
FT	REPEAT AB.
FT	REPEAT AC.
FT	REPEAT AD.
FT	REPEAT AE.
FT	REPEAT AF.
FT	REPEAT AG.
FT	REPEAT AH.
FT	REPEAT AI.
FT	REPEAT AJ.
FT	REPEAT AK.
FT	REPEAT AL.
FT	REPEAT AM.
FT	REPEAT AN.
FT	REPEAT AO.
FT	REPEAT AP.
FT	REPEAT AQ.
FT	REPEAT AR.
FT	REPEAT AS.
FT	REPEAT AT.
FT	REPEAT AU.
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FT	REPEAT AW.
FT	REPEAT AX.
FT	REPEAT AY.
FT	REPEAT AZ.
FT	REPEAT BA.
FT	REPEAT BB.
FT	REPEAT BC.
FT	REPEAT BD.
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FT	REPEAT BF.
FT	REPEAT BG.
FT	REPEAT BH.
FT	REPEAT BI.
FT	REPEAT BJ.
FT	REPEAT BK.
FT	REPEAT BL.
FT	REPEAT BM.
FT	REPEAT BN.
FT	REPEAT BO.
FT	REPEAT BP.
FT	REPEAT BQ.
FT	REPEAT BR.
FT	REPEAT BS.
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FT	REPEAT BU.
FT	REPEAT BV.
FT	REPEAT BW.
FT	REPEAT BX.
FT	REPEAT BY.
FT	REPEAT BZ.
FT	REPEAT CA.
FT	REPEAT CB.
FT	REPEAT CC.
FT	REPEAT CD.
FT	REPEAT CE.
FT	REPEAT CF.
FT	REPEAT

FT DISULFID 1144 1155 BY SIMILARITY.
 FT DISULFID 1150 1164 BY SIMILARITY.
 FT DISULFID 1166 1179 BY SIMILARITY.
 FT DISULFID 1258 1309 BY SIMILARITY.
 FT DISULFID 1304 1318 BY SIMILARITY.
 FT DISULFID 1320 1333 BY SIMILARITY.
 FT DISULFID 1339 1354 BY SIMILARITY.
 FT DISULFID 1349 1363 BY SIMILARITY.
 FT DISULFID 1365 1378 BY SIMILARITY.
 FT MOD_RES 647 HYDROXYLATION.
 FT MOD_RES 810 HYDROXYLATION.
 FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 870 870 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 923 923 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1039 1039 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 365 365 /FTID=CAR 000184.
 FT CONFLICT 504 504 Y -> H (IN REF. 2).
 FT CONFLICT 1334 1334 A -> T (IN REF. 2).
 FT CONFLICT 1394 1394 F -> V (IN REF. 2).
 SQ SEQUENCE 1394 AA; 152791 MM; DEFGA81A40B2CTD1 CRC64;

Query Match 6.7%; Score 126; DB 1; Length 1394;
 Best Local Similarity 22.5%; Pred. No. 0.22; Indels 140; Gaps 25;
 Matches 90; Conservative 37; Mismatches 133;

QY 25 PRATSAVPKPPALSYPOEATLNEFRVEHEIMEDTQHLRSAYEMKAEPAKASE 84
 DB 437 PVAKSTHPPPLPAKEP-----VEALTPSRHGAASA---EPVATAPPEKE 480
 QY 85 VMLANLPSYHNETNTDTRV-----GNNTIHYR-----EJHKTIN 120
 DB 481 I-----PSIDGP-----KTKLEPQPOLSPGISALHHPQPVVIEKTSPPVVEVAPRAS 531
 QY 121 NOTGCVWFSETVTSVDEBGRSHCEIIDED-CGSMWCOPASFOYTOQPRG-----Q 174
 DB 532 TSSASVLAFTQVTEI-----NCTVNPDLICGAG-HCINLPVRYITCTEGYRFSQ 582
 QY 175 RMLCTDSECCGDO-LCVWGHCTKATNGS-----NCTICNORDC-QPGLC 219
 DB 583 QRCVVIDECTQVQHLCGQRCEN--TEGSFLCTCPAGMASBEGINCIDVDECLRPDVC 640
 QY 220 -----CAF-----QRLPLPV---CTPLPVGEIC-HDPASRLDLIT- 253
 DB 641 GEGHCVNTVGAFCRCYCDSGYRMTQRCEDDECLNPTCPDQCNSPFSYQCVPTB 700
 QY 254 -----WE-----LEPDGALDRCPASG-----LLCOPSHSHSVYVCKPTFGSRD-----Q 294
 DB 701 GFRGWMGQCLDVDECELEPNVCANGDCSNLEGSYMSCCHKG---YTRTPDHKCRDIDECQ 757
 QY 295 DGEILLPREVPDEYEVGSF-----MEVNGELEDIE 325
 DB 758 QGNLCVNGQCKN--TEGSFRCTCGGYQLSAARDQEDID 795

RESULT 14
 ID LABEL HUMAN STANDARD; PRT; 1595 AA.
 AC Q14766;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Latent transforming growth factor beta binding protein, isoform 1L
 DE precursor (LTBP-1) (Transforming growth factor beta-1 binding protein
 DE 1) (TGF-beta1-BP-1).
 GN LTBP1
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_Taxid=9606;
 RN [1]

RP SEQUENCE OF 1-346 FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=96125117; PubMed=8537398;
 RA Olofsson A., Ichijo H., Møen A., ten Dijke P., Miyazono K.,
 RA Heldin C.-H.;
 RT "Efficient association of an amino-terminally extended form of human
 RT latent transforming growth factor-beta binding protein with the
 RT extracellular matrix";
 RL J. Biol. Chem. 270:31294-31297(1995).
 RN [2]
 RP SEQUENCE OF 347-1595 FROM N.A.
 RC TISSUE=Fibroblast, and Platelet;
 RX MEDLINE=90275601; PubMed=2350783;
 RA Kanazaki T., Olofsson A., Møen A., Wernstedt C., Hellman U.,
 RA Miyazono K., Claesson-Welsh L., Heldin C.-H.;
 RT "TGF-beta 1 binding protein: a component of the large latent complex
 RT of TGF-beta 1 with multiple repeat sequences";
 RL Cell 61:1051-1061(1990).
 RN [3]
 RP INTERACTION WITH FIBRILLIN.
 RX PubMed=12429738;
 RA Isogai Z., Ono R.N., Ushiro S., Keene D.R., Chen Y., Mazzieri R.,
 RA Chabouneau N.L., Reinhardt D.P., Rifkin D.B., Sakai L.Y.;
 RT "Latent transforming growth factor beta-binding protein 1 interacts
 RT with fibrillin and is a microfibril-associated protein";
 RL J. Biol. Chem. 278:2750-2757(2003).
 CC -1 SUBUNIT: The large latent complex of TGF-beta1 from platelets is
 CC composed of the TGF-beta1 molecule noncovalently associated with a
 CC disulfide-bonded complex of a dimer of the N-terminal propeptide
 CC of the TGF-beta1 precursor and a third component denoted TGF-
 CC beta1-BP. TGF-beta1-BP does not bind directly to active TGF-BETA1.
 CC Binds to fibrillin.
 CC -1 SUBCELLULAR LOCATION: Secreted.
 CC -1 ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=long;
 CC Name=short;
 CC Isoid=Q14766-1; Sequence=Displayed;
 CC -1 TISSUE SPECIFICITY: The long isoform is found in fibroblasts.
 CC -1 PTM: CONTAINS HYDROXYLATED ASPARAGINE RESIDUES (BY SIMILARITY).
 CC -1 SIMILARITY: Contains 16 EGF-like domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@ebi.ac.uk).
 CC DR EMBL; L48925; AAA96327.1; -;
 CC DR EMBL; M34057; AAA61160.1; ALT_INIT.
 CC DR HSSP; P08709; 1BP9.
 CC MIM; 150380;
 DR GO; GO:000578; C:extracellular matrix; NAS.
 DR GO; GO:0005024; F:transforming growth factor-beta receptor ac. .; NAS.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR002212; Fibril-assoc.
 DR Pfam; PF00068; EGF; 15.
 DR Pfam; PF00683; TB; 4.
 DR SMART; SM00119; EGF_CA; 13.
 DR PROSITE; PS00010; ASX_HYDROXYL; 13.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS01186; EGF_2; 11.
 DR PROSITE; PS01187; EGF_CA; 15.
 DR Growth factor binding; Repeat; EGF-like domain; Hydroxylation; Signal;
 KM Glycoprotein; Alternative splicing.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 1595 LATENT TRANSFORMING GROWTH FACTOR BETA
 FT BINDING PROTEIN, ISOFORM 1L.

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FT DOMAIN 501 541 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT REPEAT 549 613 REPEAT A.
FT DOMAIN 747 788 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 789 830 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 831 871 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 872 911 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 912 952 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 953 993 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1034 1075 EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1076 1117 EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1118 1159 EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1160 1202 EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
FT REPEAT 1218 1285 REPEAT B.
FT DOMAIN 1298 1340 EGF-LIKE 13, CALCIUM-BINDING (POTENTIAL).
FT REPEAT 1391 1463 REPEAT C.
FT DOMAIN 1341 1381 EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1495 1535 EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1536 1580 EGF-LIKE 16, CALCIUM-BINDING (POTENTIAL).
FT SITE 1048 1050 CELL ATTACHMENT SITE (POTENTIAL).
FT DISULFID 505 516 BY SIMILARITY.
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FT DISULFID 1367 1380 BY SIMILARITY.
FT DISULFID 1499 1510 BY SIMILARITY.
FT DISULFID 1505 1519 BY SIMILARITY.
FT DISULFID 1521 1534 BY SIMILARITY.
FT DISULFID 1540 1555 BY SIMILARITY.
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FT DISULFID 1566 1579 BY SIMILARITY.
FT MOD_RSS 848 848 HYDROXYLATION (BY SIMILARITY).
FT MOD_RSS 1011 1011 HYDROXYLATION (BY SIMILARITY).
FT CARBOHYD 495 495 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1071 1071 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1124 1124 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 1240 1240 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1595 AA; 173229 MW; 6A091EBA8556D85 CRC64;
Query Match 6.7%; Score 126; DB 1; Length 1595;
Best Local Similarity 22.5%; Pred. No. 0.26; Mismatches 133; Indels 140; Gaps 25;
Matches 90; Conservative 37;
25 PRATAPYKPGPALSYPOEATLNMFRVEELMEDTQKLSAVEEMAEAAKASSE 84
638 PVAKSTHPPPLPAKEP-----VEALFPSEHGARS-----EPVATAPPEKE 681
85 VTLALPPSYNENMTDTRV-----GNTTHVR-----EIHKTN 120
682 I-----PSLDOE---KRLLEPGQPQLSPGISALHLHPQFVVIKTPSPYVVEVAPAS 732
121 NQTGMVSEFVITVSGDEGRSHCEIIDBD-CGPMYCOPAFQYTCPCRG-----Q 174
733 TSSAQVLAIPQVTEI-----NECTVNPDIGAG-HCLNLPVRYNCICEGYRFESEQ 783
175 RMLCTRDECCGDD-LCYWGHCTKMATRGS-----NGTICDNQDC-QPGIC 219
784 QKCVDIDECTQVCHLCSQGRCEH--TEGSFLCICPAGFMASERGTNCIDVDECLRPDVC 841
220 -----CAF-----ORGLFPV---CTPLPYEGELC-HDPASRLDLIT- 253
842 GEGHCVNTVGAFCRCYCSGYRMTGRRCEDIDECLNPSTCPDECCVNSPGSYCCVPTC 901
254 ---WE---LEPDGALDRCPASG-----LTCQPHSHLVYVCKPTFGSRD---Q 294
902 GFRGNQGOCLDVECLFENVCANGDCSNLEGSYMCSCRG---YRTPDHGHCRCRDIDECQ 958
255 DGEILLPREVDEYEVGSF-----MEVRQELDELE 325
959 QGNLCVNGQCKN--TEGSFRCTCGGYQLSAKQDCEDID 996
RESULT 15
ID_SGY1 MOUSE STANDARD; PRT; 230 AA.
AC QGQZL9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Soggy-1 protein precursor (SGY-1).
GN SGY1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20035735; PubMed=10570958;
RA Krupnik V.E., Sharp J.D., Jiang C., Robison K., Chickering T.W.,
RA Amaravadi L., Brown D.B., Guyot D., Mays G., Leiby K., Chang B.,
RA Duong T., Goodheart A.D.J., Gearing D.P., Sobol S.T., McCarthy S.A.;
RT "Functional and structural diversity of the human Dickopf gene
family."
RL Gene 238:301-313(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in testis.
CC -!- SIMILARITY: TO THE N-TERMINAL SECTION OF DKX-3.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC EMBL; AF177399; AAF02679.1; -.
CC DR EMBL; MG1:1354963; SGY1.
CC KW Signal; Glycoprotein.

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FT	CHAIN	21	230	SOGV-1 PROTEIN
FT	CARBOHYD	31	31	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. . .) (POTENTIAL).
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SQ	SEQUENCE	230 AA;	26663 MW;	E3C95330935DDDBA CRC64;

Query Match
 Best Local Similarity 26.6%;
 Matches 38; Conservative 25; Mismatches 53; Indels 27; Gaps 2;

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QY	57	LMEDTQHKLRSAYEEWEAEBAAKASSEVYLANLPSSYHNETNTDTKVGNNTIHYHREIH	116
Db	61	FF-----SSPMDFRDLPRNFHQENQEHKMGKNTLSSHLQID	97
QY	117	KITNNQGMVFSEVITSVGDE	139
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Search completed: February 20, 2004, 18:49:40
 Job time : 29 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2004, 16:59:25 / Search time 686 Seconds
(without alignments)
10176.016 Million cell updates/sec

Title: US-10-063-671-7

Sequence: 1 cgcgcgcctccgcaccgcg.....aaaaaaaaaaaaaaaaaaaaa 2586

Scoring table: IDENTITY NUC
Gapop 10.0, Gapekt 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	2586	100.0	2586	22	AAK52255	Human PRO295 CDNA.
3	2586	100.0	2586	22	AAK52255	Human PRO295 CDNA.
4	2586	100.0	2586	24	ABSL74381	Human CDNA encoding
5	2586	100.0	2586	24	ABSL74381	Human CDNA encoding
6	2586	100.0	2586	24	ABSL74381	Human CDNA encoding
7	2586	100.0	2586	25	ACA55002	Novel human secret
8	2586	100.0	2586	25	ACA55002	CDNA encoding huma

9	2586	100.0	2586	25	ACA58813	CDNA encoding huma
10	2586	100.0	2586	25	ACA60194	Human CDNA for sec
11	2586	100.0	2586	25	ACA60366	Novel human secret
12	2586	100.0	2586	25	ACA63376	CDNA encoding huma
13	2586	100.0	2586	25	ACA65532	CDNA encoding huma
14	2586	100.0	2586	25	ABX36211	Human secreted/tra
15	2586	100.0	2586	25	ABX71642	Human CDNA encodin
16	2571.4	99.4	2660	22	AAH45490	Human reduced expr
17	2446.4	94.6	2632	22	AAH45491	Human reduced expr
18	2445.2	94.6	2479	22	AAI69309	Human DKK-3 DNA.
19	2440.4	94.4	2479	19	AAV07906	Human cysteine-ric
20	2440.4	94.4	2479	19	AAV75128	CDNA encoding a hu
21	2427.8	93.9	2490	19	AAV38798	Homo sapiens cereb
22	2423	93.7	2450	25	ABZ81805	Human dickkopf2 nu
23	2423	93.7	2450	25	ABZ81805	Human dickkopf3 DN
24	2423	93.7	2450	25	ABX75308	Human CDNA for dic
25	2421.4	93.6	2608	24	ABL92089	Human Tumour Endoc
26	2421.4	93.6	2608	25	ABX72014	DNA encoding human
27	2098	81.1	2124	25	ABZ81835	DKK-2 nucleic acid
28	2098	81.1	2124	25	ABZ81835	Human DKK-3 DNA.
29	2098	81.1	2124	25	ABZ81835	Human DKK-3 DNA.
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31	1053	40.7	1053	21	AAH45489	Human DKK-3 DNA.
32	1050	40.6	1050	22	AAH45489	Human reduced expr
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35	820.4	31.7	2381	19	AAV07911	Mouse cysteine-ric
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37	693.8	26.8	1050	21	AAH08847	Human DKK-3 DNA op
38	476.4	18.4	557	19	AAV52114	Homo sapiens CSP
39	422.2	16.3	439	23	AAH80820	DNA encoding novel
40	380	14.7	1383	20	AAH56833	Chicken phdxx-3 cd
41	371.4	14.4	410	19	AAV52115	Homo sapiens CSP
42	362.6	14.0	397	19	AAV52116	Homo sapiens CSP
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45	321.4	12.4	475	21	AAH41805	Human secreted exp

ALIGNMENTS

AAK52255	AAK52255 standard; DNA; 2586 BP.
AC	AAK52255;
DT	25-JUN-1999 (first entry)
XX	Protein PRO295 CDNA clone DNA38268-1188.
DE	Secreted protein; transmembrane protein; human; enterocolitis;
XX	Zollinger-Ellison syndrome; gastrointestinal ulceration;
KW	congenital microvillus atrophy; skin disease; cell growth;
KW	abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW	Parinson's disease; Alzheimer's disease; ALS; neuropathy;
KW	Fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;
KW	anti-thrombotic; wound healing; tissue repair; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO9914328-A2.
XX	
PD	25-MAR-1999.
XX	
PF	16-SEP-1998; 98WC-US19330.
XX	
PR	25-NOV-1997; 97US-0066840.
PR	17-SEP-1997; 97US-0058113.
PR	17-SEP-1997; 97US-0059115.
PR	17-SEP-1997; 97US-0059117.
PR	17-SEP-1997; 97US-0059119.

PR 17-SEP-1997; 97US-0059121.
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 PR 17-SEP-1997; 97US-0059184.
 PR 18-SEP-1997; 97US-0059263.
 PR 18-SEP-1997; 97US-0059266.
 PR 15-OCT-1997; 97US-0062125.
 PR 17-OCT-1997; 97US-0062285.
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 PR 21-OCT-1997; 97US-0063486.
 PR 24-OCT-1997; 97US-0062814.
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 PR 29-OCT-1997; 97US-0063738.
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 PR 31-OCT-1997; 97US-0063870.
 PR 31-OCT-1997; 97US-0064103.
 PR 03-NOV-1997; 97US-0064248.
 PR 07-NOV-1997; 97US-0064809.
 PR 12-NOV-1997; 97US-0065186.
 PR 17-NOV-1997; 97US-0065846.
 PR 18-NOV-1997; 97US-0065846.
 PR 21-NOV-1997; 97US-0066120.
 PR 21-NOV-1997; 97US-0066364.
 PR 24-NOV-1997; 97US-0066772.
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 PR 24-NOV-1997; 97US-0066770.
 PR 24-NOV-1997; 97US-0066511.
 PR 24-NOV-1997; 97US-0066453.
 XX (GETH) GENENTECH INC.
 PA
 PI Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;
 XX WPI, 1999-229533/19.
 DR P-PSDB; AAY13384.
 XX
 PT New isolated human genes and polypeptides used in, e.g. treatment of
 XX gastrointestinal ulceration
 PS Claim 2; Fig 83; 320pp; English.
 CC AAX52213-74 encode secreted and transmembrane human proteins, and are
 CC obtained from cDNA libraries, prepared from fetal lung, fetal kidney,
 CC fetal brain, fetal liver and fetal retina. The encoded polypeptides
 CC have specific uses based on their homology to known polypeptides,
 CC e.g. PRO211 and PRO217 can be used for disorders associated with the
 CC preservation and maintenance of gastrointestinal mucosa and the repair
 CC of acute and chronic mucosal lesions (e.g. enterocolitis,
 CC Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital
 CC microvillus atrophy), skin diseases associated with abnormal
 CC keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as
 CC lung squamous cell carcinoma of the vulva and gliomas), potent effects on
 CC cell growth and development, diseases related to growth or survival of
 CC nerve cells including Parkinson's disease, Alzheimer's disease, ALS,
 CC neuropathies or cancer. PRO265 can be used as a target for anti-tumor
 CC reducing dermal scarring. PRO264 can be used as a target for anti-tumor

CC drugs. PRO533 may be used in the treatment of Usher Syndrome or Atrophia
 CC areata; PRO269 can be used as an anti-thrombotic agent; PRO287
 CC polypeptides and portions may have therapeutic applications in wound
 CC healing and tissue repair; PRO317 can be used for treating problems of
 CC the kidney, uterus, endometrium, blood vessels, or related tissue, e.g.
 CC in the heart of genital tract.
 XX
 SQ Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;
 Query Match 100.0%; Score 2586; DB 20; Length 2586;
 Best Local Similarity 100.0%; Pred. No. 0;
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XX DE Human PRO295 cDNA.
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XX KW Human; PRO; dermatological; antipruritic; cytostatic; antiinflammatory;
XX KW antiparinsonian neurotropic; neuroprotective; vulnerary; cardiant;
XX KW antiangiogenic; vasotropic; antiaesthetic; antirheumatic; cancer;
XX KW antiaesthetic; antinfertility; antidiabetic; antiviral; diabetes;
XX KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
XX KW ischaemia; inflammation; se.
XX OS Homo sapiens.
XX PN WO200104311-A1.
XX PD 18-JAN-2001.
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XX PF 22-FEB-2000; 2000MO-US04414.
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XX PR 07-JUL-1999; 99US-0143048.
XX PR 26-JUL-1999; 99US-0145698.
XX PR 28-JUL-1999; 99US-0146222.
XX PR 08-SEP-1999; 99MO-US20594.
XX PR 13-SEP-1999; 99MO-US20944.
XX PR 15-SEP-1999; 99MO-US21090.
XX PR 15-SEP-1999; 99MO-US21547.
XX PR 05-OCT-1999; 99MO-US23089.
XX PR 29-NOV-1999; 99MO-US28214.
XX PR 30-NOV-1999; 99MO-US28313.
XX PR 16-DEC-1999; 99MO-US30095.
XX PR 20-DEC-1999; 99MO-US30911.
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XX PR 05-JAN-2000; 99MO-US00219.
XX XX
XX PA (GETH ) GENENTECH INC.
XX XX
XX PI Ashkenazi AJ, Botstein D, Deenoyers L, Eaton DL, Ferrara N;
XX PI Filvaroff E, Fong S, Gao W, Gerber H, Gertlisen ME, Goddard A;
XX PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kijavrin IJ;
XX PI Mather UP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumes D;
XX PI Williams PW, Wood WL;
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XX DR WPI; 2001-081051/09.
XX DR P-PSDB; AAB80252.
XX XX
XX PT Sixty one nucleic acids encoding PRO polypeptides which are useful in
XX PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung
XX PT squamous cell carcinoma) and neurodegenerative diseases (e.g.
XX PT Alzheimer's disease) -
XX PT
XX PS Claim 2; Fig 83; 393bp; English.
XX XX
XX CC The present sequence is one of sixty one nucleic acids encoding novel
XX CC secreted and transmembrane PRO polypeptides. The PRO polypeptides are
XX CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung
XX CC squamous cell carcinoma), gastrointestinal disorders (e.g.
XX CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,
XX CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.
XX CC endometrial bleeding angiogenesis, ischaemia such as coronary
XX CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,
XX CC rheumatoid arthritis, multiple sclerosis), infertility, AIDS and
XX CC diabetes and retinal disorders such as retinitis pigmentosa.
XX CC The PRO nucleic acids have applications in molecular biology, including
XX CC use as hybridization probes, and in chromosome and gene mapping.
XX XX
XX SQ Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other.

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Query Match 100.0%; Score 2586; DB 22; Length 2586;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 481 ATGTGACCGGAAATTCAGATGAACCAACAGAGCTGGAGCAAAATGCTTTTCAAG 540
DB 481 ATGTGACCGGAAATTCAGATGAACCAACAGAGCTGGAGCAAAATGCTTTTCAAG 540
QY 541 AGACAGTTATCACATCTGTGGAGACGAAAGAGGCAAGAGAGCCAGAGTGCATCTG 600
DB 541 AGACAGTTATCACATCTGTGGAGACGAAAGAGGCAAGAGAGCCAGAGTGCATCTG 600
QY 601 ACAGAGATGTGGGCGCGAGATGACTGCGAGTTCCAGCTTCCAGTACCTGCGACG 660
DB 601 ACAGAGATGTGGGCGCGAGATGACTGCGAGTTCCAGCTTCCAGTACCTGCGACG 660
QY 661 CATGCCGCGGCGCAGAGAGATGCTGCAACCGGAGCACTGAGTGTGTGAGACAGCTGT 720
DB 661 CATGCCGCGGCGCAGAGAGATGCTGCAACCGGAGCACTGAGTGTGTGAGACAGCTGT 720
QY 721 GTGTCTGGGCTCACTGACCAAAATGGCCACAGGGGCGAGTGGGACCAATCTGTGACA 780
DB 721 GTGTCTGGGCTCACTGACCAAAATGGCCACAGGGGCGAGTGGGACCAATCTGTGACA 780
QY 781 ACCAGAGGAGCTGCGAGCGCGGCTGTGCTGCTTCCAGAGAGGCTGTGCTCCCTG 840
DB 781 ACCAGAGGAGCTGCGAGCGCGGCTGTGCTGCTTCCAGAGAGGCTGTGCTCCCTG 840
QY 841 TGTGACACACCCCTGCGGTGAGAGGCGAGCTTTGCCATGACCCCGCAGCTCTGTG 900
DB 841 TGTGACACACCCCTGCGGTGAGAGGCGAGCTTTGCCATGACCCCGCAGCTCTGTG 900
QY 901 ACCTCATCACTGAGAGCTGAGAGCTGAGAGCTTGGACCGATGCGCTTGTGCGAGTG 960
DB 901 ACCTCATCACTGAGAGCTGAGAGCTGAGAGCTTGGACCGATGCGCTTGTGCGAGTG 960
QY 961 GCTCTCTCTGCGAGCCCGCAGCAGCAGCTGTGTATGTGTGCAAGCGACCTTGTG 1020
DB 961 GCTCTCTCTGCGAGCCCGCAGCAGCAGCTGTGTATGTGTGCAAGCGACCTTGTG 1020
QY 1021 GGAAGCGGTGCAAGATGGGGAATCTGTGCTGCGCAGAGAGGCTCCCGATGATGAG 1080
DB 1021 GGAAGCGGTGCAAGATGGGGAATCTGTGCTGCGCAGAGAGGCTCCCGATGATGAG 1080
QY 1081 TTGGCAGCTTCATGAGAGAGTGGCGCAGAGAGCTGAGAGACTGAGAGAGAGCTGACTG 1140
DB 1081 TTGGCAGCTTCATGAGAGAGTGGCGCAGAGAGCTGAGAGACTGAGAGAGAGCTGACTG 1140

QY 1141 AAGAGATGAGCGCTGGGGGAGAGCTGCGGCTGCGCGCGCTGCACTGTGGAGGGGAGAGA 1200
DB 1141 AAGAGATGAGCGCTGGGGGAGAGCTGCGGCTGCGCGCGCTGCACTGTGGAGGGGAGAGA 1200
QY 1201 TTTAGATCTGAGACCAAGCTGTGGGTAGATGTCATGAAATAGCTAATTTATTTCCCA 1260
DB 1201 TTTAGATCTGAGACCAAGCTGTGGGTAGATGTCATGAAATAGCTAATTTATTTCCCA 1260
QY 1261 GGTGTGTCTTTAGGCGTGGGCTGACACAGGCTCTTCCATCTCTTCCAGTAACTT 1320
DB 1261 GGTGTGTCTTTAGGCGTGGGCTGACACAGGCTCTTCCATCTCTTCCAGTAACTT 1320
QY 1321 TCCCTCTGCTGACAGCATGAGGTGTGTGATTTGTTCAGTCCCGCAGGCTGTCT 1380
DB 1321 TCCCTCTGCTGACAGCATGAGGTGTGTGATTTGTTCAGTCCCGCAGGCTGTCT 1380
QY 1381 CCAGGCTTCACAGCTGTGTGCTGGAGAGTCAAGCGGGTTAACTGCGAGAGCACTT 1440
DB 1381 CCAGGCTTCACAGCTGTGTGCTGGAGAGTCAAGCGGGTTAACTGCGAGAGCACTT 1440
QY 1441 GCGACCCCTGTCCAGATTTATGGCTGTGCTCTTACCACTTGCGCAGACGCGTTGT 1500
DB 1441 GCGACCCCTGTCCAGATTTATGGCTGTGCTCTTACCACTTGCGCAGACGCGTTGT 1500
QY 1501 TCTACATGCTTTGATTAATTTGTTGAGGGGAGAGATGAGAAATGTGAGTCTCCCTC 1560
DB 1501 TCTACATGCTTTGATTAATTTGTTGAGGGGAGAGATGAGAAATGTGAGTCTCCCTC 1560
QY 1561 TGATTTGTTGGGGAATGTGGAGAGAGTGGCCCTTGTGCAACATCAACTGCGCAA 1620
DB 1561 TGATTTGTTGGGGAATGTGGAGAGAGTGGCCCTTGTGCAACATCAACTGCGCAA 1620
QY 1621 AAATGCAACAAATGATTTTCCAGCGAGTTTCCATGCGGCAATGAGTAACTGTGCTT 1680
DB 1621 AAATGCAACAAATGATTTTCCAGCGAGTTTCCATGCGGCAATGAGTAACTGTGCTT 1680
QY 1681 CAGCTGTGAGAGAGAAATGTGTGCTCACCGCTGATTAATGATTTATTCACAGCA 1740
DB 1681 CAGCTGTGAGAGAGAAATGTGTGCTCACCGCTGATTAATGATTTATTCACAGCA 1740
QY 1741 GTGTGCTCAGCTCTTCACTGTGCGAGGCGAGCATTTTCATATCCAAATCAATCCC 1800
DB 1741 GTGTGCTCAGCTCTTCACTGTGCGAGGCGAGCATTTTCATATCCAAATCAATCCC 1800
QY 1801 TCTCTCAGCAGCGTGGGAGAGGGGCTCATTTGTTCTCTGCTCATGAGGATCTCAG 1860
DB 1801 TCTCTCAGCAGCGTGGGAGAGGGGCTCATTTGTTCTCTGCTCATGAGGATCTCAG 1860
QY 1861 GCTCAGAGACTGCAAGCTGTGCGCAAGTCAACACAGCTAGTGAAGCCAGAGAGTTTC 1920
DB 1861 GCTCAGAGACTGCAAGCTGTGCGCAAGTCAACACAGCTAGTGAAGCCAGAGAGTTTC 1920
QY 1921 ATCTGTGTGAGACTTAAAGCTCAGTGTCTCTCACTAACCCCAACAGGCTGTGCGCA 1980
DB 1921 ATCTGTGTGAGACTTAAAGCTCAGTGTCTCTCACTAACCCCAACAGGCTGTGCGCA 1980
QY 1981 CCAAAAGTGTCCCAAAAGAGAGAGATGAGATTTTCTTGAAGCATCAATCTGGA 2040
DB 1981 CCAAAAGTGTCCCAAAAGAGAGAGATGAGATTTTCTTGAAGCATCAATCTGGA 2040
QY 2041 ATTAAGTCAAACTAATTTTCACTCCCTCTTAAAGATTAATCTGTGAGAACAGAGT 2100
DB 2041 ATTAAGTCAAACTAATTTTCACTCCCTCTTAAAGATTAATCTGTGAGAACAGAGT 2100
QY 2101 GTTCTCACAGTGTGGGCGAGCGCTCTTCAATGAAGACATATATGACACTGTCCCT 2160
DB 2101 GTTCTCACAGTGTGGGCGAGCGCTCTTCAATGAAGACATATATGACACTGTCCCT 2160
QY 2161 CTTTGGCAGTTGCACTTGTAACTTTGAAGATATATGAGGCTGTGCACTAGGTTAA 2220
DB 2161 CTTTGGCAGTTGCACTTGTAACTTTGAAGATATATGAGGCTGTGCACTAGGTTAA 2220
QY 2221 CCTGCAAGAACAGTACTTAAAGTATGTAGGCGAGAGATTAATGAATTTGCAAAAT 2280
DB 2221 CCTGCAAGAACAGTACTTAAAGTATGTAGGCGAGAGATTAATGAATTTGCAAAAT 2280

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Db      2221 CCTGACGAAACAGTACTAGTAATTTGAGGCGACAGTTATTAATGAATTTGCAAAAT 2280
QY      2281 CACTTAGAGCACTGGAAGACAAATTTATCAACCACTGGAGAAAATCAACCGACAGGGC 2340
Db      2281 CACTTAGAGCACTGGAAGACAAATTTATCAACCACTGGAGAAAATCAACCGACAGGGC 2340
QY      2341 TGTGTGAAACATGGTTGTAATATGAGTGGAAACATGGAACCTAGCCACTCCACAAA 2400
Db      2341 TGTGTGAAACATGGTTGTAATATGAGTGGAAACATGGAACCTAGCCACTCCACAAA 2400
QY      2401 TGATGTTTCAGGTGTCATGAGCTGTTGCCACCATGATTCATCCAGAGTTCTTAAGTT 2460
Db      2401 TGATGTTTCAGGTGTCATGAGCTGTTGCCACCATGATTCATCCAGAGTTCTTAAGTT 2460
QY      2461 TAAAGTGCACATATGTTATGATAGCACTGCTTTCTTTGATTTAATTTATGATTAACAT 2520
Db      2461 TAAAGTGCACATATGTTATGATAGCACTGCTTTCTTTGATTTAATTTATGATTAACAT 2520
QY      2521 AAGTTGATTTAGCAATCAACATTAATCACTTCACTGCAAAAAA 2580
Db      2521 AAGTTGATTTAGCAATCAACATTAATCACTTCACTGCAAAAAA 2580
QY      2581 AAAAAA 2586
Db      2581 AAAAAA 2586

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RESULT 4
 ABS74381
 ID ABS74381 standard; cDNA, 2586 BP.

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XX      ABS74381;
AC      10-DEC-2002 (first entry)
DE      Human cDNA encoding secreted/transmembrane protein PRO255.
XX      Human, ss; gene, secreted protein, transmembrane protein, anti-rheumatic;
XX      antiarthritic; osteopathic; sports-related joint problem;
XX      articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX      Homo sapiens.
XX      OS
XX      US200219130-A1.
XX      23-AUG-2002.
XX      06-DEC-2001; 2001US-0006867.
XX      29-OCT-1997; 97US-063435P.
XX      29-OCT-1997; 97US-064215P.
XX      22-APR-1998; 98US-082797P.
XX      29-APR-1998; 98US-083495P.
XX      15-MAY-1998; 98US-085797P.
XX      10-JUN-1998; 98US-088811P.
XX      10-JUN-1998; 98US-088824P.
XX      10-JUN-1998; 98US-088825P.
XX      11-JUN-1998; 98US-088832P.
XX      12-JUN-1998; 98US-089105P.
XX      16-JUN-1998; 98US-089514P.
XX      16-SEP-1998; 98WO-US19330.
XX      08-MAR-1999; 99WO-US05028.
XX      14-MAY-1999; 99WO-US10733.
XX      02-JUN-1999; 99WO-US12252.
XX      01-SEP-1999; 99WO-US20111.
XX      15-SEP-1999; 99WO-US21090.
XX      15-SEP-1999; 99WO-US21194.
XX      22-DEC-1999; 99WO-US30720.
XX      18-FEB-2000; 2000WO-US04341.
XX      18-FEB-2000; 2000WO-US04342.
XX      30-MAR-2000; 2000WO-US08439.
XX      22-MAY-2000; 2000WO-US14042.

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PR      02-JUN-2000; 2000WO-US15264.
PR      23-AUG-2000; 2000WO-US23522.
PR      24-AUG-2000; 2000WO-US23328.
PR      10-NOV-2000; 2000WO-US30873.
PR      01-DEC-2000; 2000WO-US32378.
PR      20-DEC-2000; 2000WO-US34956.
PR      28-FEB-2001; 2001WO-US06520.
PR      20-JUN-2001; 2001WO-US19692.
PR      29-JUN-2001; 2001WO-US21066.
PR      09-JUL-2001; 2001WO-US21735.
XX      (GENT) GENENTECH INC.
XX      Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI      Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX      WPI; 2002-731348/79.
XX      P-PSDB; ABG93854.
XX      New isolated secreted and transmembrane PRO polypeptide useful for
PT      modulating biological activity of a cell, or for treating
PT      sports-related joint problems, osteoarthritis or rheumatoid arthritis
XX      Claim 2; Fig 7; 399pp; English.
XX      The invention relates to an isolated secreted and transmembrane PRO
XX      polypeptide having 80 % sequence identity to a sequence appearing
XX      as ABG93851-ABG93934 or their associated signal peptide, or a sequence of
XX      an extracellular domain of the proteins with their associated signal
XX      peptide or lacking its associated signal peptide. Also included are
XX      the nucleic acids encoding the proteins, vectors, host cells,
XX      fusion proteins and antibodies which specifically bind to the proteins.
XX      The proteins are useful for detecting a polypeptide designated as A, B, C
XX      or D in a sample suspected of containing an A, B, C or D polypeptide,
XX      by contacting the sample with a polypeptide designated as E, F, G, H or
XX      I (or vice versa) and determining the formation of an A/E, B/F, B/G, C/H
XX      or D/I polypeptide conjugate in the sample, where the formation of the
XX      conjugate is indicative of the presence of an A, B, C or D polypeptide
XX      in the sample, where A is a PRO10272 polypeptide, B is a PRO20110
XX      polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide,
XX      E is a PRO5801 polypeptide, F is a PRO1 polypeptide, G is a PRO20040
XX      polypeptide, H is a PRO20233 polypeptide and I is a PRO1890
XX      polypeptide. The sample comprises a cell suspected of expressing the A,
XX      B, C or D polypeptide. The B, F, G, H or I polypeptide is labeled with
XX      a detectable label or is attached to a solid support. The proteins are
XX      useful for linking a bioactive molecule to a cell expressing a
XX      polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive
XX      molecule is a toxin, a radiolabel or an antibody. The bioactive molecule
XX      causes death of the cell. A, B, C, D, E, F, G, H, or I, or antibodies
XX      against them are useful for modulating a biological activity of a cell
XX      expressing a polypeptide designated as A, B, C or D or E, F, G, H, or
XX      I. The cell is killed. The proteins are useful for identifying
XX      agonists or antagonists, for the preparation of a medicament useful in
XX      the treatment of a condition which is responsive to the proteins, as
XX      molecular weight markers for protein electrophoresis purposes, and as
XX      therapeutic agents for treating sports-related joint problems,
XX      articular cartilage defects, osteoarthritis or rheumatoid arthritis.
XX      Nucleic acids encoding the proteins are useful as hybridisation probes,
XX      in chromosome and gene mapping, in the generation of antisense RNA and
XX      DNA, for the preparation of the proteins, to generate transgenic or
XX      knockout animals which are useful in the development and screening of
XX      therapeutic useful reagents, for chromosome identification, and in gene
XX      therapy. The antibody is useful as a therapeutic agent, in a diagnostic
XX      assay and for affinity purification of the protein from recombinant
XX      cell culture natural sources. The present sequence encodes a novel
XX      secreted or transmembrane protein of the invention.
XX      Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;
SQ

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Query Match 100.0%; Score 2586; DB 24; Length 2586;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CGCGCGCTTCGCGACCCGCGCGCGCGCCACCGCGCGCTCCCGCATCTGCAACCCGCGAGC	60
Db	1	CGCGCGCTTCGCGACCCGCGCGCGCGCCACCGCGCGCTCCCGCATCTGCAACCCGCGAGC	60
QY	61	CGCGCGCGCTTCGCGCGCGCGCGCGAGGACGAGACGATCCAGTCCGCGCGCGCAGCGCAATCGAGTCCA	120
Db	61	CGCGCGCGCTTCGCGCGCGCGCGCGAGGACGAGACGATCCAGTCCGCGCGCGCAGCGCAATCGAGTCCA	120
QY	121	GTCGCGCGCGCGCGCTGCGCGCGCGACGAGACGAGATGCAACGCGCTTGGGGCCGACCTTGCTGT	180
Db	121	GTCGCGCGCGCGCGCTGCGCGCGCGACGAGCGGAGATGCAACGCGCTTGGGGCCGACCTTGCTGT	180
QY	181	GCCGCTGCTGCGCGCGCGCGGTCCCAACGCGCGCGCGCGCGCGCTTCGACGCGCGACCTCGG	240
Db	181	GCCGCTGCTGCGCGCGCGCGGTCCCAACGCGCGCGCGCGCGCGCTTCGACGCGCGACCTCGG	240
QY	241	CTCCAGTCAAGCCCGCGCGCGCTCTCAGCTTACCCTGACGAGAGAGCGCACCTTCATGAGA	300
Db	241	CTCCAGTCAAGCCCGCGCGCGCTCTCAGCTTACCCTGACGAGAGAGCGCACCTTCATGAGA	300
QY	301	TGTTCCGCGAGGTTGAGGAATGATGAGAGACACGACGCAAAATGGCGGAGCGGGGTGG	360
Db	301	TGTTCCGCGAGGTTGAGGAATGATGAGAGACACGACGCAAAATGGCGGAGCGGGGTGG	360
QY	361	AAGAGATGAGAGCGCAGAGAGAGCTGCTCTTAAGCATATCAGAGTGAACCTGGCAAACT	420
Db	361	AAGAGATGAGAGCGCAGAGAGAGCTGCTCTTAAGCATATCAGAGTGAACCTGGCAAACT	420
QY	421	TACCTCCGAGTTATCAATGAGACCAACACGACACGACGAGAGGTTGGAAATTAATACATCC	480
Db	421	TACCTCCGAGTTATCAATGAGACCAACACGACACGACGAGAGGTTGGAAATTAATACATCC	480
QY	481	ATGTGCACCCGGAATTCACAAAGATTAACCAACACAGCTGACCAATGTTTTCAG	540
Db	481	ATGTGCACCCGGAATTCACAAAGATTAACCAACACAGCTGACCAATGTTTTCAG	540
QY	541	AGACAGTTATCAATCTGTGGAGACGAGAGGCGAGAGGCGACGAGTGCATATCG	600
Db	541	AGACAGTTATCAATCTGTGGAGACGAGAGGCGAGAGGCGACGAGTGCATATCG	600
QY	601	ACGAGGATGTGGGCGCGCAGCATGTACTGCGCAGGTTTGCAGTTTCACTAACCTGCGCAGC	660
Db	601	ACGAGGATGTGGGCGCGCAGCATGTACTGCGCAGGTTTGCAGTTTCACTAACCTGCGCAGC	660
QY	661	CATGCCGCGCGCGCAGAGATGCTCTTGCAACCCGCGACAGTGAAGTGTGTGAGACGACTGT	720
Db	661	CATGCCGCGCGCGCAGAGATGCTCTTGCAACCCGCGACAGTGAAGTGTGTGAGACGAGTGT	720
QY	721	GTGTCTGGGGTCACTGCAACCAATGTGCGACCAAGGGGAGGCAATGGGACCATCTGTGACA	780
Db	721	GTGTCTGGGGTCACTGCAACCAATGTGCGACCAAGGGGAGGCAATGTGTGACA	780
QY	781	ACCAGAGGGAATGCGCAGCGCGGCGCTGTGCTTGCTTCCAGAGAGGCTGTGTTCCCTG	840
Db	781	ACCAGAGGGAATGCGCAGCGCGGCGCTGTGCTTGCTTCCAGAGAGGCTGTGTTCCCTG	840
QY	841	TGTGACACACCTTGCCTGTGAGAGGCGAGCTTTGCAATGACCCCGCAGCCGCGCTTTGCG	900
Db	841	TGTGACACACCTTGCCTGTGAGAGGCGAGCTTTGCAATGACCCCGCAGCCGCGCTTTGCG	900
QY	901	ACCTCATCACTGGGAGCTGAGAGCTGATGAGACCTTGGACGATGCTTGTGCCAGTG	960
Db	901	ACCTCATCACTGGGAGCTGAGAGCTGATGAGACCTTGGACGATGCTTGTGCCAGTG	960
QY	961	GCCTCTCTTGCCAGCCCGCAGCCACGCAACGCTGTGTATGTGTGCAAGCGCACTTTCGTG	1020
Db	961	GCCTCTCTTGCCAGCCCGCAGCCACGCAACGCTGTGTATGTGTGCAAGCGCACTTTCGTG	1020
QY	1021	GGAGCGCGTACCAAGATGGGGAGATCTGCTCCCGACGAGAGGTCCCGCATAGATGAG	1080
Db	1021	GGAGCGCGTACCAAGATGGGGAGATCTGCTCCCGACGAGAGGTCCCGCATAGATGAG	1080
QY	1081	TTGGCAGCTTCAATGAGGAGGTGCGCAGGAGCTGAGAGACTGAGAGGAGCTTGACTG	1140

D	1081	TTGGCAGCTTCAAGAGCAGAGGTGGCCGACAGAACTGGAGAACTTGGAGAGGAGCACTGACTG	1140
Q	1141	AAGAGATGGCGCTGGGGGAGCCTGCGGCTGCGCGCTGACTGCTGCGGAGGGGAAAGGA	1200
D	1141	AAGAGATGGCGCTGGGGGAGCCTGCGGCTGCGCGCTGACTGCTGCGGAGGGGAAAGGA	1200
Q	1201	TTTAGACTCTGACCAAGGCTGTGGGTAGATGTGCATAGAAATAGCTAAATTATTTCCCA	1260
D	1201	TTTAGACTCTGACCAAGGCTGTGGGTAGATGTGCATAGAAATAGCTAAATTATTTCCCA	1260
Q	1261	GGTGTGCTTTAGGGGTGGGCTGACCAAGCTTCTCCATCAATCTCTCCCAAGTAAGT	1320
D	1261	GGTGTGCTTTAGGGGTGGGCTGACCAAGCTTCTCTCAATCTTCTCCCAAGTAAGT	1320
Q	1321	TCCCTCTGGCTTGACAGCATAGAGTGTGTGCATTTGTTCAGCTCCCGAGGCTTCT	1380
D	1321	TCCCTCTGGCTTGACAGCATAGAGTGTGTGCATTTGTTCAGCTCCCGAGGCTTCT	1380
Q	1381	CCAGGCTTCAAGTCTGTGTGCTTGGGAGATCAGGAGGGTTAAATTGAGAGCAGTT	1440
D	1381	CCAGGCTTCAAGTCTGTGTGCTTGGGAGATCAGGAGGGTTAAATTGAGAGCAGTT	1440
Q	1441	GCCACCCCTGACAGATTAATGGCTGCTTTCCTCTACAGTTGGCAGACAGCCGTTGT	1500
D	1441	GCCACCCCTGACAGATTAATGGCTGCTTTCCTCTACAGTTGGCAGACAGCCGTTGT	1500
Q	1501	TCATACATGGCTTGATTAATGTTTGAAGGGAGAGATGAAATAAATGTGAGTCCCTC	1560
D	1501	TCATACATGGCTTGATTAATGTTTGAAGGGAGAGATGAAATAAATGTGAGTCCCTC	1560
Q	1561	TGATTTGTTTGGGGAAATGTGAGAGAGTGGCTGCTTTGGCAACATCAACCTGGCAA	1620
D	1561	TGATTTGTTTGGGGAAATGTGAGAGAGTGGCTGCTTTGGCAACATCAACCTGGCAA	1620
Q	1621	AAATGCAACAATGAATTTTCCAGGAGTCTTCCATGGGCAATAGGTAAAGTGTGCTT	1680
D	1621	AAATGCAACAATGAATTTTCCAGGAGTCTTCCATGGGCAATAGGTAAAGTGTGCTT	1680
Q	1681	CAGCTGTTGAGATGAATGTCTGTTCACCCGTCATTAATCATGTGTTATTCATCCAGA	1740
D	1681	CAGCTGTTGAGATGAATGTCTGTTCACCCGTCATTAATCATGTGTTATTCATCCAGA	1740
Q	1741	GTTGTGCTCAGCTCTTAATCTGTGCGCAGGGGAGCAATTCATCAATCAATCAATCCC	1800
D	1741	GTTGTGCTCAGCTCTTAATCTGTGCGCAGGGGAGCAATTCATCAATCAATCAATCCC	1800
Q	1801	TCTCTCAGCAAGCCTGGGAGGGGGTCAATGTTCTCTCTGTCATCAGGAGATCTCAG	1860
D	1801	TCTCTCAGCAAGCCTGGGAGGGGGTCAATGTTCTCTCTGTCATCAGGAGATCTCAG	1860
Q	1861	GCTCAGACACTGCAAGCTGTGTGGCCAAATGCACACACTAGTGAAGCCAGACAGTTTC	1920
D	1861	GCTCAGACACTGCAAGCTGTGTGGCCAAATGCACACACTAGTGAAGCCAGACAGTTTC	1920
Q	1921	ATCTGTTGTAATCTAAGCTCAGTGTCTCTCCACTACCCACACAGCCTTGTGTCCA	1980
D	1921	ATCTGTTGTAATCTAAGCTCAGTGTCTCTCCACTACCCACACAGCCTTGTGTCCA	1980
Q	1981	CCAAAGAGTCTCCCAAAAGAGAGAAATGGAAATTTTCTGAGGATGCAATCTGSA	2040
D	1981	CCAAAGAGTCTCCCAAAAGAGAGAAATGGAAATTTTCTGAGGATGCAATCTGSA	2040
Q	2041	ATTAAAGTCAAACTAATCTCACAATCCTCTAAAGTAAACTACTGTTAGAAACAGAGT	2100
D	2041	ATTAAAGTCAAACTAATCTCACAATCCTCTAAAGTAAACTACTGTTAGAAACAGAGT	2100
Q	2101	GTTCTCAGAGTGTGGGGAGCGGTCTCTATGTAAGACATGATATTTGACACTGTCCCT	2160
D	2101	GTTCTCAGAGTGTGGGGAGCGGTCTCTATGTAAGACATGATATTTGACACTGTCCCT	2160
Q	2161	CTTTGGCAATGCAATTAGTAACTTTGAAGGTATATGCTGAGGTAGCATACAGTTTAA	2220

	RESULT	5
ID	ABL95585	
	ABL95585 standard; cDNA; 2586 BP.	
AC	ABL95585;	
XX		
DT	19-JUL-2002 (first entry)	
DE	Human angiogenesis related CDNA PRO295 SEQ ID NO: 49.	
XX		
KW	Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;	
KM	atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;	
KW	cardiac; cytosolic; antiangiogenic; hypotensive; vulnerary;	
KM	antiarteriosclerotic; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	NC0200208284-A2.	
PD		
PF	31-JAN-2002.	
XX		
PF	09-JUL-2001; 2001MO-US21735.	
XX		
PR	20-JUL-2000; 2000US-219556P.	
PR	25-JUL-2000; 2000US-220624P.	
PR	25-JUL-2000; 2000US-220644P.	
PR	28-JUL-2000; 2000MO-US20710.	
PR	02-AUG-2000; 2000US-222695P.	
PR	17-AUG-2000; 2000US-0643657.	
PR	23-AUG-2000; 2000MO-US23522.	
PR	24-AUG-2000; 2000MO-US23328.	
PR	07-SEP-2000; 2000US-230978P.	
PR	15-SEP-2000; 2000US-000000P.	
PR	18-SEP-2000; 2000US-0664610.	
PR	18-SEP-2000; 2000US-0665350.	
PR	24-OCT-2000; 2000US-242922P.	
PR	08-NOV-2000; 2000US-0709238.	
PR	08-NOV-2000; 2000MO-US30952.	
PR	10-NOV-2000; 2000MO-US30873.	
PR	01-DEC-2000; 2000MO-US32678.	
PR	20-DEC-2000; 2000US-0747259.	
PR	20-DEC-2000; 2000MO-US34956.	

121 GTCGGGCGGCTGCGGGCGCAGAGCGGAGATGCAGCGCTTGGGCCACCCCTGCTGT 18

Db 121 GTGAGGAGCGGCTGCGGCGGAGAGCGAGATGAGCGGCTGCGGCGGAGCGGCTGCTGT 180
QY 181 GCGTGTGCTGAGGAGGAGGAGTCCGACGAGCGCGCGCGCGCTGCGGAGCGGAGCTGCG 240
Db 181 GCGTGTGCTGAGGAGGAGGAGTCCGACGAGCGCGCGCGCGCTGCGGAGCGGAGCTGCG 240
QY 241 CTCGAGTCAAGCGCGCGCGCTGCTGAGCTACCGGAGAGAGGCGACCTTCAATGAGA 300
Db 241 CTCGAGTCAAGCGCGCGCGCTGCTGAGCTACCGGAGAGAGGCGACCTTCAATGAGA 300
QY 301 TGTTCGCGAGGTTGAGGAGCTGATGAGGAGCAGGAGCAAAATGCGGAGCGGAGTGG 360
Db 301 TGTTCGCGAGGTTGAGGAGCTGATGAGGAGCAGGAGCAAAATGCGGAGCGGAGTGG 360
QY 361 AAGAGATGAGGAGAGAGAGTGTGCTAAAGCATATGAGAGTGAACCTGCGAACT 420
Db 361 AAGAGATGAGGAGAGAGAGTGTGCTAAAGCATATGAGAGTGAACCTGCGAACT 420
QY 421 TACCTCCAGCTATCAGATGAGAGCAGACAGAGAGTGGAAATATACATCC 480
Db 421 TACCTCCAGCTATCAGATGAGAGCAGACAGAGAGTGGAAATATACATCC 480
QY 481 ATGTGACACGAGAAATTCAGATTAACCAACAGAGCTGAGCAAAATGCTTTTCAG 540
Db 481 ATGTGACACGAGAAATTCAGATTAACCAACAGAGCTGAGCAAAATGCTTTTCAG 540
QY 541 AGACAGTTATOCATCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Db 541 AGACAGTTATOCATCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 601 ACAGAGCTGTGAGGCGCGAGAGTGTGAGAGCTTTCAGCTTCCAGTACCTGCGAC 660
Db 601 ACAGAGCTGTGAGGCGCGAGAGTGTGAGAGCTTTCAGCTTCCAGTACCTGCGAC 660
QY 661 CATGCGCGGAGCGAGAGAGTGTGAGAGCTTTCAGAGTGTGAGAGAGAGAGAGAG 720
Db 661 CATGCGCGGAGCGAGAGAGTGTGAGAGCTTTCAGAGTGTGAGAGAGAGAGAGAG 720
QY 721 GTGTCTGAGGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db 721 GTGTCTGAGGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 781 ACCAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Db 781 ACCAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 841 TGTGACACAGCGCGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db 841 TGTGACACAGCGCGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 901 ACCTCATCACCTGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Db 901 ACCTCATCACCTGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 961 GCGTCTCTGTGAG 1020
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QY 1021 GAGAGCGTGAACAG 1080
Db 1021 GAGAGCGTGAACAG 1080
QY 1081 TTTGACAGCTTATGAG 1140
Db 1081 TTTGACAGCTTATGAG 1140
QY 1141 AAGAGATGAG 1200
Db 1141 AAGAGATGAG 1200
QY 1201 TTTAGATCTGAGACAGAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1260
Db 1201 TTTAGATCTGAGACAGAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1260

Db 1201 TTTAGATCTGAGACAGAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1260
QY 1261 GATGTGTGCTTTAG 1320
Db 1261 GATGTGTGCTTTAG 1320
QY 1321 TCCCTCTGAGCTGAG 1380
Db 1321 TCCCTCTGAGCTGAG 1380
QY 1381 CCAGGCTTCAAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Db 1381 CCAGGCTTCAAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
QY 1441 GCAACCCCTGTCCAGATTTATGAGTGTGCTTTCAGCTTTCAGAGAGAGAGAGAG 1500
Db 1441 GCAACCCCTGTCCAGATTTATGAGTGTGCTTTCAGCTTTCAGAGAGAGAGAGAG 1500
QY 1501 TCTACATGCTTGTATATGTTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Db 1501 TCTACATGCTTGTATATGTTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
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Db 1561 TGATTTGTTTGGGAAATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
QY 1621 AAATGCAACAAATGAAATTTTCCAGAGTGTTCATGAGGAGATGAGTGTGCTT 1680
Db 1621 AAATGCAACAAATGAAATTTTCCAGAGTGTTCATGAGGAGATGAGTGTGCTT 1680
QY 1681 CAGCTGTGAGATGAAATGTTCTGTTTACCTGATTAACATGTTTATTCATCCAGCA 1740
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QY 1741 GTGTGCTGAGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
Db 1741 GTGTGCTGAGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
QY 1801 TCTCTCAGCAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
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QY 1861 GCTCAG 1920
Db 1861 GCTCAG 1920
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QY 1981 CCAAAAAGTGTCCCAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
Db 1981 CCAAAAAGTGTCCCAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
QY 2041 ATTAGAGTCAAACTAATCTCAGATCCCTTAAAGTAACTAAGTAACTAAGTAACT 2100
Db 2041 ATTAGAGTCAAACTAATCTCAGATCCCTTAAAGTAACTAAGTAACTAAGTAACT 2100
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Db 2281 CACTTGAAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
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QY 2581 AAAAAA 2586
Db 2581 AAAAAA 2586

RESULT 6
AB188096
ID AB188096 standard; cDNA; 2586 BP.
AC AB188096;
XX
XX 16-MAY-2002 (first entry)
DE Human PRO295 cDNA sequence SEQ ID NO:49.
XX
XX Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;
XX vulnerability; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
XX gene therapy; cardiovascular disorder; endothelial disorder; cancer;
XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
XX age-related macular degeneration; arterial restenosis; angina;
XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;
XX lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
XX wound healing; chromosome mapping; gene mapping; gene; ss.
XX
OS Homo sapiens.
XX
XX MO200200690-A2.
XX
PD 03-JAN-2002.
PF
XX 20-JUN-2001; 2001WO-US19692.
XX
PR 23-JUN-2000; 2000US-213637P.
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220664P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-0643657.
PR 23-AUG-2000; 2000WO-US23322.
PR 24-AUG-2000; 2000WO-US23328.
PR 07-SEP-2000; 2000US-230978P.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-0709238.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0766498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 09-MAR-2001; 2001US-0802706.

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PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 03-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17600.
XX
XX (GENTH ) GENENTECH INC.
XX
XX Baker KP, Ferrara N, Garber H, Gerritsen ME, Goddard A;
XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
XX Stephen WF, Watanabe CK, Williams PM, Wood WT, Ye W;
XX WPI; 2002-090516/12.
XX
XX P-PSDB; ABB84841.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX infarction), endothelial or angiogenic disorders in a mammal -
XX
XX Claim 2; Fig 49; 565pp; English.
XX
XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
XX ABB85003. The PRO proteins and polynucleotides have cardiac, cytosolic,
XX antiangiogenic, hypotensive, vulnerability and antiarteriosclerotic
XX activities, and can be used in gene therapy. The PRO polynucleotides,
XX proteins, agonists and antagonists are useful for treating or diagnosing
XX a cardiovascular, endothelial or angiogenic disorder in a mammal,
XX e.g. cardiac hypertrophy, trauma, cancer, age-related macular
XX degeneration, atherosclerosis, hypertension, arterial restenosis,
XX rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
XX lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
XX carcinoma) and wound healing. The PRO polynucleotides have applications
XX in molecular biology, including use as hybridisation probes, and in
XX chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
XX probes used in the exemplification of the present invention.
XX
XX Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 2586; DB 24; Length 2586;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 CCGCGCGCTCCCGCGGAGCGAGCATCTGCGCGCCGCGGAGCGCAACTCGGTCCA 120
QY 121 GTCGCGCGCGCGCTGCGCGCGCGAGCGAGATGACGCGGCTTTGCGGCACTCTGCTGT 180
Db 121 GTCGCGCGCGCGCTGCGCGCGCGAGCGAGATGACGCGGCTTTGCGGCACTCTGCTGT 180
QY 181 GCGCTGCTGCTGCGCGCGCGGTCCCGACCGCCCGCGCGCGCTCCGAGCGGCGACCTCGG 240
Db 181 GCGCTGCTGCTGCGCGCGCGGTCCCGACCGCCCGCGCGCGCTCCGAGCGGCGACCTCGG 240
QY 181 GCGCTGCTGCTGCGCGCGCGGTCCCGACCGCCCGCGCGCGCTCCGAGCGGCGACCTCGG 240
Db 181 GCGCTGCTGCTGCGCGCGCGGTCCCGACCGCCCGCGCGCGCTCCGAGCGGCGACCTCGG 240
QY 241 CTCAGTCAAGCCCGCGCGCGCTCTCAGTCAACCGCGAGAGAGGCCACCTCATAGAGA 300
Db 241 CTCAGTCAAGCCCGCGCGCGCTCTCAGTCAACCGCGAGAGAGGCCACCTCATAGAGA 300
QY 301 TGTTCGCGAGAGTTGAGGAATGATGAGAGACAGCGACCAATTTGCGAGCGCGGTGG 360
Db 301 TGTTCGCGAGAGTTGAGGAATGATGAGAGACAGCGACCAATTTGCGAGCGCGGTGG 360
QY 361 AAGAGATGAGAGAGAGAGAGAGTCTGCTAAGCATCATCAGAAAGTAACTGGCAACT 420

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OY 2581 AAAAAA 2586
 DB 2581 AAAAAA 2586
 RESULT 7
 ID ACAS5002 standard; cDNA; 2586 BP.
 AC ACAS5002;
 DT 05-JUN-2003 (first entry)
 DE Novel human secreted and transmembrane protein PRO295 cDNA.
 XX
 XX Homo sapiens.
 XX US2003017463-A1.
 PD 23-JAN-2003.
 XX
 PF 11-JUL-2001; 2001US-0903640.
 XX
 XX 10-SEP-1998; 98MO-US18824.
 PR 14-SEP-1998; 98MO-US19177.
 PR 16-SEP-1998; 98MO-US19330.
 PR 17-SEP-1998; 98MO-US19437.
 PR 01-DEC-1998; 98MO-US25108.
 PR 08-SEP-1999; 99MO-US20594.
 PR 13-SEP-1999; 99MO-US20944.
 PR 15-SEP-1999; 99MO-US21090.
 PR 15-SEP-1999; 99MO-US21547.
 PR 05-OCT-1999; 99MO-US23089.
 PR 29-NOV-1999; 99MO-US28214.
 PR 30-NOV-1999; 99MO-US28313.
 PR 01-DEC-1999; 99MO-US28301.
 PR 02-DEC-1999; 99MO-US28564.
 PR 02-DEC-1999; 99MO-US28565.
 PR 16-DEC-1999; 99MO-US30095.
 PR 20-DEC-1999; 99MO-US30911.
 PR 05-JAN-2000; 2000MO-US00219.
 PR 11-FEB-2000; 2000MO-US03565.
 PR 22-FEB-2000; 2000MO-US04414.
 PR 24-FEB-2000; 2000MO-US05004.
 PR 02-MAR-2000; 2000MO-US05841.
 PR 20-MAR-2000; 2000MO-US07377.
 PR 30-MAR-2000; 2000MO-US08439.
 PR 22-MAY-2000; 2000MO-US14042.
 PR 02-JUN-2000; 2000MO-US15264.
 PR 28-JUL-2000; 2000MO-US20710.
 PR 24-AUG-2000; 2000MO-US23328.
 PR 17-SEP-1997; 97US-059113P.
 PR 17-SEP-1997; 97US-059115P.
 PR 17-SEP-1997; 97US-059117P.
 PR 17-SEP-1997; 97US-059119P.
 PR 17-SEP-1997; 97US-059121P.
 PR 17-SEP-1997; 97US-059122P.
 PR 17-SEP-1997; 97US-059184P.
 PR 18-SEP-1997; 97US-059263P.
 PR 18-SEP-1997; 97US-059266P.
 PR 15-OCT-1997; 97US-062185P.
 PR 17-OCT-1997; 97US-062285P.

PR 17-OCT-1997; 97US-062287P.
 PR 21-OCT-1997; 97US-063486P.
 PR 24-OCT-1997; 97US-062814P.
 PR 24-OCT-1997; 97US-062816P.
 PR 24-OCT-1997; 97US-063045P.
 PR 24-OCT-1997; 97US-063120P.
 PR 24-OCT-1997; 97US-063121P.
 PR 24-OCT-1997; 97US-063127P.
 PR 24-OCT-1997; 97US-063128P.
 PR 27-OCT-1997; 97US-063327P.
 PR 27-OCT-1997; 97US-063329P.
 PR 28-OCT-1997; 97US-063541P.
 PR 28-OCT-1997; 97US-063542P.
 PR 28-OCT-1997; 97US-063544P.
 PR 28-OCT-1997; 97US-063549P.
 PR 28-OCT-1997; 97US-063550P.
 PR 28-OCT-1997; 97US-063564P.
 PR 29-OCT-1997; 97US-063435P.
 PR 29-OCT-1997; 97US-063704P.
 PR 29-OCT-1997; 97US-063732P.
 PR 29-OCT-1997; 97US-063734P.
 PR 29-OCT-1997; 97US-063735P.
 PR 29-OCT-1997; 97US-063738P.
 PR 29-OCT-1997; 97US-064215P.
 PR 31-OCT-1997; 97US-063870P.
 PR 31-OCT-1997; 97US-064103P.
 PR 03-NOV-1997; 97US-064248P.
 PR 07-NOV-1997; 97US-064809P.
 PR 12-NOV-1997; 97US-065186P.
 PR 17-NOV-1997; 97US-065846P.
 PR 18-NOV-1997; 97US-065693P.
 PR 21-NOV-1997; 97US-066120P.
 PR 21-NOV-1997; 97US-066364P.
 PR 24-NOV-1997; 97US-066453P.
 PR 24-NOV-1997; 97US-066466P.
 PR 24-NOV-1997; 97US-066511P.
 PR 24-NOV-1997; 97US-066770P.
 PR 24-NOV-1997; 97US-066772P.
 PR 25-NOV-1997; 97US-066840P.
 PR 12-DEC-1997; 97US-069425P.
 PR 04-JUN-1998; 98US-068026P.
 PR 10-SEP-1998; 98US-099803P.
 PR 14-SEP-1998; 98US-100262P.
 PR 17-SEP-1998; 98US-100858P.
 PR 13-OCT-1998; 98US-104080P.
 PR 20-NOV-1998; 98US-109304P.
 PR 22-DEC-1998; 98US-113296P.
 PR 07-JUL-1999; 99US-143048P.
 PR 26-JUL-1999; 99US-145698P.
 PR 28-JUL-1999; 99US-146222P.
 PR 18-SEP-2000; 2000US-0665350.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Ashkenazi A, Bongstein D, Desnoyers L, Baton DL, Ferrara N;
 PI Filvaroff E, Fong S, Gao W, Garber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavich IJ;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PM, Wood WI;
 XX
 XX WPI; 2003-341586/32.
 DR P-PSDB; ABU69662.
 XX
 XX
 PT New PRO polypeptides and nucleic acid molecules, useful in diagnosing
 PT or treating inflammatory diseases, organ failure, atherosclerosis,
 PT cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or
 PT Parkinson's disease -
 XX
 XX Claim 2; Fig 83; 473pp; English.
 PS
 XX
 CC The invention describes sixty one nucleic acids encoding PRO polypeptides
 CC (secreted and transmembrane). The PRO polypeptides and nucleic acids are
 CC useful in diagnosing or treating enterocolitis, gastrointestinal

CC ulceration, skin diseases associated with abnormal keratinocyte
CC differentiation, e.g. psoriasis or epithelial cancers such as squamous
CC cell carcinoma, Alzheimer's disease, Parkinson's disease, amyotrophic
CC lateral sclerosis, inflammatory diseases, e.g. rheumatoid arthritis,
CC asthma or multiple sclerosis, organ failure, atherosclerosis, cardiac
CC injury, infertility, birth defects, premature aging, AIDS, cancer,
CC diabetic complications, or mutations in general. The polypeptides are
CC also useful for wound repair and associated therapies concerned with
CC re-growth of tissue. The PRO polypeptides and nucleic acid molecules
CC are also useful in gene therapy, and as molecular weight markers for
CC protein electrophoresis purposes. The anti-PRO antibodies may be used
CC in diagnostic assays for PRO, or for the affinity purification of PRO
CC from recombinant cell culture or natural sources. This sequence
CC encodes a novel human PRO polypeptide.

XX Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;

Query Match 100.0%; Score 2586; DB 25; Length 2586;

Best Local Similarity 100.0%; Pred. No. 0; Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CGCGCGCTCCGCGACCGCGCGCCGCCACCGCGCGCTCCCGCATCTGACCCGCGAGC 60
QY 61 CGCGCGCGCTCCGCGCGCGAGCGAGCATCTGACCGCGCGCGCATCTGAGTCCA 120
DB 61 CGCGCGCGCTCCGCGCGCGAGCGAGCATCTGACCGCGCGCGCATCTGAGTCCA 120
QY 121 GTGCGGCGCGCGCGCTGCGGCGCGAGCGAGCATCTGAGTCCA 180
DB 121 GTGCGGCGCGCGCGCTGCGGCGCGAGCGAGCATCTGAGTCCA 180
QY 181 GCGTGTCTGCGGCGCGCGCTGCGGCGCGAGCGAGCATCTGAGTCCA 240
DB 181 GCGTGTCTGCGGCGCGCGCTGCGGCGCGAGCGAGCATCTGAGTCCA 240
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DB 241 CTCAGTCAAGCGCGCGCGCGCTGCGGCGCGAGCGAGCATCTGAGTCCA 300
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DB 481 ATGTGACCGAGAAATTCAGAAATTAACAGCAACAGAGTGAACCTGTTTCA 540
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DB 541 AGACAGTTATCAATCTGTGGAGAGCAAGAGGCAAGAGTGAACCTG 600
QY 601 ACAGAGATCTGTGGAGAGCAAGAGTGAACCTGTTTCAAGCTGCACTG 660
DB 601 ACAGAGATCTGTGGAGAGCAAGAGTGAACCTGTTTCAAGCTGCACTG 660
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QY 721 GTGTCTGCGGCTACCTGACCAAAATGAGCAACGAGGCGAGCAATGAGGACCATCTG 780
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QY 841 TGTGACACCCCTGCGCGCGAGGAGGAGTGTGCAATGACCCCGCAGCGGCTTGG 900
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DB 1081 TTTGAGAGCTTCAATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
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QY 1201 TTTAGATCTGAGACGAGCTGTGGGTAGATGTGCAATGAGGAGGAGGAGGAGGAG 1260
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QY 1321 TCCCTCTGAGCTTGAAGAGTGAAGTGTGCAATTTGTTCAAGCTCCCGAGCTGTT 1380
DB 1321 TCCCTCTGAGCTTGAAGAGTGAAGTGTGCAATTTGTTCAAGCTCCCGAGCTGTT 1380
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DB 1381 CCAAGCTTCAAGCTGTGCTTGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1440
QY 1441 GCGACCCCTGCAAGATTTATGCTGCTTGAAGAGTGAAGTGAAGTGAAGTGAAG 1500
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Db 301 TGTTCGCGAGGTTGAGGAACTGATGAGAGACAGCGAGACAAATTGCGCGAGCGGTTG 360
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Db 361 AAGAGATGAGGCGAG 420
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QY 541 AGACAGTTATCATCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Db 541 AGACAGTTATCATCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 601 ACGAGAGCTGTGAGGCGCGAGAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 601 ACGAGAGCTGTGAGGCGCGAGAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 CATGCGCGGCGCGAG 720
Db 661 CATGCGCGGCGCGAG 720
QY 721 GTGTCTGAGGCTGATGCAACCAAAATGCGCACCGAGGCGAGCAATGAGCACTGTGACA 780
Db 721 GTGTCTGAGGCTGATGCAACCAAAATGCGCACCGAGGCGAGCAATGAGCACTGTGACA 780
QY 781 ACCAG 840
Db 781 ACCAG 840
QY 841 TGTGACACACCTGCGCGAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
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QY 901 ACCTATACCTCTGAG 960
Db 901 ACCTATACCTCTGAG 960
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Db 961 GCTCTCTGCGAGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
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Db 1021 GAGAGCGGTGACCAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1081 TTGGCAGCTTCACTGAG 1140
Db 1081 TTGGCAGCTTCACTGAG 1140
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Db 1441 GCCACCCCTGTCAGATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
QY 1501 TCTACATGAGCTTGAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Db 1501 TCTACATGAGCTTGAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
QY 1561 TGAATGAGTTTGGGAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
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Db 1741 GTGTGCTGAGCTTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
QY 1801 TCTCTGAGCAGAGCTGAG 1860
Db 1801 TCTCTGAGCAGAGCTGAG 1860
QY 1861 GCTCAG 1920
Db 1861 GCTCAG 1920
QY 1921 ATCTGTGTGAGCTTAAG 1980
Db 1921 ATCTGTGTGAGCTTAAG 1980
QY 1981 CCAAAAGTGTCCCAAAAG 2040
Db 1981 CCAAAAGTGTCCCAAAAG 2040
QY 2041 ATTAAGTCAAACTAATTTCTCACTCCCTCTAATAAGTAATCTGTTAGAGAGAGAG 2100
Db 2041 ATTAAGTCAAACTAATTTCTCACTCCCTCTAATAAGTAATCTGTTAGAGAGAGAG 2100
QY 2101 GTTCTCAGAGTGTGAGGAG 2160
Db 2101 GTTCTCAGAGTGTGAGGAG 2160
QY 2161 CTTTGGCAGTTGATTAATGATTTGAAAGATTAATGAGAGAGAGAGAGAGAGAGAGAG 2220
Db 2161 CTTTGGCAGTTGATTAATGATTTGAAAGATTAATGAGAGAGAGAGAGAGAGAGAGAG 2220
QY 2221 CTTGAG 2280
Db 2221 CTTGAG 2280

Db 301 TGTTCGCGAGGTTGAGAACTGATGAGAGACCGGACCAAAATTGCCGACGGGTGG 360
QY AAGAGATGAGGAGGAGAAAGCTGTCTAAAGCATCATCAGAAAGTGAACCTGGGAAA 420
Db 361 AAGAGATGAGGAGGAGAAAGCTGTCTAAAGCATCATCAGAAAGTGAACCTGGGAAA 420
QY 421 TACTCCGAGCTTCACTCAATGAGACCAAGACAGACGAAAGGTGGAAATAATACATCC 480
Db 421 TACTCCGAGCTTCACTCAATGAGACCAAGACAGACGAAAGGTGGAAATAATACATCC 480
QY 481 ATGTGACCGGAGAAATTCAGAAAGATTAACCAACAGACGATGGAACAAATGCTTTTGG 540
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QY 541 AGCACTTATCAATCTGTGGAGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
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QY 1201 TTTAGATCTGGAGCAGAGCTGTGGGATGATGTGCAATGAATGCTAATTTATTTCCCA 1260
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Db 1321 TCCCTCTGTGCTTGAAGAGAGTGTGTGATTTGTTCAGCTTCCAGAGGAGGAGGAGGAG 1380
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Db 1921 ATCTGATGTGACTTAAGTCAAGTGTCTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
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QY 2521 AAGTTCATTAGAAATCAAGCATTAATCACTTCAACTGCAGAAAAA 2580
DB 2521 AAGTTCATTAGAAATCAAGCATTAATCACTTCAACTGCAGAAAAA 2580
QY 2581 AAAAAA 2586
DB 2581 AAAAAA 2586
RESULT 10
AC60194
ID AC60194 standard; cDNA; 2586 BP.
AC60194;
AC ACAA0194;
XX 12-JUN-2003 (first entry)
XX
DE Human cDNA for secreted/transmembrane protein PRO25.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW gene therapy; chromosome identification; chromosome marker.
XX
OS Homo sapiens.
XX
PN US2003003530-A1.
XX
PD 02-JAN-2003.
XX
XX 11-JUL-2001; 2001US-0904011.
XX
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 01-DEC-1998; 98WO-US25108.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 05-JAN-2000; 2000WO-US00219.
PR 11-FEB-2000; 2000WO-US03565.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 22-MAY-2000; 2000WO-US14042.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 17-SEP-1997; 97US-0591133.
PR 17-SEP-1997; 97US-0591155.
PR 17-SEP-1997; 97US-0591176.
PR 17-SEP-1997; 97US-0591197.
PR 17-SEP-1997; 97US-0591212.
PR 17-SEP-1997; 97US-0591229.
PR 17-SEP-1997; 97US-0591849.
PR 18-SEP-1997; 97US-0592633.
PR 18-SEP-1997; 97US-0592666.
PR 15-OCT-1997; 97US-0621256.
PR 17-OCT-1997; 97US-0622856.
PR 17-OCT-1997; 97US-0622876.
PR 21-OCT-1997; 97US-0634866.

PR 24-OCT-1997; 97US-0628146.
PR 24-OCT-1997; 97US-0628166.
PR 24-OCT-1997; 97US-0630456.
PR 24-OCT-1997; 97US-0631206.
PR 24-OCT-1997; 97US-0631216.
PR 24-OCT-1997; 97US-0631276.
PR 24-OCT-1997; 97US-0631286.
PR 27-OCT-1997; 97US-0633276.
PR 27-OCT-1997; 97US-0633296.
PR 28-OCT-1997; 97US-0635416.
PR 28-OCT-1997; 97US-0635426.
PR 28-OCT-1997; 97US-0635446.
PR 28-OCT-1997; 97US-0635496.
PR 28-OCT-1997; 97US-0635506.
PR 28-OCT-1997; 97US-0635566.
PR 29-OCT-1997; 97US-0634356.
PR 29-OCT-1997; 97US-0637046.
PR 29-OCT-1997; 97US-0637326.
PR 29-OCT-1997; 97US-0637346.
PR 29-OCT-1997; 97US-0637356.
PR 29-OCT-1997; 97US-0637386.
PR 29-OCT-1997; 97US-0642156.
PR 31-OCT-1997; 97US-0638706.
PR 31-OCT-1997; 97US-0641036.
PR 03-NOV-1997; 97US-0642486.
PR 07-NOV-1997; 97US-0648096.
PR 12-NOV-1997; 97US-0651866.
PR 17-NOV-1997; 97US-0658466.
PR 18-NOV-1997; 97US-0656936.
PR 21-NOV-1997; 97US-0661206.
PR 21-NOV-1997; 97US-0663646.
PR 24-NOV-1997; 97US-0664536.
PR 24-NOV-1997; 97US-0664666.
PR 24-NOV-1997; 97US-0665116.
PR 24-NOV-1997; 97US-0667706.
PR 24-NOV-1997; 97US-0667726.
PR 18-SEP-2000; 2000US-0665350.
XX
XX (GENTH) GENENTECH INC.
XX
XX Ashkenazi A, Botstein D, Desnovers L, Eaton DL, Ferrara N,
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
PI Gutowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Klayman J,
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D,
PI Williams PM, Wood WI;
XX
XX WPI; 2003-329602/31.
XX
XX P-PSDB; AB071931.
XX
XX New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
PT chromosome markers, in generating probes and in tissue typing
XX
XX
XX Claim 2; Fig 83; 484pp; English.
XX
XX The invention relates to an isolated nucleic acid with at least 80%
CC nucleic acid sequence identity to a nucleotide sequence encoding one of
CC 61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a
CC PRO protein extracellular domain. Also included are a vector comprising
CC the PRO nucleic acid, a host cell comprising the vector, producing a PRO
CC polypeptide (by culturing the host cell for the expression of the PRO
CC polypeptide, and recovering the host cell from the cell culture),
CC an isolated PRO polypeptide (having at least 80% sequence identity
CC to: (a) an amino acid sequence selected from the 61 PRO proteins;
CC (b) an amino acid sequence encoded by a nucleic acid molecule deposited
CC with an ATCC number (detailed in the specification); or (c) an
CC extracellular domain of a PRO polypeptide or to a PRO polypeptide lacking
CC its associated signal peptide), a chimeric molecule comprising a PRO
CC polypeptide of fused to a heterologous amino acid sequence, an anti-PRO
CC antibody, detecting a PRO245 or PRO186 in a sample suspected of
CC containing the polypeptide, linking a bioactive molecule to a cell
CC expressing a PRO245 or PRO186 and modulating at least one biological
CC activity of a cell expressing a PRO245 or PRO186. Nucleic acids which


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QY 1921 ATCTGGTGTGACTTAAGCTCAGTGTCTCTCCACTACCCACACAGCCTTGTCGA 1980
DB 1921 ATCTGGTGTGACTTAAGCTCAGTGTCTCTCCACTACCCACACAGCCTTGTCGA 1980
QY 1981 CCAAAAGTGTCTCCCAAAAGGAGAGAAATGGGATTTTCTTGAAGCATGCACTGTGA 2040
DB 1981 CCAAAAGTGTCTCCCAAAAGGAGAGAAATGGGATTTTCTTGAAGCATGCACTGTGA 2040
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DB 2041 ATTAAGGTCAAACTAATTTCTCACATCCCTCTAAAAGTAACCTAGTGAACAAGCAGT 2100
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DB 2101 GTTCTCAGAGTGGGGGAGCGCTCTCTTAATGAAGACATATATTTGACACTGTCCCT 2160
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DB 2161 CTTTGGCAGTTGCACTAGTAATTTGAAAAGTATATGACTGAGCGATACAGGTTAA 2220
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DB 2341 TGTGTGAACAGTGTGTATATATGCGATGCGAACACTGAACCTTAACGCGCACTCCACAAA 2400
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DB 2401 TGAATGTTTAAAGTGTGCATGAGCACTGTTGCCACATGATTTCAACCCGAGTTCTTAAGTT 2460
QY 2461 TAAAGTTGACATGATTTGTAATGAACATGCTTTCTTGAAGTTTAAATTAATTAACAT 2520
DB 2461 TAAAGTTGACATGATTTGTAATGAACATGCTTTCTTGAAGTTTAAATTAATTAACAT 2520
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DB 2521 AAAGTTGATTTAAGATTAACAGCATTAATCACTTCAACTGCAAAAAA 2580
QY 2581 AAAAAA 2586
DB 2581 AAAAAA 2586

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XX (GETH ) GENENTECH INC.
PA Eaton DL, Filvarcoff E, Gerritsen ME, Goddard A, Godowski PJ,
XX Grimaldi JC, Guiney AL, Watanabe CK, Wood WI,
PI WPI, 2003-330984/31.
XX P-PSDB; ABU71955.
DR
XX New secreted and transmembrane PRO polypeptides and nucleic acid
XX molecules encoding the polypeptides, useful in gene therapy or
XX PT preparing a medicament for treating a condition that is responsive to
XX the PRO polypeptide or antibody
XX
XX Disclosure; Fig 7; 409pp; English.
XX
XX The invention describes novel isolated PRO polypeptides. The PRO
XX polypeptides or anti-PRO antibodies are useful in preparing a medicament
XX for treating a condition that is responsive to the PRO polypeptide or
XX antibody. The PRO nucleotide sequences may be used as hybridisation
XX probes in chromosome and gene mapping, or in generating antisense RNA
XX and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides,
XX in assays to identify other proteins or molecules involved in binding
XX reaction, to generate transgenic animals or knockout animals, which in
XX turn are useful in the development and screening of therapeutically
XX useful reagents, for chromosome identification, and tissue typing. The
XX PRO polypeptides and nucleic acid molecules are also useful in gene
XX therapy, and as molecular weight markers for protein electrophoresis
XX purposes. The anti-PRO antibodies may be used in diagnostic assays for
XX PRO, or for the affinity purification of PRO from recombinant cell
XX culture or natural sources. This sequence encodes a novel human
XX secreted and transmembrane PRO polypeptide.
XX
XX Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 2586; DB 25; Length 2586;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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D	541	AGACAGTTATCACTCTGTGGGAGACGAAGAAGCCAGAAGCCACGATGCATCATCG	600
Q	601	ACAGAGACTGTGGGCCAGACATGATACAGTTTGACAGTTTCCAGTATCACTCGCCAGC	660
D	601	ACAGAGACTGTGGGCCAGACATGATACAGTTTGACAGTTTCCAGTATCACTCGCCAGC	660
Q	661	CATGCCGGGSCCAGAGGATGCTTGCACCCGGGACAGTGAETGCTGTGGAGACCACTGT	720
D	661	CATGCCGGGSCCAGAGGATGCTTGCACCCGGGACAGTGAETGCTGTGGAGACCACTGT	720
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D	901	ACCTCATCACCTTGGAGACTAGAGCCTATGAGAGCCTTGAAACCAATGCCCTTGTGCCAGTG	960
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D	961	GCTCTCTCTGCGACGCCCAACGCCACAGCTGTGTATGTGTGCAAGCCGACTTCGTGG	1020
Q	1021	GGAGCCGTGACCAAGATGGGGAGATCTGTGCTGCCACAGAGAGTCCCGCATAGATGAAG	1080
D	1021	GGAGCCGTGACCAAGATGGGGAGATCTGTGCTGCCACAGAGAGTCCCGCATAGATGAAG	1080
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D	1081	TTGGCAGCTTCATGGAAGAGGTGCGCCAGAGACTGGAAGACCTGGAAGAGAGCTTGACTG	1140
Q	1141	AAGAGATGGGCGCTGGGGGAGCCTGCGGTGCGCGCGTGCACCTGTGGGAGAGGGAGAAGA	1200
D	1141	AAGAGATGGGCGCTGGGGGAGCCTGCGGTGCGCGCGTGCACCTGTGGGAGAGGGAGAAGA	1200
Q	1201	TTTAGATCTGAGACCAGGCTGTGGGTAGATGTGCAATAGAAATAGACTAATTTATTTCCCA	1260
D	1201	TTTAGATCTGAGACCAGGCTGTGGGTAGATGTGCAATAGAAATAGACTAATTTATTTCCCA	1260
Q	1261	GGTGTGTGCTTTAGCGCTGGGCTGACACAGAGCTTCTCTTAATCATCTTCTTCCAGTAAGTT	1320
D	1261	GGTGTGTGCTTTAGCGCTGGGCTGACACAGAGCTTCTCTTAATCATCTTCTTCCAGTAAGTT	1320
Q	1321	TCCCTCTGTGCTTACACAGCATGAGAGTGTGTGCAATTTGTTCAAGCTGCCCCAGCGTGTCT	1380
D	1321	TCCCTCTGTGCTTACACAGCATGAGAGTGTGTGCAATTTGTTCAAGCTGCCCCAGCGTGTCT	1380
Q	1381	CCAGGCTTCACAGTCTGTGCTTTGGAGAGATCAGGACAGGTTAAATCTGACAGAGCATTT	1440
D	1381	CCAGGCTTCACAGTCTGTGCTTTGGAGAGATCAGGACAGGTTAAATCTGACAGAGCATTT	1440
Q	1441	GCCACCCCTGTCCAGATATATGGCTGTCTCTCTACCAAGTTGGCAGACAGCCGTTGT	1500
D	1441	GCCACCCCTGTCCAGATATATGGCTGTCTCTCTCTACCAAGTTGGCAGACAGCCGTTGT	1500
Q	1501	TCTACATGTGCTTTGATTAATTTGTTGAGGGAGAGATGGAACAATGTGAGTCTTCCTC	1560
D	1501	TCTACATGTGCTTTGATTAATTTGTTGAGGGAGAGATGGAACAATGTGAGTCTTCCTC	1560
Q	1561	TGATTTGGTTTGGGGAAATGTGGAGAAAGTCCCTGTTTGCAAAACATCAACTCGGCAA	1620
D	1561	TGATTTGGTTTGGGGAAATGTGGAGAAAGTCCCTGTTTGCAAAACATCAACTCGGCAA	1620

QY	1622	AAATGCAACAATGAAATTTTCCAGCAGATCTTTTCAATGGGAGATAGATAGCTTGACCTT	1680
Db	1621	AAATGCAACAATGAAATTTTCCAGCAGATCTTTTCAATGGGAGATAGATAGCTTGACCTT	1680
QY	1681	CAGCTTTGCAGATGAAATGTTCTGTTCACCTTGATTAACATGTGTATTTATTCACAGA	1740
Db	1681	CAGCTTTGCAGATGAAATGTTCTGTTCACCTTGATTAACATGTGTATTTATTCACAGA	1740
QY	1741	GGTGTCTCAGCTCCCACTCTGTGCGAGGGAGCATTTTCAATCCAAAGATCAATCCC	1800
Db	1741	GGTGTCTCAGCTCCCACTCTGTGCGAGGGAGCATTTTCAATCCAAAGATCAATCCC	1800
QY	1801	TCTCTCAGCAACAGCTGGGAGGGAGGTCAATTGTTCTCTGTCCATCAGGATCTCAGAG	1860
Db	1801	TCTCTCAGCAACAGCTGGGAGGGAGGTCAATTGTTCTCTGTCCATCAGGAGTCTCAGAG	1860
QY	1861	GCCTCAGACGTCGACAGCTGCTTGCCCAATCACAACAGCTAGTGAAGACACAGACAGTTTC	1920
Db	1861	GCCTCAGACGTCGACAGCTGCTTGCCCAATCACAACAGCTAGTGAAGACACAGACAGTTTC	1920
QY	1921	ATCTGTTGTACTCTTAAGCTCAGTGTCTCTTCCACTACCCCAACACAGCCTTGTCGA	1980
Db	1921	ATCTGTTGTACTCTTAAGCTCAGTGTCTCTTCCACTACCCCAACACAGCCTTGTCGA	1980
QY	1981	CCAAAAGTGCTCCCAAAGGAGAGGAAATGGAGATTTTCTTGAGGCAATGCATCTGGA	2040
Db	1981	CCAAAAGTGCTCCCAAAGGAGAGGAAATGGAGATTTTCTTGAGGCAATGCATCTGGA	2040
QY	2041	ATTAAAGTCAAACTAATCTCAACATCCCTCTAAAGTAACTACTGTAGGAACAGCACT	2100
Db	2041	ATTAAAGTCAAACTAATCTCAACATCCCTCTAAAGTAACTACTGTAGGAACAGCACT	2100
QY	2101	GTTCTCAGAGTGAGGAGCAGCGCTCTTCTTAATGAAGACAATGATATTCAACTGTCCCT	2160
Db	2101	GTTCTCAGAGTGAGGAGCAGCGCTCTTCTTAATGAAGACAATGATATTCAACTGTCCCT	2160
QY	2161	CTTTGGCAGTTGCATTAATGTAACCTTTGAANAGTAAATGACTGAGCGTAGATCAGGTTAA	2220
Db	2161	CTTTGGCAGTTGCATTAATGTAACCTTTGAANAGTAAATGACTGAGCGTAGATCAGGTTAA	2220
QY	2221	CTTGCGAAGAACAGTACTTAAAGTAAATGTAGGAGCGAGGATTAATAATGAATTTGCCAAAT	2280
Db	2221	CTTGCGAAGAACAGTACTTAAAGTAAATGTAGGAGCGAGGATTAATAATGAATTTGCCAAAT	2280
QY	2281	CACCTAGCAGCACTGAAGACAATTAACAACAACGTCGAGAAATCAACCGAGCAGGGCC	2340
Db	2281	CACCTAGCAGCACTGAAGACAATTAACAACAACGTCGAGAAATCAACCGAGCAGGGCC	2340
QY	2341	TGTGTGAACAATGATGTTGAATATGAGCAGTCGCAACACTGAACCTTAAGCACTCCGACAA	2400
Db	2341	TGTGTGAACAATGATGTTGAATATGAGCAGTCGCAACACTGAACCTTAAGCACTCCGACAA	2400
QY	2401	TGATGTTTCAAGTGTCAATGAGACTGTGCGAACCATGATTAATCCAGAGTTCTTAAAGTT	2460
Db	2401	TGATGTTTCAAGTGTCAATGAGACTGTGCGAACCATGATTAATCCAGAGTTCTTAAAGTT	2460
QY	2461	TAAAGTTGCACTGATGTGTAATAGCATGCTTCTTGAAGTTTAAATATGTAATAACAT	2520
Db	2461	TAAAGTTGCACTGATGTGTAATAGCATGCTTCTTGAAGTTTAAATATGTAATAACAT	2520
QY	2521	AAAGTTGATTTAGAAATCAAGCACTTAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAA	2580
Db	2521	AAAGTTGATTTAGAAATCAAGCACTTAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAA	2580
QY	2581	AAAAAA 2586	
Db	2581	AAAAAA 2586	

RESULT 12
ACA63376
ID ACA63376 standard; cDNA; 2586 BP.

Dh	138	CCAGGCTTCAACAGCTGCTGTGCTTGGAGAGTCAAGCAGGGGTTAACTGACAGAGCAAGTTT	144h
Qy	144i	GCCACCCCTGTCCAGATATTATGGCTGCTTTGGCTCTACAGTTGGGAGACAGCCGTTTGT	150i
Dh	144i	GCCACCCCTGTCCAGATATTATGGCTGCTTTGGCTCTACAGTTGGGAGAGAGCTTGT	150i
Qy	150i	TCTACATGGCTTTGATATAATGTTTTAGGGGAGAGATGTAACAAATGAGTCTCCCTC	156i
Dh	150i	TCTACATGGCTTTGATATAATGTTTTAGGGGAGAGATGTAACAAATGAGTCTCCCTC	156i
Qy	156i	TGATTTGGTTTTGGGGAAAATGTGAGAGAGAGGCCCTGTTTGCAAACTCAACTGGCA	162i
Dh	156i	TGATTTGGTTTTGGGGAAAATGTGAGAGAGAGGCCCTGTTTGCAAACTCAACTGGCA	162i
Qy	162i	AAATGCCAACAAATGMAATTTTCCAGCAGTTCTTTCCATGGCATAGTAACTGTGCTT	168i
Dh	162i	AAATGCCAACAAATGMAATTTTCCAGCAGTTCTTTCCATGGCATAGTAACTGTGCTT	168i
Qy	168i	CAGCTGTTGCAGATGAAATGTCTGTTCCACCTGATACATGTTGTTATTCATCCAGCA	174i
Dh	168i	CAGCTGTTGCAGATGAAATGTCTGTTCCACCTGATACATGTTGTTATTCATCCAGCA	174i
Qy	174i	GTTGTTGCTCAGCTCCTACCTCTGTGCCAGGAGAGCAATTTTCAATCCAGATCAATTC	180i
Dh	174i	GTTGTTGCTCAGCTCCTACCTCTGTGTGCCAGGAGAGCAATTTTCAATCCAGATCAATTC	180i
Qy	180i	TCTCTCCAGCAAGCTGGGGAGGGGGATGTTCTCCTGTCATCAGAGATCTCAGAG	186i
Dh	180i	TCTCTCCAGCAAGCTGGGGAGGGGGATGTTCTCCTGTCATCAGAGATCTCAGAG	186i
Qy	186i	GCTCAGAGACTGCAAGCTGTTGCCCAAGTCACACAGCTAATGAAAGCAGAGCAGTTTC	192i
Dh	186i	GCTCAGAGACTGCAAGCTGTTGCCCAAGTCACACAGCTAATGAAAGCAGAGCAGTTTC	192i
Qy	192i	ATCTGTTGTGATCTTAAGCTCAGTGCCTCTCCACTACCCCAACAGCCTTGATGCA	198i
Dh	192i	ATCTGTTGTGATCTTAAGCTCAGTGCCTCTCCACTACCCCAACAGCCTTGATGCA	198i
Qy	198i	CCAAAAGTGTCCCCCAAAAAGGAGAGATGGATTTTCTTGAAGCATGCAACTTGA	204i
Dh	198i	CCAAAAGTGTCCCCCAAAAAGGAGAGATGGATTTTCTTGAAGCATGCAACTTGA	204i
Qy	204i	ATTAAAGTCAAACCTAATTTCTCAACATCCCTCTAAAGTAACTACCTGTAGGAACAGCAGT	210i
Dh	204i	ATTAAAGTCAAACCTAATTTCTCAACATCCCTCTAAAGTAACTACCTGTAGGAACAGCAGT	210i
Qy	210i	GTTCTCACAGTGTGGGAGCCGCTCTTCTAATGAAGCAATGATATGACACGTCCCT	216i
Dh	210i	GTTCTCACAGTGTGGGAGCCGCTCTTCTAATGAAGCAATGATATGACACGTCCCT	216i
Qy	216i	CTTTGGCAGTTGCATTAAGTAATCTTGAAGGAATGATGATGAGGTAGCATACAGTTAA	222i
Dh	216i	CTTTGGCAGTTGCATTAAGTAATCTTGAAGGAATGATGATGAGGTAGCATACAGTTAA	222i
Qy	222i	CCTGCAGAAACGTACTTAGGTAATTTGAGGCGAGATTTAAATGMAATTTTCAAAAT	228i
Dh	222i	CCTGCAGAAACGTACTTAGGTAATTTGAGGCGAGATTTAAATGMAATTTTCAAAAT	228i
Qy	228i	CACCTTAGCAGCACTGAGACAAATTAATCAACCTGAGAGAAATCAAAACGAGACAGGCG	234i
Dh	228i	CACCTTAGCAGCACTGAGACAAATTAATCAACCTGAGAGAAATCAAAACGAGACAGGCG	234i
Qy	234i	TGTGTGAAAACATGTTGTAATATGCGACTGGAACCTGAACCTGACGCCCTGCACAA	240i
Dh	234i	TGTGTGAAAACATGTTGTAATATGCGACTGGAACCTGAACCTGACGCCCTGCACAA	240i
Qy	240i	TGATGTTTTCAAGGTGATGAGTGTGATTAAGAGTCTTTCTTGAAGTTTAAATTAATTAACAT	246i
Dh	240i	TGATGTTTTCAAGGTGATGAGTGTGATTAAGAGTCTTTCTTGAAGTTTAAATTAATTAACAT	246i
Qy	246i	TAAAGTGCACATGATTTGTAATTAAGAGTCTTTCTTGAAGTTTAAATTAATTAACAT	252i
Dh	246i	TAAAGTGCACATGATTTGTAATTAAGAGTCTTTCTTGAAGTTTAAATTAATTAACAT	252i

YY		2521	AAGTGCATTGAGAATCAACAAATGAATCCTTCACCTGCAAAAAAAAAAAAAA	2586
DB		2521	AAGTGCATTGAGAATCAACAAATGAATCCTTCACCTGCAAAAAAAAAAAAAA	2586
QY		2581	AAAAA	2586
Db		2581	AAAAA	2586
<hr/>				
		RESULT 13		
ID		ACA05532		
XX		ACA05532 standard; cDNA, 2586 BP.		
XX		ACA05532;		
AC				
DT		29-MAY-2003	(first entry)	
XX				
DE		cDNA encoding human secreted protein PRO295.		
KX		Human; gene therapy; mucosal lesion; ulcer; enterocolitis; skin disease;		
KW		psoriasis; cancer; lung cancer; colon cancer; nerve cell disease;		
KM		Alzheimer's disease; Parkinson's disease; Usher syndrome; angiogenesis;		
KX		atrophia areata; inflammatory disease; asthma; rheumatoid arthritis;		
KX		ischaemia; ss; gene.		
OS		Homo sapiens.		
XX		US2003023054-A1.		
PN				
PD		30-JAN-2003.		
XX				
PF		16-JUL-2001; 2001US-0906742.		
XX				
ER		10-SEP-1998; 98WO-US18824.		
FR		14-SEP-1998; 98WO-US19177.		
PR		16-SEP-1998; 98WO-US19330.		
PR		17-SEP-1998; 98WO-US19437.		
PR		01-DEC-1998; 98WO-US21108.		
PR		08-SEP-1999; 99WO-US20594.		
PR		13-SEP-1999; 99WO-US20944.		
PR		15-SEP-1999; 99WO-US21090.		
PR		15-SEP-1999; 99WO-US21547.		
PR		05-OCT-1999; 99WO-US23089.		
PR		29-NOV-1999; 99WO-US28214.		
PR		30-NOV-1999; 99WO-US28313.		
PR		01-DEC-1999; 99WO-US28301.		
PR		02-DEC-1999; 99WO-US28564.		
PR		02-DEC-1999; 99WO-US28565.		
PR		16-DEC-1999; 99WO-US30099.		
PR		20-DEC-1999; 99WO-US30911.		
PR		20-DEC-1999; 99WO-US30999.		
PR		05-JAN-2000; 2000WO-US00219.		
PR		11-FEB-2000; 2000WO-US03565.		
PR		22-FEB-2000; 2000WO-US04414.		
PR		24-FEB-2000; 2000WO-US05004.		
PR		02-MAR-2000; 2000WO-US05841.		
PR		20-MAR-2000; 2000WO-US07377.		
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PR		28-JUL-2000; 2000WO-US20710.		
PR		24-AUG-2000; 2000WO-US23328.		
PR		17-SEP-1997; 97US-059113B.		
PR		17-SEP-1997; 97US-059115B.		
PR		17-SEP-1997; 97US-059117B.		
PR		17-SEP-1997; 97US-059119B.		
PR		17-SEP-1997; 97US-059121B.		
PR		17-SEP-1997; 97US-059122B.		
PR		17-SEP-1997; 97US-059184B.		
PR		18-SEP-1997; 97US-059263B.		
PR		18-SEP-1997; 97US-059266B.		
PR		15-OCT-1997; 97US-062125B.		

17-OCT-1997; 97US-062285P.
 PR 17-OCT-1997; 97US-062287P.
 PR 21-OCT-1997; 97US-063486P.
 PR 24-OCT-1997; 97US-062814P.
 PR 24-OCT-1997; 97US-062816P.
 PR 24-OCT-1997; 97US-063045P.
 PR 24-OCT-1997; 97US-063120P.
 PR 24-OCT-1997; 97US-063121P.
 PR 24-OCT-1997; 97US-063127P.
 PR 24-OCT-1997; 97US-063128P.
 PR 27-OCT-1997; 97US-063327P.
 PR 27-OCT-1997; 97US-063329P.
 PR 28-OCT-1997; 97US-063541P.
 PR 28-OCT-1997; 97US-063542P.
 PR 28-OCT-1997; 97US-063544P.
 PR 28-OCT-1997; 97US-063549P.
 PR 28-OCT-1997; 97US-063550P.
 PR 28-OCT-1997; 97US-063564P.
 PR 29-OCT-1997; 97US-063435P.
 PR 29-OCT-1997; 97US-063704P.
 PR 29-OCT-1997; 97US-063722P.
 PR 29-OCT-1997; 97US-063734P.
 PR 29-OCT-1997; 97US-063735P.
 PR 29-OCT-1997; 97US-063738P.
 PR 29-OCT-1997; 97US-064215P.
 PR 31-OCT-1997; 97US-063870P.
 PR 31-OCT-1997; 97US-064103P.
 PR 03-NOV-1997; 97US-064248P.
 PR 07-NOV-1997; 97US-064809P.
 PR 12-NOV-1997; 97US-065186P.
 PR 17-NOV-1997; 97US-065846P.
 PR 18-NOV-1997; 97US-065693P.
 PR 21-NOV-1997; 97US-066120P.
 PR 21-NOV-1997; 97US-066434P.
 PR 24-NOV-1997; 97US-066453P.
 PR 24-NOV-1997; 97US-066466P.
 PR 24-NOV-1997; 97US-066511P.
 PR 24-NOV-1997; 97US-066770P.
 PR 24-NOV-1997; 97US-066772P.
 PR 25-NOV-1997; 97US-066840P.
 PR 12-DEC-1997; 97US-069425P.
 PR 04-JUN-1998; 98US-088026P.
 PR 10-SEP-1998; 98US-099803P.
 PR 14-SEP-1998; 98US-100282P.
 PR 17-SEP-1998; 98US-100858P.
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 PR 20-NOV-1998; 98US-109304P.
 PR 22-DEC-1998; 98US-113296P.
 PR 07-JUL-1999; 99US-143048P.
 PR 26-JUL-1999; 99US-145698P.
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 PR 18-SEP-2000; 2000US-0665350.

(GETH) GENENTECH INC.

PI Ashkenazi A, Botstein D, Desnoyers L, Baton DL, Ferrara N,
 PI Rilyavoff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
 PI Godowski PJ, Grimaldi UC, Gurney AL, Hillan KJ, Kijavini IJ,
 PI Mather JF, Pan J, Paoni NF, Roy WA, Stewart TA, Tumas D,
 PI Williams PM, Wood WI,
 XX WPI; 2003-331485/31.
 DR P-PSDB; AB067385.

XX Sixty one isolated nucleic acids encoding a PRO polypeptide, e.g.
 PT PRO245 or PRO1868, useful in chromosome and gene mapping, in generating
 PT antisense RNA and DNA, and in treating cancer and Alzheimer's disease -
 XX Example 38; Fig 83; 481pp; English.

XX The invention relates to sixty one nucleic acids encoding PRO
 CC polypeptides (secreted and transmembrane). The polynucleotide is useful
 CC in molecular biology, including uses as hybridisation probes, in

CC chromosome and gene mapping, in generating antisense RNA and DNA, and in
 CC gene therapy. The polynucleotide may also be used in preparing PRO
 CC polypeptides by recombinant techniques, and in generating either
 CC transgenic animals or knock-out animals which, in turn, are useful in the
 CC development and screening of therapeutically useful reagents. The PRO
 CC polypeptide or the antibody is used in preparing a medicament for
 CC treating a condition responsive to the polypeptide or antibody, such as
 CC mucosal lesions e.g. ulcers and enterocolitis, skin disease e.g.
 CC psoriasis, cancer e.g. lung cancer and colon cancer, nerve cell disease
 CC e.g. Alzheimer's disease and Parkinson's disease, Usher syndrome,
 CC atrophial areata, angiogenesis, inflammatory disease e.g. asthma and
 CC rheumatoid arthritis, ischaemia, and in various diagnostic assays. The
 CC present sequence represents an cDNA which encodes a PRO polypeptide.

XX Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;

Query Match 100.0%; Score 2586; DB 25; Length 2586;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGCGCTCCCGACCCCGGCGCCCGCCACCGCGCGCTCCCGCATCTGCACCCGAGC 60
 DB 1 CGCGGCGCTCCCGACCCCGGCGCCCGCCACCGCGCGCTCCCGCATCTGCACCCGAGC 60
 QY 61 CGCGGCGCTCCCGGCGGAGCGAGCATCCAGTCCGCGCCCGCAGCGCACTCGTCCA 120
 DB 61 CGCGGCGCTCCCGGCGGAGCGAGCATCCAGTCCGCGCCCGCAGCGCACTCGTCCA 120
 QY 121 GTGCGGCGCGCGCGGTGTGGGCGCGAGCGAGCATCGACGCGCTTTGGGCGCACTCGTGT 180
 DB 121 GTGCGGCGCGCGCGGTGTGGGCGCGAGCGAGCATCGACGCGCTTTGGGCGCACTCGTGT 180
 QY 121 GTGCGGCGCGCGCGGTGTGGGCGCGAGCGAGCATCGACGCGCTTTGGGCGCACTCGTGT 180
 DB 121 GTGCGGCGCGCGCGGTGTGGGCGCGAGCGAGCATCGACGCGCTTTGGGCGCACTCGTGT 180
 QY 181 GCCTGCTGCTGCGCGCGCGCGGTGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
 DB 181 GCCTGCTGCTGCGCGCGCGCGGTGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
 QY 181 GCCTGCTGCTGCGCGCGCGCGGTGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
 DB 181 GCCTGCTGCTGCGCGCGCGCGGTGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
 QY 241 CTCGAGTCAAGCCCGCGCGCGCTCTCACTGACCGCGAGAGAGCGCCATCAATAGA 300
 DB 241 CTCGAGTCAAGCCCGCGCGCGCTCTCACTGACCGCGAGAGAGCGCCATCAATAGA 300
 QY 241 CTCGAGTCAAGCCCGCGCGCGCTCTCACTGACCGCGAGAGAGCGCCATCAATAGA 300
 DB 241 CTCGAGTCAAGCCCGCGCGCGCTCTCACTGACCGCGAGAGAGCGCCATCAATAGA 300
 QY 301 TGTTCGCGAGGTGAGGAAGTGTGAGGAGCAGCGCAAAATTGCGAGCGCGGTGG 360
 DB 301 TGTTCGCGAGGTGAGGAAGTGTGAGGAGCAGCGCAAAATTGCGAGCGCGGTGG 360
 QY 301 TGTTCGCGAGGTGAGGAAGTGTGAGGAGCAGCGCAAAATTGCGAGCGCGGTGG 360
 DB 301 TGTTCGCGAGGTGAGGAAGTGTGAGGAGCAGCGCAAAATTGCGAGCGCGGTGG 360
 QY 301 TGTTCGCGAGGTGAGGAAGTGTGAGGAGCAGCGCAAAATTGCGAGCGCGGTGG 360
 DB 301 TGTTCGCGAGGTGAGGAAGTGTGAGGAGCAGCGCAAAATTGCGAGCGCGGTGG 360
 QY 361 AAGAGATGAGGAGCAAGAAAGCTGCTCTTAAGCATATCAAGATTAACCTGCAAACT 420
 DB 361 AAGAGATGAGGAGCAAGAAAGCTGCTCTTAAGCATATCAAGATTAACCTGCAAACT 420
 QY 361 AAGAGATGAGGAGCAAGAAAGCTGCTCTTAAGCATATCAAGATTAACCTGCAAACT 420
 DB 361 AAGAGATGAGGAGCAAGAAAGCTGCTCTTAAGCATATCAAGATTAACCTGCAAACT 420
 QY 421 TACCTCCAGCTATCATATGAGCAACAAGCAAGAGTTGGAATAATACATCC 480
 DB 421 TACCTCCAGCTATCATATGAGCAACAAGCAAGAGTTGGAATAATACATCC 480
 QY 421 TACCTCCAGCTATCATATGAGCAACAAGCAAGAGTTGGAATAATACATCC 480
 DB 421 TACCTCCAGCTATCATATGAGCAACAAGCAAGAGTTGGAATAATACATCC 480
 QY 481 ATGTGACCGAGAAATTCAAGATTAACAACAACCAAGCTGGAACAAATGGTCTTTTCA 540
 DB 481 ATGTGACCGAGAAATTCAAGATTAACAACAACAAGCTGGAACAAATGGTCTTTTCA 540
 QY 481 ATGTGACCGAGAAATTCAAGATTAACAACAACAAGCTGGAACAAATGGTCTTTTCA 540
 DB 481 ATGTGACCGAGAAATTCAAGATTAACAACAACAAGCTGGAACAAATGGTCTTTTCA 540
 QY 541 AGAGATTATCACTGTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
 DB 541 AGAGATTATCACTGTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
 QY 541 AGAGATTATCACTGTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
 DB 541 AGAGATTATCACTGTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
 QY 601 ACGAGAGCTGTGGCGCGAGCATGTACTGCGAGTTGCGAGCTTCAGTACACCTGCAGC 660
 DB 601 ACGAGAGCTGTGGCGCGAGCATGTACTGCGAGTTGCGAGCTTCAGTACACCTGCAGC 660
 QY 601 ACGAGAGCTGTGGCGCGAGCATGTACTGCGAGTTGCGAGCTTCAGTACACCTGCAGC 660
 DB 601 ACGAGAGCTGTGGCGCGAGCATGTACTGCGAGTTGCGAGCTTCAGTACACCTGCAGC 660
 QY 661 CATGCCGCGGCGCAAGAGATGTGTGACCCCGGAGCAATGAGTGTGTGGAGACAGCTGT 720
 DB 661 CATGCCGCGGCGCAAGAGATGTGTGACCCCGGAGCAATGAGTGTGTGGAGACAGCTGT 720
 QY 661 CATGCCGCGGCGCAAGAGATGTGTGACCCCGGAGCAATGAGTGTGTGGAGACAGCTGT 720
 DB 661 CATGCCGCGGCGCAAGAGATGTGTGACCCCGGAGCAATGAGTGTGTGGAGACAGCTGT 720
 QY 721 GTGTCTGGGGTCACTGACCAAAATGGCCACAGGGGCAAGATGGAGCATCTGTGACA 780
 DB 721 GTGTCTGGGGTCACTGACCAAAATGGCCACAGGGGCAAGATGGAGCATCTGTGACA 780
 QY 721 GTGTCTGGGGTCACTGACCAAAATGGCCACAGGGGCAAGATGGAGCATCTGTGACA 780
 DB 721 GTGTCTGGGGTCACTGACCAAAATGGCCACAGGGGCAAGATGGAGCATCTGTGACA 780
 QY 781 ACCAAGGAGACTGCGACCGCGGCGGTGTGTGCTTCCAGAGAGGCTCTGTCCCTG 840

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Db 781 ACCAAGAGGAGCTGCAGCCGGGCTGTGTGTGCTTCAGAGAGAGGCTGTGTTCCCTG 840
QY 841 TGTGCAACCCCTGCCCCGTTGAGGGGCGAGCTTTGCAATGACCCCGCCAGCCGGCTTCGG 900
Db 841 TGTGCAACCCCTGCCCCGTTGAGGGGCGAGCTTTGCAATGACCCCGCCAGCCGGCTTCGG 900
QY 901 ACCCTATCACTGGAGAGCTAGAGCTGTATGAGACCTTGAGACCGATGCCCTTGTGCAAGT 960
Db 901 ACCCTATCACTGGAGAGCTAGAGCTGTATGAGACCTTGAGACCGATGCCCTTGTGCAAGT 960
QY 961 GCTCTCTCTGCAAGCCCAACAGCCACAGCTGTGTATGTGTGCAAGCCCACTTCCTGG 1020
Db 961 GCTCTCTCTGCAAGCCCAACAGCCACAGCTGTGTATGTGTGCAAGCCCACTTCCTGG 1020
QY 1021 GGAGCCGTGACCAAGATGGAGAGATCTGTCTGCCAGAGAGGTCCCGATGATGTAAG 1080
Db 1021 GGAGCCGTGACCAAGATGGAGAGATCTGTCTGCCAGAGAGGTCCCGATGATGTAAG 1080
QY 1081 TTGGCAGCTTTCATGAGAGAGTGGCCGAGAGAGCTGAGAGACCTGAGAGAGAGCTGACTG 1140
Db 1081 TTGGCAGCTTTCATGAGAGAGTGGCCGAGAGAGCTGAGAGACCTGAGAGAGAGCTGACTG 1140
QY 1141 AAGAGATGGCGCTGGGGGAGAGCTGGCGGCTGCCGCGAGCTGCACTGCTGGAGGGGAGAGA 1200
Db 1141 AAGAGATGGCGCTGGGGGAGAGCTGGCGGCTGCCGCGAGCTGCACTGCTGGAGGGGAGAGA 1200
QY 1201 TTTAGATCTGACACAGAGCTGTGGGTATGATGTGCAATAGAAATAGCTAATTTATTTCCCA 1260
Db 1201 TTTAGATCTGACACAGAGCTGTGGGTATGATGTGCAATAGAAATAGCTAATTTATTTCCCA 1260
QY 1261 GGTGTGTGCTTTAGAGGCTGGGCGTGCAGAGCTTCTTCTCAATCTTCTTCCAGTAAGT 1320
Db 1261 GGTGTGTGCTTTAGAGGCTGGGCGTGCAGAGCTTCTTCTCAATCTTCTTCCAGTAAGT 1320
QY 1321 TCCCTCTGTGCTTGCAGACATGAGGTGTGTGCAATTTGTTGAGCTTCCCGAGGCTGTCT 1380
Db 1321 TCCCTCTGTGCTTGCAGACATGAGGTGTGTGCAATTTGTTGAGCTTCCCGAGGCTGTCT 1380
QY 1381 CCAAGCTTTCAGAGCTGTGTGCTTGGAGAGTCAAGGAGGTTAACTGAGAGAGAGT 1440
Db 1381 CCAAGCTTTCAGAGCTGTGTGCTTGGAGAGTCAAGGAGGTTAACTGAGAGAGAGT 1440
QY 1441 GCCACCCCTGTCCAGATTAATGTGCTTGTGCTTCAACAGTTGGAGAGCAGCCGTTGT 1500
Db 1441 GCCACCCCTGTCCAGATTAATGTGCTTGTGCTTCAACAGTTGGAGAGCAGCCGTTGT 1500
QY 1501 TCTACATGGCTTTGATTAATGTGTTGAGGGAGAGATGGAACCAATGTGAGATCTCCCTC 1560
Db 1501 TCTACATGGCTTTGATTAATGTGTTGAGGGAGAGATGGAACCAATGTGAGATCTCCCTC 1560
QY 1561 TGAATGATTTTGGGGAATGTGAGAGAGTGCCTGTTTGCAACATCAACTGAGCA 1620
Db 1561 TGAATGATTTTGGGGAATGTGAGAGAGTGCCTGTTTGCAACATCAACTGAGCA 1620
QY 1621 AAATGCAACAAATGAAATTTTCCAGCAGTTCCTTCCATGAGGCAATGAGTGTGCTT 1680
Db 1621 AAATGCAACAAATGAAATTTTCCAGCAGTTCCTTCCATGAGGCAATGAGTGTGCTT 1680
QY 1681 CAGCTGTGAGATGAAATGTTCTGTTCACTCCCTGATCAATGATGTTTATCATCAGCA 1740
Db 1681 CAGCTGTGAGATGAAATGTTCTGTTCACTCCCTGATCAATGATGTTTATCATCAGCA 1740
QY 1741 GGTGTGCTGAGCTTCACTCTGTGTGCGAGGAGCAGATTTTCAATCAAGATCAATTTCC 1800
Db 1741 GGTGTGCTGAGCTTCACTCTGTGTGCGAGGAGCAGATTTTCAATCAAGATCAATTTCC 1800
QY 1801 TCTCTCAGCAGAGCTGGAGAGGAGGAGGATGTTTCTCTCTGCTCAGAGAGCTCAGAG 1860
Db 1801 TCTCTCAGCAGAGCTGGAGAGGAGGAGGATGTTTCTCTCTGCTCAGAGAGCTCAGAG 1860
QY 1861 GCTCAGAGCTGCAAGCTGTGCTTGCACAGTCAACAGCTATGTAAGACAGAGCAGTTTC 1920

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Db 1861 GCTCAGAGCTGCAAGCTGCTTGCACAGTCAACAGCTATGTAAGACAGAGCAGTTTC 1920
QY 1921 ATCTGTTGATCTTAAGCTCAGTGTCTCTCTCACTACCCACACAGCCTTGTGCA 1980
Db 1921 ATCTGTTGATCTTAAGCTCAGTGTCTCTCTCACTACCCACACAGCCTTGTGCA 1980
QY 1981 CCAAAAGTGTCTCCCAAAAGAGAGAAATGGGATTTTCTTGAAGCATGCACTGTGA 2040
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QY 2041 ATTAAGTCAAACTAATTTCTCACTACCTCTTAAGTAAGTAAGTATGTAAGACAGCAGT 2100
Db 2041 ATTAAGTCAAACTAATTTCTCACTACCTCTTAAGTAAGTAAGTATGTAAGACAGCAGT 2100
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QY 2161 CTTGGCAGTTGATTAATGATTAATGAAAGTATGATGATGAGCTGAGCTAGACATAGGTTAA 2220
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Db 2221 CTTGCAAGAACAGTACTTAAATGATTAATGAGGAGATTAATGAAATTTGCAAAAT 2280
QY 2281 CACTTACAGCACTGAAGCAATTAATCAACGCTGAGAAATGAAATGAAATGCAAGGCG 2340
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Db 2521 AAGTTGATTTAAGAAATCAAGCATTAATCACTCACTGCAAAAAAATTTTTAAAAA 2580
QY 2581 AAAAAA 2586
Db 2581 AAAAAA 2586

RESULT 14
ABX96211
ID ABX96211 standard; cDNA; 2586 BP.
XX
AC ABX96211;
XX
DT 13-MAY-2003 (first entry)
XX
DE Human secreted/transmembrane protein cDNA, #43.
XX
KW Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;
KW diagnostic; biosensor; bioreactor; therapeutic; hyperplasia;
KW endometriosis; cancer; tumor; ischemia; coronary arterial disease;
KW polycystic kidney disease; renal failure; inflammatory response; asthma;
KW rheumatoid arthritis; psoriasis; multiple sclerosis; gene therapy;
KW cytostatic; gynecological; cardiac; nephrotoxic; hepatotoxic;
KW antiinflammatory.
XX
OS Homo sapiens.
XX
PN US2002160374-A1.
XX

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Dh 301 TGTTCGGAGGTTGAGAACTGATGAGAGACCGACGCAAAATTGGCGACCGCGGTG 360
Qy 361 AAGAGATGAGGCGAGAGAAAGCTGTGCTAAAGCATCATAGAAAGTGAACCTGGCAAACT 420
Db 361 AAGAGATGAGGCGAGAGAAAGCTGTGCTAAAGCATCATAGAAAGTGAACCTGGCAAACT 420
Qy 421 TACCTCCAGCTATCACTGATGAGACCAACAGACCGAAGGTTGAAATATACATCC 480
Db 421 TACCTCCAGCTATCACTGATGAGACCAACAGACCGAAGGTTGAAATATACATCC 480
Qy 481 ATGTGACCGAGAAATTCACAGATTAACCAACAGACCTGAGCAAAATGTCTTTTGG 540
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Qy 541 AGACAGTTATCACTGTGAGAGACGAAAGAGGCAAGAGGCAAGAGTGCATCATCG 600
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Db 1921 ATCTGTGTGATCTTAAGCTGATGCTCTCTCTCACTACCCCAACAGGCTTGTGCA 1980
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 DB 2521 AAGTGCATTAGAAATCAAGCATTAATCACTTCACTGCAAAAAA 2580
 QY 2581 AAAAAA 2586
 DB 2581 AAAAAA 2586
 RESULT 15
 ABX71642
 ID ABX71642 standard; CDNA; 2586 BP.
 XX
 AC ABX71642;
 XX
 DT 10-MAR-2003 (first entry)
 XX
 DE Human CDNA encoding secreted/transmembrane protein PRO295.
 XX
 KW Human; PRO; secreted protein; transmembrane protein; enterocolitis;
 KW gastrointestinal ulceration; skin disease; ss; gene;
 KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
 KW squamous cell carcinoma; Alzheimer's disease; Parkinson's disease;
 KW amyotrophic lateral sclerosis; inflammatory disease;
 KW rheumatoid arthritis; asthma; multiple sclerosis; organ failure;
 KW atherosclerosis; cardiac injury; infertility; birth defect;
 KW premature aging; AIDS; acquired immunodeficiency syndrome; cancer;
 KW diabetic complication; wound repair.
 XX
 OS Homo sapiens.
 XX
 XX US2002132240-A1.
 XX
 PD 19-SEP-2002.
 XX
 PF 18-JUL-2001; 2001US-0909320.
 XX
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19177.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 01-DEC-1998; 98WO-US25108.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 13-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 01-DEC-1999; 99WO-US28301.
 PR 02-DEC-1999; 99WO-US28564.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 06-JAN-2000; 2000WO-US00219.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 17-SEP-1997; 97US-059113P.
 PR 17-SEP-1997; 97US-059115P.
 PR 17-SEP-1997; 97US-059117P.
 PR 15-OCT-1997; 97US-062125P.
 PR 17-OCT-1997; 97US-062285P.
 PR 17-OCT-1997; 97US-062287P.
 PR 21-OCT-1997; 97US-063486P.
 PR 24-OCT-1997; 97US-062814P.
 PR 24-OCT-1997; 97US-062816P.
 XX
 PA (GENETH) GENENTECH INC.
 XX
 XX Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
 PI Filvaroff E, Fong W, Gao W, Garber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavlin IJ;

PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams EM, Wood WI;
 XX
 DR WPI; 2003-147434/14.
 XX
 DR P-PSDB; ABUS4387.
 XX
 PT New PRO polypeptides and nucleic acid molecules, useful in diagnosing
 PT or treating inflammatory diseases, organ failure, atherosclerosis,
 PT cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or
 PT Parkinson's disease -
 XX
 PS Claim 2; Fig 83; 473pp; English.
 XX
 XX The invention relates to an isolated PRO polypeptide having at least 80%
 CC amino acid sequence identity to: (a) any one of 61 fully defined amino
 CC acid sequences given in the specification (appearing as ABUS4347-
 CC ABUS4407); (b) an amino acid sequence encoded by the nucleotide sequence
 CC deposited under American Type Culture Collection (accession numbers
 CC listed in the specification); (c) any one of the PRO sequences which
 CC lacks its associated signal peptide; (d) an extracellular domain of the
 CC PRO polypeptide with its associated signal peptide; or (e) an
 CC extracellular domain of the PRO polypeptide which lacks its associated
 CC signal peptide. Also include are the nucleic acids encoding the PRO
 CC polypeptides, vectors, host cells and anti-PRO antibodies.
 CC The PRO polypeptides and nucleic acids are useful in diagnosing
 CC or treating enterocolitis, gastrointestinal ulceration, skin diseases
 CC associated with abnormal keratinocyte differentiation, e.g. psoriasis
 CC or epithelial cancers such as squamous cell carcinoma, Alzheimer's
 CC disease, Parkinson's disease, amyotrophic lateral sclerosis,
 CC inflammatory diseases, e.g. rheumatoid arthritis, asthma or multiple
 CC sclerosis, organ failure, atherosclerosis, cardiac injury, infertility,
 CC birth defects, premature aging, AIDS, cancer, diabetic complications,
 CC or mutations in general. The polypeptides are also useful for wound
 CC repair and associated therapies concerned with re-growth of tissue. The
 CC nucleotide sequences may be used as hybridisation probes in chromosome
 CC and gene mapping, or in generating antisense RNA and DNA. PRO nucleic
 CC acids are also useful in preparing PRO polypeptides, in assays to
 CC identify other proteins or molecules involved in binding reaction, to
 CC generate transgenic animals or knockout animals, which in turn are
 CC useful in the development and screening of therapeutically useful
 CC reagents, for chromosome identification, and tissue typing. The PRO
 CC polypeptides and nucleic acid molecules are also useful in gene
 CC therapy, and as molecular weight markers for protein electrophoresis
 CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
 CC PRO, or for the affinity purification of PRO from recombinant cell
 CC culture or natural sources. The present sequence encodes a PRO
 CC polypeptide.
 XX
 SQ Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;
 QY
 Query Match 100.0%; Score 2586; DB 25; Length 2586;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGCCGGGCTCCGCAACCGCGGCGCCGCGCGCTCCGATTCGACCCGACG 60
 DB 1 CGCCGGGCTCCGCAACCGCGGCGCCGCGCGCTCCGATTCGACCCGACG 60
 QY 61 CGCGGGGCTCCCGCGGAGGAGCAAGATCCAGCCGCGCGGCAATCGATCA 120
 DB 61 CGCGGGGCTCCCGCGGAGGAGCAAGATCCAGCCGCGCGGCAATCGATCA 120
 QY 121 GTCGGGGCGGCGGCTGCGGGCGCAGAGCGGAGATCAGCGGCTTGAGCTGCT 180
 DB 121 GTCGGGGCGGCGGCTGCGGGCGCAGAGCGGAGATCAGCGGCTTGAGCTGCT 180
 QY 181 GCGTGTGCTGCGCGCGCGGCGGCGGCGGCGGCGGCGGCTCCGAGCGGACTCGG 240
 DB 181 GCGTGTGCTGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCTCCGAGCGGACTCGG 240
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Db 301 TGTTCGCGCGAGGTTGAGGAACTGATGAGAGACAACGAGACAAATTTCGCGACGCGGTGG 360
QY 361 AAGAGATGAGGAGAGAGAGAGCTGTCTGTAAAGCATCATCAGAGTGAAGACTGTGGAAACT 420
Db 361 AAGAGATGAGGAGAGAGAGAGCTGTCTGTAAAGCATCATCAGAGTGAAGACTGTGGAAACT 420
QY 421 TACCTCCAGCTTATCACAATGAGACCAACACAGACAAGAGTTGGAATTAATACATCC 480
Db 421 TACCTCCAGCTTATCACAATGAGACCAACACAGACAAGAGTTGGAATTAATACATCC 480
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Db 481 ATGTGACCCGAGAAATTCAAAATTAACCAACAACAGACTGGAACAAATGTCTTTTCAG 540
QY 541 AGACAGTTATCACATCTGTGAGAGACGAAAGAGAGAGAGACGAGTGCATCATCG 600
Db 541 AGACAGTTATCACATCTGTGAGAGACGAAAGAGAGAGAGACGAGTGCATCATCG 600
QY 601 ACAGAGACTGTGGGCCCCAGAGTGTATCTGCCAGTTTTCGAGCTTCCAGTACACTTCCAGC 660
Db 601 ACAGAGACTGTGGGCCCCAGAGTGTATCTGCCAGTTTTCGAGCTTCCAGTACACTTCCAGC 660
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Db 661 CATGCCGAGGCGCAGAGGATGCTCTGACACCGGAGCAGTAGAGTGTCTGAGACAGCTGT 720
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Db 721 GTGTCTGGGGGTCACTGACCAAAATGACCAACAGGAGCAGATGAGAGCAATCTGTGACA 780
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Db 781 ACCAGAGGAGCTGCGACGCGGAGCTGTGCTGTGCTTCCAGAGAGGCTGTGTTCCCTG 840
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Db 841 TGTGACACCCCTGCGCGTGTGAGAGGAGAGCTTTGCCATGACCCCGCAGACCGGCTTCTGG 900
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QY	2581	AAAAAA 2586	
Db	2581	AAAAAA 2586	

Search completed: February 19, 2004, 18:41:11
Job time : 701 secs

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 5' mRNA sequence.
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 VERSION BUI57365.1 GI:22670897
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 1002)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
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 /clone_lib="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOT7; Site_1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGACAGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."
 BASE COUNT 204 a 258 c 288 g 252 t
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 Query Match 36.5% Score 945; DB 13; Length 1002;
 Best Local Similarity 97.7%; Pred. No. 2e-114;
 Matches 980; Conservative 0; Mismatches 20; Indels 3; Gaps 2;
 QY 849 CCCCTGCCCGTGAAGAGGAGACCTTGGCATGACCCCGACCGGCTTCTGAGCCTATC 908
 Db 1 CCCCTGCCCGTGAAGAGGAGACCTTGGCATGACCCCGACCGGCTTCTGAGCCTATC 60
 QY 909 ACCGTGGAGCTAGAGCCCTGATGAGAGCCCTGGAACCGATGCTGTGCGAGTGGCTCCTC 968
 Db 61 ACCGTGGAGCTAGAGCCCTGATGAGAGCCCTGGAACCGATGCTGTGCGAGTGGCTCCTC 120
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 Db 301 GCGCTGGGGAGAGCTGCGGCTGCGCGCTGCACTGCTGGAGGGGAGAGATTTAATC 360
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RESULT 3
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 5', mRNA sequence.
 ACCESSION BO690088
 VERSION BO690088.1 GI:21815404
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 1 (bases 1 to 936)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: csabbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILN at:
 http://image.llnl.gov
 Plate: LLCM2365 row: n column: 09
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 /clone_lib="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOTB7, Site_1: XhoI;
 Site_2: EcoRI; CDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAAGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University

FEATURES
 source

of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library. 1 others
 BASE COUNT 186 a 224 c 275 g 240 t
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 Query Match 35.4%; Score 916.6; DB 13; Length 936;
 Best Local Similarity 99.4%; Pred. No. 1.1e-110;
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 Db 1 CCCCTGCCGTGAGGAGGCGGAGCTTTGCAATGACCCCGGAGCGGCTTTGACCTCATC 60
 Qy 909 ACCTGGAGCTAGAGCTGATGAGAGCTTGAGCCGATGACCTTTGTCAGAGCTCTC 968
 Db 61 ACCTGGAGCTAGAGCTGATGAGAGCTTGAGCCGATGACCTTTGTCAGAGCTCTC 120
 Qy 969 TGGCAGCCCAAGCCCAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1028
 Db 121 TGGCAGCCCAAGCCCAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 180
 Qy 1029 GACCAAGATGGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1088
 Db 181 GACCAAGATGGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 Qy 1089 TTGATGAGAGAGGTGCGCCAGAGCTGAGAGAGCTGAGAGAGAGAGAGAGAGAGAGATG 1148
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 Db 301 GCGCTGAGGAGAGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 360
 Qy 1209 TGAACACAGCTGTGAGTAGATGTCATTAAGAAATAGCTAATTTATTTCCACAGTGTG 1268
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 Qy 1749 CAGCTCTTACCTGTG--GCCAGGAGAGCATTTTCAT 1783
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RESULT 4
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LOCUS AGENCOURT 8034028 NIH_MGC_110 Homo sapiens CDNA clone IMAGE:6208256
DEFINITION 5', mRNA sequence.
ACCESSION BO690888 GI:21816204
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 951)
NIH-MGC <http://mgi.nci.nih.gov/>,
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
AUTHORS Contact: Robert Strausberg, Ph.D.
TITLE Email: cgabs-remail.nih.gov
COMMENT Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLCM2365 row: k column: 09
High quality sequence stop: 698.
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/clone_lib="NIH_MGC_110"
/note="Organ: pancreas; Vector: pOTB7; Site: 1; XhoI;
Site 2: EcoRI; CDNA made by oligo-dt priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 191 a 239 c 276 g 244 t 1 others
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Query Match 35.4%; Score 914.8; DB 13; Length 951;
Best Local Similarity 98.9%; Pred. No. 1.8e-110;
Matches 941; Conservative 0; Mismatches 8; Indels 2; Gaps 2;
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QY 909 ACCTGGGAGCTAGAGCTTATGAGAGCTTTGACCGATGCCCTTGTGCGCAGTGCCTTC 968
DB 61 ACCTGGGAGCTAGAGCTTATGAGAGCTTTGACCGATGCCCTTGTGCGCAGTGCCTTC 120
QY 969 TGGCAGCCCGACAGCCAGCTGCTGATATGTATGTGCAAGCCGATCTTCTGAGGAGACCT 1028
DB 121 TGGCAGCCCGACAGCCAGCTGCTGATATGTATGTGCAAGCCGATCTTCTGAGGAGACCT 180
QY 1029 GACCAATATGGGAGATCTCTGCTGCCAGAGAGGTCCCGATGATGATGAAGTTGGCAGC 1088
DB 181 GACCAATATGGGAGATCTCTGCTGCCAGAGAGGTCCCGATGATGATGAAGTTGGCAGC 240
QY 1089 TTGATGAGAGAGGGGCGCCAGAGCTGAGAGAGCTTGGAGAGAGAGCTGATGAAGAGATG 1148
DB 241 TTGATGAGAGAGGGGCGCCAGAGCTGAGAGAGCTTGGAGAGAGAGCTGATGAAGAGATG 300

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DB 421 CTTTGGGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
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DB 601 TGTCCAGATTTATGCTGT 660
QY 1509 GCTTGTATTAATGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1568
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QY 1569 TTTGGGGAG 1628
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QY 1629 CAATGATTTTCCAG 1688
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ACCESSION BO686792 GI:21812108
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 932)
NIH-MGC <http://mgi.nci.nih.gov/>,
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
AUTHORS Contact: Robert Strausberg, Ph.D.
TITLE Email: cgabs-remail.nih.gov
COMMENT Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLCM2393 row: f column: 15
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Location/Qualifiers

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/lab_host="DH10B (phage-resistant)"
/notes="Organ: pancreas; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT      184 a      235 c      279 g      234 t
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Best Local Similarity 98.8%; Pred. No. 1.3e-105;
Matches 905; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

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DB 558 TTCAAGTCTGTGCTTGGAGAGTCAAGGAGGTTAACTGAGAGAGAGTTTGCACCC 617
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RESULT 6
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LOCUS
DEFINITION
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B0689559      GI:21814875
VERSION
B0689559.1 GI:21814875
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EST.
SOURCE
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ORGANISM
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
REFERENCE
AUTHORS
NIH-MGC
TITLE
Unpublished
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ARCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LCM392 row: n column: 04
High quality sequence stop: 584.
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/mol_type="mrna"
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/clone="IMAGE:6250179"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_110"
/notes="Organ: pancreas; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT      181 a      232 c      272 g      237 t
ORIGIN
Query Match      33.9%; Score 876.2; DB 13; Length 926;
Best Local Similarity 97.9%; Pred. No. 2e-105;
Matches 906; Conservative 0; Mismatches 17; Indels 2; Gaps 2;

QY 849 CCCCCTGCCGTGAGGGCGAGCTTTGCCATGACCCCGCAGCCGAGCTTCTGAGACCTATC 908
DB 1 CCCCCTGCCGTGAGGGCGAGCTTTGCCATGACCCCGCAGCCGAGCTTCTGAGACCTATC 60
QY 909 ACCTGGAGCTAGAGCCTGATGAGAGCTTGAACGATGACCTTGTGCACTGAGCTTCTC 968
DB 61 ACCTGGAGCTAGAGCCTGATGAGAGCTTGAACGATGACCTTGTGCACTGAGCTTCTC 120

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QY 969 TGGCAGCCCCCAGCCAGCCTGCTGTATGTGTGAGACCCAGCTTCTGTGGAGCCGT 1028
 DB 121 TGGCAGCCCCCAGCCAGCCTGCTGTATGTGTGAGACCCAGCTTCTGTGGAGCCGT 180
 QY 1029 GACCAAGATGGGGAGATCTCTGCTGCCAGAGAGTCCCGATGATGATGAATTTGGCAGC 1088
 DB 181 GACCAAGATGGGGAGATCTCTGCTGCCAGAGAGTCCCGATGATGATGAATTTGGCAGC 240
 QY 1089 TTGATGAGAGAGTGGCGGAGAGCTGAGAGAGCTTGGAGAGAGAGCTGATGAAGAGATG 1148
 DB 241 TTGATGAGAGAGTGGCGGAGAGCTGAGAGAGCTTGGAGAGAGAGCTGATGAAGAGATG 300
 QY 1149 GCGCTGGGGAGAGCTGGCGGCTGCCCGCTGCACTGCTGGAGGGGAGAGATTTAGATC 1208
 DB 301 GCGCTGGGGAGAGCTGGCGGCTGCCCGCTGCACTGCTGGAGGGGAGAGATTTAGATC 360
 QY 1209 TGGACCAAGGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTATTTCCCGAGGTGTG 1268
 DB 361 TGGACCAAGGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTATTTCCCGAGGTGTG 420
 QY 1269 CTTTAAAGCGGGGCTGACAGAGCTTCTCTCACTCTTCTCCAGTAGTTCCCTCT 1328
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 DB 481 GCGTTGACAGCATGAGAGTGTGTGCAATTTGTCAGCTCCCGAGGCTGTCTCCAGGCTT 540
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 QY 1509 GCTTTGATTAATTTGTTGAGAGGAGAGAGATGAAACAATGTGAGTCTCCCTGATGTT 1568
 DB 661 GCTTTGATTAATTTGTTGAGAGGAGAGAGATGAAACAATGTGAGTCTCCCTGATGTT 720
 QY 1569 TTTGGGGAAATGTGAGAGAGAGAGCTGTTGCAAAACATCACTGGCAAAATGCA 1628
 DB 721 TTTGGGGAAATGTGAGAGAGAGAGCTGTTGCAAAACATCACTGGCAAAATGCA 779
 QY 1629 CAAATGATTTTTCACGAGCTTTCTTCAATGGGCAATAGGTAAGCTGTGCTTCACTGTT 1688
 DB 780 CAAATGATTTTTCACGAGCTTTCTTCAATGGGCAATAGGTAAGCTGTGCTTCACTGTT 839
 QY 1689 GCAGATGAAATGTTCTGTTCAACCTGATTAATGATGTTTATTCATCCAGCAGTG- TTGC 1747
 DB 840 GCAGATGAAATGTTCTGTTCAACCTGATTAATGATGTTTATTCATCCAGCAGTGTTTGC 899
 QY 1748 TCAGCTCTTACTCTGTGCCAGGAC 1772
 DB 900 TCAGCTCTTACTCTGTGCCAGGAC 924

RESULT 7
 LOCUS B0691927 912 bp mRNA linear EST 15-JUL-2002
 DEFINITION AGENCOURT 8034941 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6207089
 5', mRNA sequence.
 ACCESSION B0691927 GI:21817255
 VERSION B0691927.1 GI:21817255
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 912)
 AUTHORS NIH-MGC http://mgc.ncl.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: sgabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: L10M2362 row: 5 column: 18
 High quality sequence stop: 654.
 Location/Qualifiers
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 /clone="IMAGE:6207089"
 /tissue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_idb="NIH MGC 110"
 /note="Organ: pancreas; Vector: pOT87; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC library."
 BASE COUNT 180 a 228 c 270 g 231 t 3 others
 ORIGIN
 Query Match 33.7%; Score 872.2; DB 13; Length 912;
 Best Local Similarity 98.6%; Pred. No. 6.8e-105;
 Matches 899; Conservative 0; Mismatches 11; Indels 2; Gaps 2;
 QY 849 CCCCTGCCCGTGGAGGGGAGCTTTGCCATGACCCGCGAGCGGCTTGGACCTCATC 908
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 QY 909 ACCTGGAGCTAGAGCTGTATGAGAGCTTTGAGCCGATGCCCTTGTGCAAGTGCCTCTC 968
 DB 61 ACCTGGAGCTAGAGCTGTATGAGAGCTTTGAGCCGATGCCCTTGTGCAAGTGCCTCTC 120
 QY 969 TGGCAGCCCCCAGCCACAGCTGTGTATGTGTGCAAGCGACCTTCGTGGAGAGCGT 1028
 DB 121 TGGCAGCCCCCAGCCACAGCTGTGTATGTGTGCAAGCGACCTTCGTGGAGAGCGT 180
 QY 1029 GACCAAGATGGGGAGATCTCTGCTGCCAGAGAGTCCCGATGATGAAGTTGGCAGC 1088
 DB 181 GACCAAGATGGGGAGATCTCTGCTGCCAGAGAGTCCCGATGATGAAGTTGGCAGC 240
 QY 1089 TTGATGAGAGAGTGGCGGAGAGCTGAGAGAGCTTGGAGAGAGAGCTGATGAAGATG 1148
 DB 241 TTGATGAGAGAGTGGCGGAGAGCTGAGAGAGCTTGGAGAGAGAGCTGATGAAGATG 300
 QY 1149 GCGCTGGGGAGAGCTGGCGGCTGCCCGCTGCACTGCTGGAGGGGAGAGATTTAGATC 1208
 DB 301 GCGCTGGGGAGAGCTGGCGGCTGCCCGCTGCACTGCTGGAGGGGAGAGATTTAGATC 360
 QY 1209 TGGACCAAGGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTATTTCCCGAGGTGTG 1268
 DB 361 TGGACCAAGGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTATTTCCCGAGGTGTG 420
 QY 1269 CTTTAAAGCGGGGCTGACAGAGCTTCTCTCACTCTTCTCCAGTAGTTCCCTCT 1328
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 DB 481 GCGTTGACAGCATGAGAGTGTGTGCAATTTGTCAGCTCCCGAGGCTGTCTCCAGGCTT 540
 QY 1389 CACAGCTGTGTGTTGGAGAGTCAAGGAGGTTAACTGCGAGAGCATTTGGCCACCC 1448

Db 541 CACAGCTGGTGGTGGAGAGTCAAGAGGTTAACTGAGAGCAAGTTGGCAACCC 600
 1449 TGTCCAGATTATGGCTGCTTTGCTCCTTACCAAGTTGGAGACAGCCGTTTGTCTACATG 1508
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 1509 GCTTTGATTAATGTTGAGGGAGAGAGATGAAACAATGAGAGTCCCTCTGATAGGT 1568
 Db 661 GCTTTGATTAATGTTGAGGGAGAGAGATGAAACAATGAGAGTCCCTCTGATAGGT 720
 1569 TTTGGGAAATGTGAGAGAGTGGCTGCTTTGCAACATCAACCTGGCAAAATGCA 1628
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 1629 CAAATGAATTTCCAGCAGCTTTTCCATGAGGCAATGAGTGGTCCCTGAGCTGT 1688
 Db 780 CAAATGAATTTTTCAGCAGCTTTTCCATGAGGCAATGAGTGGTCCCTGAGCTGT 839
 1689 GCAGATGAATGTTGTTGTTCACTGATGATGATGTTT-ATTGATCCAGAGTGTGC 1747
 Db 840 GCAGATGAATGTTGTTGTTCACTGATGATGATGTTT-ATTGATCCAGAGTGTGC 899
 QY 1748 TGAGCTCTTACC 1759
 Db 900 TCAGCTCTTACC 911

RESULT 8
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 LOCUS AL535720 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 DEFINITION CS0DF016YJ11 5-PRIME, mRNA sequence.
 ACCESSION AL535720
 VERSION AL535720.2 GI:31260722
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 977)
 L1,W.B., Gruber,C., Jesse,J. and Polayes,D.
 Full-length cDNA libraries and normalization
 Unpublished
 On Feb 13, 2001 this sequence version replaced gi:12799213.
 CONTACT Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 6027.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DF016CE06QPLcluster=6027.r. Contact :
 Feng Liang Email: fliang@life.techn.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DF016CE06QPL.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /note="Organ: brain; Vector: PCWVSORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with NotI and
 cloned into the NotI and EcoRV sites of the PCWVSORT 6
 vector. Library was not normalized."

BASE COUNT
 ORIGIN

222 a 294 c 296 g 165 t

Query Match 33.7%; Score 872; DB 9; Length 977;
 Best Local Similarity 99.9%; Pred. No. 7e-105; Mismatches 0; Indels 1; Gaps 1;
 Matches 883; Conservative 0;

126 GGGCGGGCTGGCGGGCGGAGCGGAGATGACAGCGCTTGGGGCCACCTGCTGCTG 185
 Db 95 GGGCGGGCTGGCGGGCGGAGCGGAGATGACAGCGCTTGGGGCCACCTGCTGCTG 154
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 Db 155 CTCTGGCGGGCGGGCTTCCCAAGCGCCCGCGCCGCTCCAGCGGCACTGGCTGCA 214
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 QY 306 CGGAGGTTGAGGAATGATGAGGACAGCAGCACAATTTGGCAGCGCGGTGAGAG 365
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 QY 906 ATCACTGGAGGCTAGAGCTGTATGAGCTTGTGAGCTTGTGAGCTTGTGAGCTTGTG 965
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 QY 966 CTCTGCCAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCC 1009
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RESULT 9
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 LOCUS BU149689
 DEFINITION AGENCOURT_8049944 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6083782
 5', mRNA sequence.
 ACCESSION BU149689
 VERSION BU149689.1 GI:22663221

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 949)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: scapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: <http://image.liml.gov>
Plate: LIM2314 row: h column: 23
High quality sequence start: 19
Location/Qualifiers
1. 949

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/clone="IMAGE:6083782"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_110"
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald W. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and SuperScript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 188 a 236 c 288 g 237 t

ORIGIN

Query Match 33.6%; Score 870; DB 13; Length 949;
Best Local Similarity 98.1%; Pred. No. 1,3e-104;
Matches 901; Conservative 0; Mismatches 15; Indels 2; Gaps 2;

QY 848 ACCCTGCGCGTGGAGGGCGAGCTTTGCGCATGACCCCGACGCGGCTTCTGACCTCAT 907
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QY 908 CACCTGGAGCTAGAGCTGTATGAGACCTTGAGCCGATGCTTTGTGCCAGTGGCTTCT 967
DB 91 CACCTGGAGCTAGAGCTGTATGAGACCTTGAGCCGATGCTTTGTGCCAGTGGCTTCT 150
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DB 151 CTGGCAGCCCAACGACGACCTGTGTATGTATGACGACGACCTTCTGAGGAGACCG 210
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QY 1088 CTTCAATGAGAGAGTGTGGCCGACGAGACTGTGAGAGAGCTTGAAGAGAT 1147
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QY 1208 CTGAGACCAAGCTGTGTGGTATGATGTCAATTAAGTAATTTATTTCCCAAGGTGT 1267
DB 391 CTGAGACCAAGCTGTGTGGTATGATGTCAATTAAGTAATTTATTTCCCAAGGTGT 450

QY 1268 GCTTTAGGCGTGGGCTGACCAAGGCTTCTTCTACATCTTCTTCCAGTAAGTTCCCTC 1327
DB 451 GCTTTAGGCGTGGGCTGACCAAGGCTTCTTCTACATCTTCTTCCAGTAAGTTCCCTC 510
QY 1328 TGGCTTGACAGATAGAGTGTGTGATTTGTCATTTGTCAGTCCCGCAGGCTGTCTCAGGCT 1387
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DB 751 TTTTGGGGAATGTGAGAGAGTCCCTGCTTGGCAATCAACCTTGGCAAAATGCA 810
QY 1628 ACAATGAATTTTCCAGCAG-TTCTTCCATGGGATAGGTAAGTGTGCTTCCAGCTG 1686
DB 811 ACAATGAATTTTCCAGCAGTTCTTCCATGGGATAGGTAAGTGTGCTTCCAGCTG 870
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DB 871 TTGCAGATGAATTTGTTGTTTCACTTGCATTAATGTC-TTTATTCAATCCAGAGTGT 930
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DB 931 GCTCAGCTCTTCACTCTG 948

RESULT 10
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LOCUS
DEFINITION
AL566024 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
CS0DP016Y011.3-PRIME, mRNA sequence.
ACCESSION
AL566024
VERSION
AL566024.1 GI:12917976
KEYWORDS
SOURCE
ORGANISM
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
Li, W.B., Gruber, C., Jessup, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: secref@genoscope.cns.fr; Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6027.r For
more information about this cluster, see
<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DP016CE06NP1&cluster=6027.r>. Contact :
Peng Liang Email: liang@life.techn.com URL: <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0DP016CE06NP1.
Location/Qualifiers
1. 959
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DP016Y011"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"

/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: Brain; Vector: PCWVSORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the PCWVSORT 6 vector. Library was not normalized."
BASE COUNT 241 a 195 c 221 g 266 t 36 others
ORIGIN
Query Match 33.3%; Score 862.2; DB 9; Length 959;
Best Local Similarity 93.4%; Pred. No. 1.3e-103;
Matches 897; Conservative 31; Mismatches 28; Indels 4; Gaps 3;
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959 AATGTGAGAAAGAGGCGCTGTTTGGCAACATCACTGGCAAAATGACAAACAAATGA 900
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899 ATTTCCAGCAGTCTTTCATGAGGAGTAAGTAAGCTGCTTCACTGCTTGGAGATG 840
1696 AATGTTCTGTACCTGATTAATGTTTATTCATCCAGAGTGTGCTTCAGCTCC 1755
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1816 TGGGAGAGGGGATATTGTTCTCTGTCATCAAGGATTCAGAGGCTCAGAGCTGCA 1875
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1876 GCTGCTTGGCCAGTACACAGTAGTGAAGACAGAGCTTCACTGTTGATGATC 1935
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599 TAAGCTCAGTCTCTCTCCATCAACCCACACAGCCTTGGTGCACCAAAAGTGTCCCC 540
1996 AAAGAGAGAGAGATGGAGATTTTTC--TGAGGAGCAGCAGTCTGGAATTAAGTCAAC 2053
539 AAAGAGAGAGAGATGGAGATTTTTC--TGAGGAGCAGCAGTCTGGAATTAAGTCAAC 480
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2114 GGGGAGAGCCTCTCTTAATGAAGACATGATTAATGACATGCTCTCTTGGCAGTGC 2173
419 GGGGAGAGCCTCTCTTAATGAAGACATGATTAATGACATGCTCTCTTGGCAGTGC 360
2174 ATTAGTAATCTTGAAGAGTATAGTGAAGCAGTGAAGTAACTGAGGAGAAACAG 2233
359 ATTAGTAATCTTGAAGAGTATAGTGAAGCAGTGAAGTAACTGAGGAGAAACAG 300
2234 TACTTAGTAATCTTGAAGAGTATTAATGAAGATTTGCAAAATCACTTAGAGCA 2293
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179 GATATATATGCGACGCGCAACCTGAATCTAGCGCATCCCAAAATATATGTTTCAG 120
2414 TGTATGAGACTGTGCGACGCGCATTTATTCACAGAGTCTTAAAGTTAAAGTTCAGAT 2473
119 TGTATGAGACTGTGCGACGCGCATTTATTCACAGAGTCTTAAAGTTAAAGTTCAGAT 61

2474 GATTGATTAAGCATGCTTCTTTGAGTTTAAATATGATTAACATTAAGTTCATTAG 2533
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LOCUS AL572550 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION AL572550 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
ACCESSION AL572550
VERSION AL572550
KEYWORDS GI:31293927
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 16, 2001 this sequence version replaced gi:1293928.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6027.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1008G04NP1&cluster=6027.r. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0D1008G04NP1.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
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/clone="CS0D1008Y07"
/issue_type="PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoRV sites of the PCWVSORT 6 vector. Library was normalized."
BASE COUNT 311 a 254 c 261 g 311 t 64 others
ORIGIN
Query Match 33.2%; Score 858.4; DB 9; Length 1201;
Best Local Similarity 95.6%; Pred. No. 3.8e-103;
Matches 970; Conservative 14; Mismatches 18; Indels 13; Gaps 10;
Db 1509 GCTTTGTAATTTGTTGAGGAGAGAGATGAACATGATGAGTCTCTCTGATTTGT 1568
1031 GCTTTGTAATTTGTTGAGGAGAGAGATGAACATGATGAGTCTCTCTGATTTGT 976
1569 TTTGGGAAATGAGAAAGAGTCCCTGCTTGGCAACATCAACCTGGAAATGCA 1628
975 TTT-GGAAATGAGAAAGAGTCCCTGCTTGGCAACATCAACCTGGAAATGCA 918
1629 CAATGAAATTTTCCAGCAGTCTTTCATGAGGAGATAGTAAGTGTGCTTCACTGCT 1688
917 CAATGAAATTTTCCAGCAGTCTTTCATGAGGAGATAGTAAGTGTGCTTCACTGCT 860
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859 GCAATGAAATTTTCCAGCAGTCTTTCATGAGGAGATAGTAAGTGTGCTTCACTGCT 800
1748 TCACTCTCTA-CCTCTGTCAGGAGCAGATTTTCAATATCAAGATCAATTCCTCTCTC 1806
799 TCACTCTCTA-CCTCTGTCAGGAGCAGATTTTCAATATCAAGATCAATTCCTCTCTC 740

QY 1807 AGCAGAGCTGGGGAGGGGCTCATTTGTTCTCTGTCATCAGAGATCTCAGAGGCTCAG 1866
 DB 739 AGCAGAGCTGGGGAGGGGCTCATTTGTTCTCTGTCATCAGAGATCTCAGAGGCTCAG 680
 QY 1867 AGACTGCAAGCTCTGCTCCCAAGTCAACAGCTAGTGAAGACCAAGAGCTTCACTGG 1926
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 DB 139 GTTTTCAGTGTCAATGAGCTGTTGCCACATGATTTATCAGAGTTCTTAAAGTTTAA 80
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 DEFINITION AGENCOURT_8074271 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6085826
 ACCESSION BU146060
 VERSION BU146060.1 GI:22659592
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 Mammalia; Euteleostomi; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 893)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: c9apds-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:

http://image.lnl.gov
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 High quality sequence stop: 644.
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 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(C). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

BASE COUNT
 179 a 225 c 269 g 220 t
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Query Match 33.0%; Score 854; DB 13; Length 893;
 Best Local Similarity 98.7%; Freq. No. 1.6e-102;
 Matches 882; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

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 QY 909 AACTGGAGCTTAGAGCTTGATGAGAGCTTGGACCGATGCTTGTGCTAGTGGCTCTC 968
 DB 61 AACTGGAGCTTAGAGCTTGATGAGAGCTTGGACCGATGCTTGTGCTAGTGGCTCTC 120
 QY 969 TGCCAGCCCAAGCAGACAGCTGATGATGTGCAAGCCGACCTTGTGAGAGCCGT 1028
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 DB 181 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGTCCCGATGATGATGAGTGGCAGC 240
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 DB 241 TTCAATGAGAGAGTGTGCGGCAAGAGCTGAGAGCTGAGAGAGCTGATGAGAGATG 300
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RESULT 13

LOCUS B0686834 934 bp mRNA linear EST 15-JUL-2002

DEFINITION AGENCOURT_8345:189 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6250143

ACCESSION B0686834

VERSION B0686834

KEYWORDS EST.

SOURCE Homo sapiens (human).

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 934)

AUTHORS NIH-MGC http://mgs.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cga@pds-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.lnl.nih.gov

Plate: LLCM2392 row: 1 column: 16

High quality sequence stop: 607.

Location/Qualifiers

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/issue_type="ductal carcinoma, cell line"

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/note="Organ: pancreas; Vector: pORF7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming

Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGGCAAGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC library."

BASE COUNT 185 a 234 c 276 g 231 t 8 others

ORIGIN

Query Match 33.0%; Score 852.4; DB 13; Length 934;

Best Local Similarity 97.0%; Pred. No. 2.6e-102;

Matches 906; Conservative 0; Mismatches 24; Indels 4; Gaps 4;

QY 849 CCCCTGCCGAGGAGGAGGAGCTTTGGCATGACCCCGGCGGCTTGGAGCTTCATC 908

Db 1 CCCCTGCCGAGGAGGAGGAGCTTTGGCATGACCCCGGCGGCTTGGAGCTTCATC 60

QY 909 ACCTGGAGCTTAAGCTGATGAGAGCTTGGACCGATGCCCTTGGCCAGTGGCTCTTC 968

Db 61 ACCTGGAGCTTAAGCTGATGAGAGCTTGGACCGATGCCCTTGGCCAGTGGCTCTTC 120

QY 969 TGCCAGCCCCCAGCCAGAGCTTGTGTATGTGTGCAAGCCGACCTTCGTGGGAGGCCCT 1028

Db 121 TGCCAGCCCCCAGCCAGAGCTTGTGTATGTGTGCAAGCCGACCTTCGTGGGAGGCCCT 180

QY 1029 GACCAAGATGGGAGATCTCTGCTCCAGAGAGGTCCCGCATGATGATGAAGTTGGAGC 1088

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QY 1089 TTCAATGAGAGAGTGGCCGACAGAGACTGAGAGACTGAGAGAGCTGATGAGAGATG 1148

Db 241 TTCAATGAGAGAGTGGCCGACAGAGACTGAGAGACTGAGAGAGCTGATGAGAGATG 300

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RESULT 14

LOCUS B0890463 878 bp mRNA linear EST 16-AUG-2002

DEFINITION AGENCOURT_8064243 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6207928

ACCESSION B0890463

VERSION B0890463

KEYWORDS EST.

SOURCE Homo sapiens (human).

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 878)

AUTHORS NIH-MGC http://mgs.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINT)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINT at:
 http://image.lnl.gov
 Plate: LINC2364 row: n column: 17
 High quality sequence stop: 677.
 Location/Qualifiers
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 /lab_host="DH10B (phage-resistant)"
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 /note="Organ: pancreas; Vector: pOTB7; Site: 1; XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGACAGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."
 BASE COUNT 175 a 218 c 264 g 219 t 2 others
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 Best Local Similarity 99.2%; Pred. No. 2.6e-100;
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 DB 1 CCCCTGCGGCTGGAGGGCGAGCTTTGCCATGACCCCGCAGCGGCTTCTGACCTCARTC 60
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 QY 1029 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGTCCCGCATAGATATGAAGTTGGCAGC 1088
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 VERSION BX391733.1 GI:30611681
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 6027.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0BA1021ZG05_CS01959_1&cluster=6027.r.
 Contact: Feng Liang Email: fliang@lifetech.com URL: <http://fulllength.invitrogen.com/>
 Faraday Avenue Genoscope sequence ID: CS0BA1021ZG05_CS01959_1.
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 /note="1st strand cDNA was primed with a NotI-oligo (dT)
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 sites of the pCMVSPORT 6 vector. Library was normalized."
 BASE COUNT 245 a 261 c 213 g 192 t 11 others
 ORIGIN
 Query Match 32.2%; Score 833; DB 13; Length 922;
 Best Local Similarity 97.4%; Pred. No. 9e-100;
 Matches 894; Conservative 0; Mismatches 19; Indels 5; Gaps 5;
 QY 919 TAGACCTGATGAGACCTTTGAGC-GATGCCCTTGTGCAAGTGGCCTCTGCGACGCC 977

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DEFINITION	AT534481 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
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VERSION	CSD0F004YG01-5-PRIME, mRNA sequence.
KEYWORDS	AL534481.2 GI:30540322 EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1) W.B., Gruber C.; Jesssee J. and Polayes D. Full-length cDNA libraries and normalization Unpublished On Feb 13, 2001 this sequence version replaced gi:12797974.
REFERENCE	Contact : Genoscope
AUTHORS	Genoscope - Centre National de Sequencage
TITLE	BP 191 91006 EVRY cedex - France
JOURNAL	Email: segr@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6027.r For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CSD0F004D01QIP ; cluster=6027.r. Contact :
COMMENT	Feng Liang Email : fliang@life tech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Paradey Avenue Genoscope sequence ID : CSD0F004D01QIP.

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/notes=Torgans: brain; Vector: pCMVSPOK 6; 1st strand cDNA
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enriched, double-strand cDNA was digested with NotI and
cloned into the NotI and EcoRI sites of the pCMVSPOK 6
vector. Library was not normalized."
BASE COUNT      209 a      266 c      274 g      153 t
ORIGIN           4 others

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Query Match	31.9%	Score 825.4	DB 9	Length 906
Best Local Similarity	98.7%	Pred. No. 8.9e-997		
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QY	177	CTGTGCTCTGCTGTGTGGCGGCGCGGCTGCCACAGGCGCCCGGCGCGCTCCGAGCGGCGACC	236	
Db	110	CTGTGCTGTGTGTGTGGCGGCGGCGGCTGCCACAGGCGCCCGGCGCGCTCCGAGCGGCGACC	169	
QY	237	TGCGCTCCAGTCAAGTCAAGCCCGGCGCGGCTCTCAGCTACCCGCGAGAGAGGACACCTCTAAT	236	
Db	170	TGCGCTCCAGTCAAGTCAAGCCCGGCGCGGCTCTCAGCTACCCGCGA-GAGAGGCGACCTCTAAT	228	
QY	297	GAGATGTTCCGCGAGGTTGAGGAATCTGATGAGAGCACGCGACCAAAATTGGCGAGGCG	356	
Db	229	GAGATGTTCCGCGAGGTTGAGGAATCTGATGAGAGCACGCGACCAAAATTGGCGA-SCGG	287	
QY	357	GTGGAAGAGATGGAGGCGAGAAAGACTCTCTAAAGCATCATCAGAAGTGAACCTTGCA	416	
Db	288	GTGGAAGAGATGGAGGCGAGAAAGACTCTCTCTAAAGCATCATCAGAAGTGAACCTTGCA	347	
QY	417	AACCTTACCTCCAGCTATATACATAGACCAACACAGACAGAAAGTTGGAATTAATACC	476	
Db	348	AACCTTACCTCCAGCTATATACATAGACCAACACAGACAGAAAGTTGGAATTAATACC	407	
QY	477	ATCCATGTGACCGAGAAATTACAAAGATTAACCAACCGAGCTGGACAAATGCTTT	536	
Db	408	ATCCATGTGACCGAGAAATTACAAAGATTAACCAACCGAGCTGGACAAATGCTTT	467	
QY	537	TCAGAGACAGTTATTCATCTGTGGAGAGCGAAGAGGCGAGAGAGCCACGAGTGCATC	556	
Db	468	TCAGAGACAGTTATTCATCTGTGGAGAGCGAAGAGGCGAGAGAGCCACGAGTGCATC	527	
QY	597	ATGAGAGAGGACGTGTGGGCGCCGAGCATGTATCTGCCAGTTTGCACCTTCCAGTACACTGC	656	
Db	528	ATGAGAGAGGACGTGTGGGCGCCGAGCATGTATCTGCCAGTTTGCACACTTCCAGTACACTGC	587	
QY	657	CAGCCATGCCGGGCGCCAGAGATGCTCTTGCACCCGGGACAGTGAAGTCTGTGAGACAG	716	
Db	588	CAGCCATGCCGGGCGCCAGAGATGCTCTTGCACCCGGGACAGTGAAGTCTGTGAGACAG	647	
QY	717	CTGTGTGTCTGGGGTCCATCGCACCAAAATGGCCACAGGGGCGACCAATGGGACCATCTGT	776	
Db	648	CTGTGTGTCTGGGGTCCATCGCACCAAAATGGCCACAGGGGCGACCAATGGGACCATCTGT	707	
QY	777	GACAAACGAGGAGCTGCCAGCCGGGCGTGTGCTGTGCTTCCAGAGAGGCTGTGTTTC	836	
Db	708	GACAAACGAGGAGCTGCCAGCCGGGCGTGTGCTGTGCTTCCASAGAGGCTGTGTTTC	767	
QY	837	CCGTGTGTGACACCCCTGTGCCGTGAGAGGGCGAGCTTTGCCATGACCCCGGCAAGCCGGCTT	896	
Db	768	CCGTGTGTGACACCCCTGTGCCGTGAGAGGGCGAGCTTTGCCATGACCCCGGCAAGCCGGCTT	827	
QY	897	CTGAGACTCATCACTTGGAGGCTTAGAGCTTAGAGAGCTTGAACGATGCCCTTGTGCC	956	
Db	828	CTGAGACTCATCACTTGGAGGCTTAGAGCTTAGAGAGCTTGAACGATGCCCTTGTGCC	887	
QY	957	AGTGGCTCTCTGTGCCAGC 975		
Db	888	AGTGGCTCTCTGTGCCAGC 906		

RESULT 18	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	TITLE	JOURNAL	COMMENT
BU190800	1007 bp	MRNA	linear	EST_04-SEP-2002							
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5'	NIH sequence.										
BU190800											
BU190800.1	GI:22704784										
EST.											
Homo sapiens											
Homo sapiens											
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;											
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.											
1 (bases 1 to 1007)											
NIH-MGC	http://mgc.nci.nih.gov/										
National Institutes of Health, Mammalian Gene Collection (MGC)											
Unpublished											
Contact: Robert Strausberg, Ph.D.											
Email: csapbs@email.nih.gov											
Tissue Procurement: ATCC											
cDNA Library Preparation: Rubin Laboratory											
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)											
DNA Sequencing by: Agencourt Bioscience Corporation											
Clone distribution: MGC clone distribution information can be											
found through the I.M.A.G.E. Consortium/LNLN at:											
http://image.lnl.gov											
Plate: L1CM2313	row: c	column: 05									
High quality sequence stop: 575.											
Location/Qualifiers											
1..1007											
/organism="Homo sapiens"											
/mol_type="mRNA"											
/dd_xref="taxon:9606"											
/clone="IMAGE:6083260"											
/tissue_type="ductal carcinoma, cell line"											
/lab_host="DH10B (phage-resistant)"											
/clone_11b="NIH_MGC_110"											
/note="Organ: pancreas; Vector: pOTB7; Site:1: XhoI;											
Site 2: EcoRI; cDNA made by oligo-dT priming.											
directionally cloned into EcoRI/XhoI sites using the											
following 5' adaptor: GGCACGAG(G). Library constructed by											
ling Hong in the laboratory of Gerald M. Rubin (University											
of California, Berkeley) using ZAP-cDNA synthesis kit											
(Stratagene) and Superscript II RT (Life Technologies).											
Note: this is a NIH_MGC library."											
BASE COUNT	159 a	261 c	297 g	250 t							
ORIGIN											
Query Match	31.9%	Score 825.2	DB 13	Length 1007							
Best Local Similarity	95.0%	Pred. No. 9e-99	39	Indels 11	Gaps 8						
Matches 939	Conservative 0	Mismatches 0									
849	CCCTGCGCCGTGGAGGGGAGCCTTGGCATGACCCCGCAGCCGCTTCTGAGCCTCATC	908									
1	CCCCGTGCCCCGTGGAGGGGAGCCTTGGCATGACCCCGCAGCCGCTTCTGAGCCTCATC	60					</				

Oy		1149	GCAGCTGGGAGAGCCTGGGCGTGCACGCCGTGCACATGCTGGAGAGGGAAGATTAGATC	1208
Db		301	GCAGTGAGGAGAGCCCTGGCGCTGCACGCCCGCTGCACATGCTGGAGAGGGAAGATTAGATC	360
Oy		1209	TGAAACAAGGCTGTGGGTAGATATGTGCAATAGAAAATAGCTAATTTTATTTCCCAGATGTGTG	1268
Db		361	TGAGCAAGAGGCTGTGGGTAGATATGTGCAATAGAAAATAGCTAATTTTATTTCCCAGATGTGTG	420
Oy		1269	CTTTAGAGCGTAGGAGTCACAGGCTTCTCCATACTCTCTCCAGTAAGTTTCCCCTCT	1328
Db		421	CTTTAGAGCGTAGGAGTCACAGGCTTCTCTTACTATCATCTTCTCCAGTAAGTTTCCCCTCT	480
Oy		1329	GGCCTTGAACAGATAGAGTGTTTGTGCAATTTGTTCAGCTCCCCAGGCTGTCTCCAGGCTT	1388
Db		481	GGCTTGAACAGATAGAGTGTTTGTGCAATTTGTTCAGCTCCCCAGGCTGTCTCCAGGCTT	540
Oy		1389	CACAGCTGTGTGCTTGGAGAGTCACAGGCAAGGATTAACTGACAGAGACAGTTTGCCACCC	1448
Db		541	CACAGCTGTGTGCTTGGAGAGTCACAGGCAAGGATTAACTGACAGAGACAGTTTGCCACCC	600
Oy		1449	TGTCCAAATTAATATGGCTGTCTTGGCTTGCCTTACCAGTTGGCAGACAGCCGTGTGTTCTACATG	1508
Db		601	TGTCCAAATTAATATGGCTGTCTTGGCTTGCCTTACCAGTTGGCAGACAGCCGTGTGTTCTACATG	660
Oy		1509	GCTTTGATTAATTTGTTTGGAGGGAGAGATGAAAAATATGTGAGTCTCCCTGTGATTTGCT	1568
Db		661	GCTTTGATTAATTTGTTTGGAGGGAGAGATGAAAAATATGTGAGTCTCCCTGTGATTTG-719	-719
Oy		1569	TTTTGGGGAAATGTGTGAGAAAGAATGECCTGCTTTTGCAAACATCAACTCGCAAAAATGCCAA	1628
Db		720	TTTTGGGGAAATGTGTGAGAAAGAATGECCTGCTTTTGCAAACATCAACTCGGGCAAAAATGCCAA	779
Oy		1629	CAATGAAATTTTCCACGACAGATCTTTTCCATGAGGCAT-AGGTAAAGCTGTG-CCTTTCAGCTG	1686
Db		780	CAATGAAATTTTCCACGACAGATCTTTTCCATGAGGCAT-AGGTAAAGCTGTG-CCTTTCAGCTG	839
Oy		1687	TTTGAGATGAAAT-GTTCTGTTCACCTCGCATTA--CATGTGTTTATCATNCCAGCAGCTG	1743
Db		840	TTTGAGATGAAATGTTCTGTTCCTCCCTGTGATTAACATGCGGTTTATCATNCCAGCAGCAGG	899
Oy		1744	TTGCT-CAGCTCTACCTCTGTGTCAGAGGCGCAGCATTTTTCATA--TCCAAGATCAATT-C	1798
Db		900	TTGCTCCAGCTCTACCTCTGTGTCAGAGGCGCAGCATTTTTCATAATTTCAGATCAATTCC	959
Oy		1799	CCTTCTTCAGCACAGCCTGGGAGAGGGG	1826
Db		960	CCCTCTTCACAAAGCCGTGCGGAGAGG	987
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RESULT 19				
AKO04853				
LOCUS		3357 bp	mRNA	linear HTC 05-DEC-2002
DEFINITION		Mus musculus adult male liver cDNA, RIKEN full-length enriched library, clone1300002I07 product:dickopf homolog 3 (Xenopus laevis), full insert sequence.		
ACCESSION		AKO04853		
VERSION		AKO04853.1 GI:12836349		
KEYWORDS		HTC; CAP trapper.		
SOURCE		Mus musculus (house mouse)		
ORGANISM		Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
<hr/>				
REFERENCE		1	Carninci, P. and Hayashizaki, Y.	
AUTHORS			High-efficiency full-length CDNA cloning	
TITLE			Method. Enzymol. 303, 19-44 (1999)	
JOURNAL				
MEDLINE				
PUBMED			10349636	
REFERENCE		2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komio, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	
AUTHORS			Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	
TITLE				

Accession	Organism	Source	Version	Keywords	Definition	LOCUS	Result
Dp							410 AGCAGCGAACCAGGAGTGGAAATTAACAAGTCCATGTGTGACAGGAAGTTCCAAAGATA 469
Qy							507 ACCAACAACCAAGCTGAGCAAAATGGTCTTTTTCAGAGACAGTTATTCATCTGGGGAGAC 566
Dp							470 ACCAACAACCAAGTGGACAGGTGTCTTTTCTGAGACAGTCAATTCATCTGTAGGGAT 529
Qy							567 GAAGAAGGCAAGAGGCCAGAGTGCATCATGCAAGAGACTGTGGGCCAGCATATAC 626
Dp							530 GAAGAAGGCAAGAGGCCATGAATGTTCAATTATGAACATGTGGGCCACAGATAC 589
Qy							627 TGCAGATTGCCAGCTTCCAGTACACCTGCCAGGCATGCGGGGCCAGAGATGCTCTGC 686
Dp							590 TGCAGATTCTCCAGGCTTCAAGTACACCTGCCAGGCATGCGGGGCCAGAGATGCTATGC 649
Qy							687 ACCCGGGAACAGTGAAGTCTGTGGAGACCACTGTGTGTCTGGGGTCACTGCACAAATG 746
Dp							650 ACCCGGAACAGTGAAGTCTGTGGAGACCAAGTGTGTCTGGGGTCACTGCACCAAAAG 709
Qy							747 GCCACAGAGGGAGAGCAATGGAGCACTGTGTACAACAAGAGGAGACTGCCAGCCGGGCTG 806
Dp							710 GCCACAAAGTGGAGATGGACCACTGTGTACAACAAGAGGATTTGCCAGCTGGCTGTG 769
Qy							807 TGTGTGCTTTCAGAGAGGCTGCTGTTCCTGTGTGTGCAACACCCTGCTGGAGGGC 866
Dp							770 TGTGTGCTTTCCAAAGAGGCTGTGTTCCTGTGTGCAACACCCTGCTGGAGGGCA 829
Qy							867 GAGCTTGGCATGACCCCGCAGCCGAGCTTTCTGAGACTCATCACTGGAGCTAGAGCT 926
Dp							830 GAGCTTGGCATGACCCCAACAGCCAGTGTGTGATCTCATCACTGGAGACTAGAGCT 889
Qy							927 GATGAGCTTGTGACCGATGCTCTGTGTGSCAGTGGCTCTCTGCGACGCCCAAGACCA 986
Dp							890 GAAGAGCTTGTGACCGATGCTCTGTGTGSCAGTGGCTCTCTGCGACGCCCAAGACCA 949
Qy							987 AGCTGTGTATGTGTGCAAGCCGACCTTCGTGGGAGAGCTGACCAAGATGGGAGATC 1046
Dp							950 AGCTGTGTGTATGTGTGCAAGCCGACCTTCGTGGGAGAGCTGACCAAGATGGGAGATC 1009
Qy							1047 CTGTCTCCCAAGAGAGTCCCCGATGATGATTAAGTGTGGCAGCTTCATGAGAGGTGC 1106
Dp							1010 CAGCTCCCAAGAGAGGCCCCGATGATGATTAAGTGTGGCTTCATGAGAGAGTGC 1063
Qy							1107 CAGAGCTGAGAGACCTGGAGAGAGAGCTGTACTGAAGAATGGCGCTGGGGAGCCTTGC 1166
Dp							1070 CAGGAGCTGAGAGACCTGGAGAGAGAGCCTTACCCAGAGAGATGGCATTTAGAGGGCCTTGC 1125
Qy							1167 GCTGCGCCGCTGTCACTGCTGTGGAGGGGAGAGATTTAGATCTGAGACAGAGCTGTG --- 1222
Dp							1130 CCT--GTGAGATCTACTAGGCGGAGAGAGAGATTTAGGCCAGACCAAGCTGATGCAC 1186
Qy							1223 -GGTAGATGTGCAATAGAAATAGTAATTTATTTTCCAGAGTGTGCTTTAGAGCTGGG 1281
Dp							1187 TGGTAAATGTGCAATAGAAATAGGCTAATTTATTTTCCAGAGATGTGCCAAGTGTGGAA 1246
Qy							1282 CTGACCAAGGCTTCTTCTACATCTTCTTCC 1311
Dp							1247 TGGCGCGAGACTCTTCCAGTAGACTTTTTC 1276
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LOCUS							
DEFINITION							
ACCESSION							
VERSION							
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							

AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: LINC2368 row= a column= 11 High quality sequence stop= 584.
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BASE COUNT	170 a 212 c 263 g 212 t
ORIGIN	
Query Match	31.7%; Score 819; DB 13; Length 858;
Best Local Similarity	99.1%; Pred. No. 6.3e-98;
Matches	844; Conservative 0; Mismatches 6; Indels 2; Gaps 2;
D	849 CCCCTGCCCTGTGGAGGGGGAAGCTTTGCCATGACCCCGCAGCCGGCTTGTCAGACTCATC 908
Q	1 CCCCTGCCCTGTGGAGGGGGAAGCTTTGCCATGACCCCGCAGCCGGCTTGTCAGACTCATC 60
D	909 ACCCTGGAGCTAGAAGCTGTAGAGAGCTTGTGACCAGTAGCCCTTGTGTCCAGTCCCTCTC 968
Q	61 ACCTGGAGCTAGAAGCTGTAGAGAGCTTGTGACCAGTAGCCCTTGTGTCCAGTCCCTCTC 120
D	969 TGGCAGCCCCCAGCAGCCAGCCTTGTGTATGTGTGCAAGCCACCTTGTGTGGGAGCCGT 1022
Q	121 TGGCAGCCCCCAGCAGCCTTGTGTATGTGTGCAAGCCACCTTGTGTGGGAGCCGT 180
D	1029 GACCAAGATGGGAGAGATCCTGTGCCCGAGAGAGGTCCCGATAGATTAGTAAGTTGGCAGC 1088
Q	181 GACCAAGATGGGAGAGATCCTGTGCCCGAGAGAGGTCCCGATAGATTAGTAAGTTGGCAGC 240
D	1089 TTTCATGGAGAGAGTGGCCGACAGAGCTGAGAGACTGTGAGAGAGAGCCTGTACTAAGAGTG 1148
D	241 TTTCATGGAGAGAGTGGCCGACAGAGCTGAGAGAGCTGAGAGAGAGCCTGTACTAAGAGTG 300
Q	1149 GGGCTGGGAGAGCCTGTGGGCTGCCCGCGCTGTGCACTGTGTGGAGGGGAAAGATTAGATC 1208
D	301 GGGCTGGGAGAGCCTGTGGGCTGCCCGCGCTGTGCACTGTGTGGAGGGGAAAGATTAGATC 360
Q	1209 TGGACCAAGCTGTGGGTATGATGTGCATAATAAATACCTAATTATTTCCCAGAGGTGTG 1266
D	361 TGGACCAAGCTGTGGGTATGATGTGCATAATAAATACCTAATTATTTCCCAGAGGTGTG 420
Q	1269 CTTTAGGGGTGGGCTGACCAAGGCTTCTCTACATCTTCTTCCAGTAAGTTCCCTCT 1328
D	421 CTTTAGGGGTGGGCTGACCAAGGCTTCTCTACATCTTCTTCCAGTAAGTTCCCTCT 480
Q	1329 GGCTTGACAGCATAGAGTGTGTGCAATTGTTCAGCTCCGCCAGAGGTGTCTTCCAGAGGT 1388
D	481 GGCTTGACAGCATAGAGTGTGTGCAATTGTTCAGCTCCGCCAGAGGTGTCTTCCAGAGGT 540

QY 1389 CACAGTCTGCTGCTTGGGAGAGTCAAGCAGGCTTAACTGACAGAGAGCTTTGCCACCCC 1448
Db 541 CACAGTCTGCTGCTTGGGAGAGTCAAGCAGGCTTAACTGACAGAGAGCTTTGCCACCCC 600
QY 1449 TGTCCAGATTATTTGGCTGCTTTGGCTTACCAAGTTGGCAGACAGCCCTTTGTTCTACATG 1508
Db 601 TGTCCAGATTATTTGGCTGCTTTGGCTTACCAAGTTGGCAGACAGCCCTTTGTTCTACATG 660
QY 1509 GCTTTGATTAATTTGTTGAGGGGAGAGATGAAACAAATGTAGTCTCCCTTGATTTGGT 1568
Db 661 GCTTTGATTAATTTGTTGAGGGGAGAGATGAAACAAATGTAGTCTCCCTTGATTTGGT 720
QY 1569 TTTGGGGAATGTGAGAGAGTGCCTGCTTTGCAACATCAACCTGGGCAAAATGCA 1628
Db 721 TTTGGGGAATGTGAGAGAGTGCCTGCTTTGCAACATCAACCTGGGCAAAATGCA 780
QY 1629 CAAATGAATTTTCCACGAGCTTTCTTCATGAGGAT-AGGTAAAGTGTGCC-TTCAAGCTG 1686
Db 781 CAAATGAATTTTCCACGAGCTTTCTTCATGAGGAT-AGGTAAAGTGTGCC-TTCAAGCTG 840
QY 1687 TTGAGATGAAA 1698
Db 841 TTGAGATGAAA 852

RESULT 21
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LOCUS AL565532 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION CS0DF004YG01 3-PRIME, mRNA sequence.
ACCESSION AL565532
VERSION AL565532.2 GI:30549640
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 896)
Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
COMMENT On Feb 16, 2001 this sequence version replaced gi:12917002.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6027.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DF004AD01NP1&cluster=6027.r. Contact :
Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DF004AD01NP1.

FEATURES
source

1 896

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DF004YG01"

/tissue_type="FETAL BRAIN"

/dev_stage="fetal"

/clone_lib="Homo sapiens FETAL BRAIN"

/note="Torgan: brain; Vector: PCMSPORT 6; 1st strand cDNA
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cloned into the Not I and EcoRV sites of the PCMSPORT 6
vector. Library was not normalized."

BASE COUNT 234 a 189 c 207 g 250 t 16 others

Query Match 31.6%, Score 817.2; DB 9; Length 896;

Best Local Similarity 96.6%; Pred. No. 1.1e-97;
Matches 845; Conservative 9; Mismatches 18; Indels 3; Gaps 2;
QY 1647 AGTTCTTTCCATGGGACATAGTAACTGCTGCTTCAAGCTGTGCAAGATGAATGTTCTGT 1706
Db 896 AGTTCTTTCCATGGGACATAGTAACTGCTGCTTCAAGCTGTGCAAGATGAATGTTCTGT 837
QY 1707 TCACCTGATTAACATGTGTTTATTCATCCAGACATGTTGCTCAGCTCTACCTGTGCG 1766
Db 836 TCACCTGATTAACATGTGTTTATTCATCCAGACATGTTGCTCAGCTCTACCTGTGCG 777
QY 1767 CAGGACAGATTTTCTATTCACAGATCAATTCCTCTCTCAACAGCTGGGAGGGG 1826
Db 776 CAGGACAGATTTTCTATTCACAGATCAATTCCTCTCTCAACAGCTGGGAGGGG 717
QY 1827 TCATTGTTCTCTGCTGCTTCCATCAGGATCTCAGAGCTCAGAGACTGCAAGCTGTGCC 1886
Db 716 TCATTGTTCTCTGCTGCTTCCATCAGGATCTCAGAGCTCAGAGACTGCAAGCTGTGCC 657
QY 1887 AAGTCAACAGCTAGTGAAGACCAAGAGATTTCACTGTGTTGACTCTAAGCTCAATG 1946
Db 656 AAGTCAACAGCTAGTGAAGACCAAGAGATTTCACTGTGTTGACTCTAAGCTCAATG 597
QY 1947 CTCTCTCCATCCCAACCAACAGCTTGGTGCACCAAAAGTGTGCCCAAAAGGAGAGA 2006
Db 596 CTCTCTCCATCCCAACCAACAGCTTGGTGCACCAAAAGTGTGCCCAAAAGGAGAGA 537
QY 2007 GAATGGGATTTTTC--TTGAGGACATGACATCTGGAATTTAAGTCAAACTAATTCACA 2064
Db 536 GAATGGGATTTTTC--TTGAGGACATGACATCTGGAATTTAAGTCAAACTAATTCACA 477
QY 2065 TCCCTTTAAAGTAACTAAGTGAAGAAACAGAGCTGTTCACAGTGTGGGAGCCGT 2124
Db 476 TCCCTTTAAAGTAACTAAGTGAAGAAACAGAGCTGTTCACAGTGTGGGAGCCGT 417
QY 2125 CCTTCTTAATGAAGAAATGATTTGACACTGCTGCTTGGGAGTGCATTAAGTACT 2184
Db 416 CCTTCTTAATGAAGAAATGATTTGACACTGCTGCTTGGGAGTGCATTAAGTACT 357
QY 2185 TGAAGATTAATGACTGAGCGTAGCATAGTTAAGTGCAGAAACAGTAAAGTAA 2244
Db 356 TGAAGATTAATGACTGAGCGTAGCATAGTTAAGTGCAGAAACAGTAAAGTAA 297
QY 2245 TTGTAGGGGAGAGATTTAATGAATTTGCAATTCATTAGCGAATCGAAGACAT 2304
Db 296 TTGTAGGGGAGAGATTTAATGAATTTGCAATTCATTAGCGAATCGAAGACAT 237
QY 2305 TATCAACCAAGTGAAGAAATCAACCGAGAGGCTGTGTAACATGTTGTAATG 2364
Db 236 TATCAACCAAGTGAAGAAATCAACCGAGAGGCTGTGTAACATGTTGTAATG 177
QY 2365 GCACTGCGAACAAGTACTCTTACGCACTCCCAAAATGATGTTTTCAGGTGTCAGT 2424
Db 176 GCACTGCGAACAAGTACTCTTACGCACTCCCAAAATGATGTTTTCAGGTGTCAGT 117
QY 2425 GTTGCAACCATGATTCATCCAGATCTTAAAGTTAAAGTGAACATGATGATAAG 2484
Db 116 GTTGCAACCATGATTCATCCAGATCTTAAAGTTAAAGTGAACATGATGATAAG 58
QY 2485 CATGCTTTCTTGAAGTTTAAATTAATGATTAACA 2519
Db 57 CATGCTTTCTTGAAGTTTAAATTAATGATTAACA 23
RESULT 22
LOCUS BQ878479 871 bp mRNA linear EST 16-AUG-2002
DEFINITION AGENCOURT_8064671 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6206301
5', mRNA sequence.
ACCESSION BQ878479
VERSION BQ878479.1 GI:22270487
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 871)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LCM2360 row: 1 column: 22
 High quality sequence stop: 686.
 Location/Qualifiers
 1. 871
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 /clone="IMAGE:6206301"
 /tissue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 110"
 /note="Organ: pancreas; Vector: pOTB7; Site: 1; XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGACAGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH MGC Library." 1 others

BASE COUNT 173 a 219 c 262 g 216 t

Query Match 31.5%; Score 815.2; DB 13; Length 871;
 Best Local Similarity 99.5%; Pred. No. 2e-97;
 Matches 828; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

849 CCCCTGCCGCTGAGGCGGAGCTTTGCGATGACCCGCGCGGCTTGTGAGCCCTC 508
 1 CCCCTGCCGCTGAGGCGGAGCTTTGCGATGACCCGCGCGGCTTGTGAGCCCTC 60

909 ACCTGGAGCTAGAGCTTGAAGAGCTTGAACCGATGCTTGTGCAAGTGGCTCTC 968
 61 ACCTGGAGCTAGAGCTTGAAGAGCTTGAACCGATGCTTGTGCAAGTGGCTCTC 120

969 TGGCAGCCCAACAGCCAGACCTGTGTATGTGTGAGAGCCGACTTGTGAGGAGCCGT 1028
 121 TGGCAGCCCAACAGCCAGACCTGTGTATGTGTGAGAGCCGACTTGTGAGGAGCCGT 180

1029 GACCAAGATGGGAGATCTGCTGCGCCAGAGAGGTCGCCGATGATGATGAGTTGACAG 1088
 181 GACCAAGATGGGAGATCTGCTGCGCCAGAGAGGTCGCCGATGATGATGAGTTGACAG 240

1089 TTCTATGAGAGAGTGTGCGCCAGAGCTTGAAGAGAGCTTGAAGAGAGTGTGAG 1148
 241 TTCTATGAGAGAGTGTGCGCCAGAGCTTGAAGAGAGCTTGAAGAGAGTGTGAG 300

1149 GCGCTGGGAGAGCTTGGGCTGCGCGCGCTGCACTGTGGAGAGGAGATTAGATC 1208
 301 GCGCTGGGAGAGCTTGGGCTGCGCGCGCTGCACTGTGGAGAGGAGATTAGATC 360

1209 TGGACCAAGCTGTGGGTGTGATGTGATAGAAATAGTATTTATTTCCCAAGTGTG 1268
 361 TGGACCAAGCTGTGGGTGTGATGTGATAGAAATAGTATTTATTTCCCAAGTGTG 420

1269 CTTTGGAGCTGGGCTGACAGAGGCTTCTTCTACATCTTCTCCAGTATGTTCCCTCT 1328
 421 CTTTGGAGCTGGGCTGACAGAGGCTTCTTCTACATCTTCTCCAGTATGTTCCCTCT 480

1329 GGCTTGCAGAGATAGAGTGTGTGATTTTGTAGCTCCCGCAGGCTGTCTCAGGCTT 1388
 481 GGCTTGCAGAGATAGAGTGTGTGATTTTGTAGCTCCCGCAGGCTGTCTCAGGCTT 540

1389 CACAGCTGTGCTTGGGAGAGTGCAGAGGTTAACTGACAGAGAGTGGCCACCCC 1448
 541 CACAGCTGTGCTTGGGAGAGTGCAGAGGTTAACTGACAGAGAGTGGCCACCCC 600

1449 TGTCCAGATTATTTGCTGCTTGTCTTACAGTTGGCAGACAGCCGTTGTTCTACATG 1508
 601 TGTCCAGATTATTTGCTGCTTGTCTTACAGTTGGCAGACAGCCGTTGTTCTACATG 660

1509 GCTTTGATATTTGTTTGAAGGAGAGATGGAACATGTGTGATCCCTGATTTGT 1568
 661 GCTTTGATATTTGTTTGAAGGAGAGATGGAACATGTGTGATCCCTGATTTGT 720

1569 TTTGGGGAATGTGAGAGAGTGCCTGCTTGTGCAACATCAACCTGGCAAAATGCAA 1628
 721 TTTGGGGAATGTGAGAGTGCCTGCTTGTGCAACATCAACCTGGCAAAATGCAA 779

1629 CAATGATTTTCCAGCAGCTTCTTCCATGGGATAGTAACTGTGCTT 1680
 780 CAATGATTTTCCAGCAGCTTCTTCCATGGGATAGTAACTGTGCTT 831

RESULT 23
 BU196879 985 bp mRNA linear EST 04-SEP-2002
 AGENCOURT 8076102 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6084891
 5', mRNA sequence.
 BU196879
 BU196879.1 GI:22710863
 EST.

ACCESSION
 VERSION
 KEYWORDS

SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 985)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LCM2317 row: 5 column: 04
 High quality sequence stop: 644.
 Location/Qualifiers
 1. 985
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6084891"
 /tissue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 110"
 /note="Organ: pancreas; Vector: pOTB7; Site: 1; XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGACAGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH MGC Library." 1 others

BASE COUNT 199 a 256 c 282 g 248 t

Query Match 31.5%; Score 813.4; DB 13; Length 985;
 Best Local Similarity 98.3%; Pred. No. 3.2e-97;
 Matches 844; Conservative 0; Mismatches 11; Indels 4; Gaps 2;

QY 849 CCCCCTGCCCTGGAGGGCGAGCTTTGGCCATGACCCCGCAGCCGGCTTGTGACCTCANC 908
 1 CCCCCTGCCCTGGAGGGCGAGCTTTGGCCATGACCCCGCAGCCGGCTTGTGACCTCANC 60

QY 909 ACCTGGGAGCTAAGAGCTGTATGAGAGCTTGGACCGATGCCCTTGTGCTGAGTGCCTCTC 968
 61 ACCGGGAGCTAAGAGCTGTATGAGAGCTTGGACCGATGCCCTTGTGCTGAGTGCCTCTC 120

QY 969 TGGCAGCCCGCAGCAGCCAGCCTGCTGTATGTGTGCAAGCCGACCTTGTGAGGAGACCTT 1028
 121 TGGCAGCCCGCAGCAGCCAGCCTGCTGTATGTGTGCAAGCCGACCTTGTGAGGAGACCTT 180

QY 1029 GACCAAGATGGGAGATCTCTGTGCCCCAGAGAGGTCCCCGATAGTATGAAATTGGCAGC 1088
 181 GACCAAGATGGGAGATCTCTGTGCCCCAGAGAGGTCCCCGATAGTATGAAATTGGCAGC 240

QY 1089 TTCAATGAGAGAGTGGCCAGAGAGCTGAGAGACCTGAGAGAGAGCTGACTGAAGAAGATG 1148
 241 TTCAATGAGAGAGTGGCCAGAGAGCTGAGAGACCTGAGAGAGAGCTGACTGAAGAAGATG 300

QY 1149 GCGCTGGGGGAGCCTGTGCGCTGCCCGCGCTGCACTGCTGGGAGGGGAGAGATTAGATC 1208
 301 GCGCTGGGGGAGCCTGTGCGCTGCCCGCGCTGCACTGCTGGGAGGGGAGAGATTAGATC 360

QY 1209 TGGAGCAGGCGTGGGGAGATGTCATAGAAATAGCTATTTATTTCCCGAGTGTG 1268
 361 TGGAGCAGGCGTGGGGAGATGTCATAGAAATAGCTATTTATTTCCCGAGTGTG 420

QY 1269 CTTTAGGCGTGGGGTGAACAAGCTTCTTCTAATCTTCTTCCAGTAATTTCCCTCT 1328
 421 CTTTAGGCGTGGGGTGAACAAGCTTCTTCTAATCTTCTTCCAGTAATTTCCCTCT 480

QY 1329 GCGTTGACACATAGAGTGTGTGCAATTTGTGACCTCCCGAGCGCTTCTTCCAGGCTT 1388
 481 GCGTTGACACATAGAGTGTGTGCAATTTGTGACCTCCCGAGCGCTTCTTCCAGGCTT 540

QY 1389 CACAGCTGTGCTTGGAGAGTCAAGAGGTTAACTGACAGAGAGATTGGCCACCC 1448
 541 CACAGCTGTGCTTGGAGAGTCAAGAGGTTAACTGACAGAGAGATTGGCCACCC 600

QY 1449 TGTCCAAATTAATTTGGCTGCTTGTGCTTCAACAGTTGGCAACAGCGCTTGTCTACATG 1508
 601 TGTCCAAATTAATTTGGCTGCTTGTGCTTCAACAGTTGGCAACAGCGCTTGTCTACATG 660

QY 1509 GCTTGTGAATTTGTTAGAGGGAGAGATGAAACAATGTGAGTCTCCCTCTGATTTG 1568
 661 GCTTGTGAATTTGTTAGAGGGAGAGATGAAACAATGTGAGTCTCCCTCTGATTTG 720

QY 1569 TTTGGGAAAATGTGAGAAAGTGCCCTGCTTGGCAACATCAACCTGGCAAAAATGCAA 1628
 721 TTTGGGAAAATGTGAGAAAGTGCCCTGCTTGGCAACATCAACCTGGCAAAAATGCAA 780

QY 1629 CAAATGAA-TTTTCAAGCAGTTCTTCCATGGGCATAGGTAAGC--TGTGCTTCAG 1684
 781 CAAATGAAATTTTCCCGCAGCTTCTTCCATGGGCATAGGTAAGCTGTGCTTCCTCCT 840

QY 1685 TGTGAGATGAAATGTTT 1703
 841 GGTTCAGATGAAATGTTT 859

Db 841 GGTTCAGATGAAATGTTT 859

RESULT 24
 B0879213
 LOCUS B0879213 936 bp mRNA EST 16-AUG-2002
 DEFINITION AGENCOURT 8229317 Lupski, dorsal root ganglion Homo sapiens cDNA
 ACCESSION B0879213
 VERSION B0879213.1 GI:22271221
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 936)
 AUTHORS NIH-MGC
 TITLE NIH-MGC
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished
 Contact: Robert Strusberg, Ph.D.
 Email: cgsab@remail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 Plate: LLM13571 row: f column: 17
 High quality sequence stop: 708.

FEATURES
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 1..936
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6183568"
 /sex="male"
 /tissue_type="dorsal root ganglia"
 /dev_stage="adult, 36 yr"
 /lab_host="MDH10B"
 /clone_lib="Lupski, dorsal root ganglion"
 /note="Vector: pCMV-SPORT6 (Life Technologies); Site 1:
 NotI; Site 2: SalI; cDNA made by oligo-dT priming.
 Directionally cloned using the following adaptors:
 5'-TGCACACAGCGCTCG-3' and
 5'-GACGTGCTTGTATGAGGAGGCGGCGCTT(15)-3'. Size selected >
 1 kb for average insert length 1.7 kb. This is a primary
 library, non-amplified. Library constructed by Life
 Technologies and donated by U. Lupski, M.D./Ph.D. (Baylor
 College of Medicine) and is available through Life
 Technologies."

BASE COUNT 213 a 249 c 289 g 185 t

Query Match 31.4%; Score 811.2; DB 13; Length 936;
 Best Local Similarity 96.3%; Pred. No. 6.3e-97;
 Matches 880; Conservative 0; Mismatches 23; Indels 5; Gaps 5;

QY 401 AGAAGTGAACCTGGCAAACTTACCTCCAGCTATCAAAATGAGACCAACAGACAGAA 460
 1 AGAAGTGAACCTGGCAAACTTACCTCCAGCTATCAAAATGAGACCAACAGACAGAA 60

QY 461 GGTGGAAATTAATCAATCCATGTGCAACCGAGAAATTACAAAGTAAACCAACACAGAC 520
 61 GGTGGAAATTAATCAATCCATGTGCAACCGAGAAATTACAAAGTAAACCAACACAGAC 120

QY 521 TGGACAAATGCTCTTTTCAAGACAGTTATCAATCTGTGGGAGACGAAGAAGCAGAG 580
 121 TGGACAAATGCTCTTTTCAAGACAGTTATCAATCTGTGGGAGACGAAGAAGCAGAG 180

QY 581 GAGCCACAGATGATCATGACAGAGAGATGTGGGCGCCAGCATGTATCTGCGACCTTTGGCAG 640
 181 GAGCCACAGATGATCATGACAGAGAGATGTGGGCGCCAGCATGTATCTGCGACCTTTGGCAG 240

QY 641 CTTCCAGTACACCTGSCAGCAGCAGTGGGGGCGAGAGATGCTTGCACCCGGGACAGTGA 700
 241 CTTCCAGTACACCTGSCAGCAGCAGTGGGGGCGAGAGATGCTTGCACCCGGGACAGTGA 300

QY 701 GTGCTGTGAGACAGCGCTGTGTGTGGGGTCACTGCAACCAAAATGGCCACAGGGGAG 760
 301 GTGCTGTGAGACAGCGCTGTGTGTGGGGTCACTGCAACCAAAATGGCCACAGGGGAG 360

QY 761 CAATGGAGCATCTGTGACCAACAGAGGAGCTGCCAGCGGGGCTGTGCTGTGCTTCA 820

Db 361 CAATGGAGCAATCTGTGACACACAGAGGAGCTGCCAGCCGGGCTGTGTGCTTCCA 420

QY 821 GAGAGCCCTGCTGTTCCCTGTGTGACACACCCCTGCGCGTGAAGGAGACTTGGCATGA 880

Db 421 GAGAGCCCTGCTGTTCCCTGTGTGACACACCCCTGCGCGTGAAGGAGACTTGGCATGA 480

QY 881 CCCCCGACCGGCTTCTGAGACTTATCACTGGAGACTAGAGCTGATGAGCTTGA 940

Db 481 CCCCCGACCGGCTTCTGAGACTTATCACTGGAGACTAGAGCTGATGAGCTTGA 540

QY 941 CCGATGCCCTTGTGCGCAGTGGCTCTGTGCGAGCCCGACAGCCAGCTGATGT 1000

Db 541 CCGATGCCCTTGTGCGCAGTGGCTCTGTGCGAGCCCGACAGCCAGCTGATGT 600

QY 1001 GTGCAAGCCGACCTTCTGTGGAGAGCCGTGACCAAGATGGGGAGATCTGTGCCAGGA 1060

Db 601 GTGCAAGCCGACCTTCTGTGGAGAGCCGTGACCAAGATGGGGAGATCTGTGCCAGGA 660

QY 1061 GGTCCCGCATGATGATGAAGTTGGAGCTTCAATGAGAGAGTGGCGCAGAGCTGGAAGA 1120

Db 661 GGTCCCGCATGATGATGAAGTTGGAGCTTCAATGAGAGAGTGGCGCAGAGCTGGAAGA 720

QY 1121 CCTGAGAGAGAGCTGACTGAAAGATGGCGCT-GGGGGAGCCTTGGCGCTGCGCGCTG 1179

Db 721 CCTGAGAGAGAGCTGACTGAAAGATGGCGCTGAGAGAGTGGCGCTGCGCGCTG 780

QY 1180 CACTGC-TGGAGAGGGAGAGATTTAGATCTGGAACAGCTGT-GGGTATGATGCA-T 1236

Db 781 CACTGCTTGGAGAGAGATTTAGATCTGGAACAGCTGTGGGGTAAATGTCAATT 840

QY 1237 AGAATAGCTAAATT-TTCCCGAGTGTGTCTTGTAGCGTGGAGCTGACAGGCTTCT 1295

Db 841 AGAATAGCTAAATT-TTCCCGAGTGTGTCTTGTAGCGTGGAGCTTGTAGCGGAGGTGACAGGCT 900

QY 1296 TCCTACAT 1303

Db 901 TCCTTCT 908

RESULT 25
AL519269 901 bp mRNA linear EST 12-MAY-2003
LOCUS CS0DA012YB24 5-PRIME, mRNA sequence.
DEFINITION
ACCESSION AL519269
VERSION AL519269.2 GI:30538385
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 901)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 13, 2001 this sequence version replaced gi:12782762.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6027.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DA012DA12QPLcluster=6027.r. Contact :
Feng Liang, Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DA012DA12QPL.
Location/Qualifiers
1..901
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

/clone="CS0DA012YB24"
/tissue_type="NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT 212 a 266 c 259 g 153 t 11 others
ORIGIN

Query Match 31.3%; Score 810; DB 9; Length 901;
Best Local Similarity 97.8%; Pred. No. 9.2e-97;
Matches 829; Conservative 11; Mismatches 6; Indels 2; Gaps 2;

128 CCGCGGCTGCGGCGCGCAGAGCGGATGACGCGCTTGGGGCCACCTGTGCTGCT 187

Db 56 CCGGGAATTGGCGGCGCAGAGCGGATGACGCGCTTGGGGCCACCTGTGCTGCT 115

QY 188 GCTGGCGGCGGCGGCTGCCAGCGGCGGCGGCGGCTGCCAGCGGCGGCGGCTGCCAGT 247

Db 116 GCTGGCGGCGGCGGCTGCCAGCGGCGGCGGCGGCTGCCAGCGGCGGCGGCTGCCAGT 175

QY 248 CAAGCCCGGCGGCGGCTGCCAGCTTACCAGAGAGAGCGGCGGCGGCGGCGGCTGCCAGT 307

Db 176 CAAGCCCGGCGGCGGCTGCCAGCTTACCAGAGAGAGCGGCGGCGGCGGCGGCTGCCAGT 234

QY 308 CGAGTTGAGAACTGATGAGAGACAGCGACAAATTGGCGAGCGGCTGGAAGAGAT 367

Db 235 CGAGTTGAGAACTGATGAGAGACAGCGACAAATTGGCGAGCGGCTGGAAGAGAT 293

QY 368 GAGGCGAGAAAGCTGCTGCTAAGCATCATGAAAGTGAAGTGAAGTGAAGTGAAGT 427

Db 294 GAGGCGAGAAAGCTGCTGCTAAGCATCATGAAAGTGAAGTGAAGTGAAGTGAAGT 353

QY 428 CAGCTATCAATGAGACCAACAGACAGAGGTTGGAAATTAATCAATCATGTGCA 487

Db 354 CAGCTATCAATGAGACCAACAGACAGAGGTTGGAAATTAATCAATCATGTGCA 413

QY 488 CCGAATAATCACAGATTAACCAACACAGCTGACCAATGCTTTTCAAGACAGT 547

Db 414 CCGAATAATCACAGATTAACCAACACAGCTGACCAATGCTTTTCAAGACAGT 473

QY 548 TATACATCTGTGGAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 607

Db 474 TATACATCTGTGGAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 533

QY 608 CTGTGGGCGCAGCATGATGATGCGGCTTGGCAGCTTCAAGTACACCTGCGAGCATGCCG 667

Db 534 CTGTGGGCGCAGCATGATGATGCGGCTTGGCAGCTTCAAGTACACCTGCGAGCATGCCG 593

QY 668 GGGCGAGAGATGCTGTGCAACCCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 727

Db 594 GGGCGAGAGATGCTGTGCAACCCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 653

QY 728 GGGTCACTGACCAAAATGAGCAAGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 787

Db 654 GGGTCACTGACCAAAATGAGCAAGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 713

QY 788 GAGTGCAGACCCGGGCTGTGTGTGCTTCCAGAGAGGCTGTGTTCCCTGTGTGAC 847

Db 714 GAGTGCAGACCCGGGCTGTGTGTGCTTCCAGAGAGGCTGTGTTCCCTGTGTGAC 773

QY 848 ACCCTGCGCGGTGAG 907

Db 774 ACCCTGCGCGGTGAG 833

QY 908 CACCTGAGAGCTAGAGCTGATGAGAGCTTGAACCATGCTGCTTGTGCGAGCTCTCT 967

Db 834 CACCTGAGAGCTAGAGCTGATGAGAGCTTGAACCATGCTGCTTGTGCGAGCTCTCT 893

QY 968 CTGCGAGC 975

Db 894 CTGCCAAC 901

RESULT 26
BO897122 906 bp mRNA linear EST 16-AUG-2002
LOCUS AGENCOURT 8074293 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6085612
DEFINITION 5', mRNA sequence.

ACCESSION
BO897122
VERSION BO897122.1 GI:22289136
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1CM2319 row: e column: 05
High quality sequence stop: 607.

FEATURES
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1..906
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6085612"
/issue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/ad_host="NIH_MGC_110"
/note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dt priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 183 a 227 c 271 g 225 t
ORIGIN

Query Match 31.2%; Score 807.4; DB 13; Length 906;
Best Local Similarity 97.9%; Pred. No. 2e-96;
Matches 872; Conservative 0; Mismatches 11; Indels 8; Gaps 5;

QY 849 CCCCTGCCCGTGGAGGGGAGCTTGGCATGACCCCGCAAGCCGCTTCTGACCTTCATC 908
Db 1 CCCCTGCCCGTGGAGGGGAGCTTGGCATGACCCCGCAAGCCGCTTCTGACCTTCATC 60

QY 909 ACCCTGGAGCTAGAGCTGATGAGCTTGGACCGATGCCCTTGTGCATGGCTTCTC 968
Db 61 ACCCTGGAGCTAGAGCTGATGAGCTTGGACCGATGCCCTTGTGCATGGCTTCTC 120

QY 969 TGGCAGCCCAACACCAAGCCTGTGTATGTGTCAAGCCGACCTTGTGGAGAGCCGT 1028
Db 121 TGGCAGCCCAACACCAAGCCTGTGTATGTGTCAAGCCGACCTTGTGGAGAGCCGT 180

QY 1029 GACCAAGATGGGGAGATCTCTGCTGCCAGAGAGGTCCCGATGATGATGAAGTTGGAGC 1088
Db 181 GACCAAGATGGGGAGATCTCTGCTGCCAGAGAGGTCCCGATGATGATGAAGTTGGAGC 240

QY 1089 TTCAATGAGAGGTGGCGCAGAGAGCTGAGAGAGCTGAGAGAGAGCTGATGAAGAGATG 1148
Db 241 TTCAATGAGAGGTGGCGCAGAGAGCTGAGAGAGCTGAGAGAGAGCTGATGAAGAGATG 300

QY 1149 GCGCTGGGGAGAGCTTGGCGCTGCCCGCCGCTGCATCTGCTGGAGAGGAGAAATTTAGATC 1208
Db 301 GCGCTGAGAGAGAGCTTGGCGCTGCCCGCCGCTGCATCTGCTGGAGAGGAGAAATTTAGATC 360

QY 1209 TGAACCAAGCTGTGGGTAGATGTGCAATAGAAATAGCTAAATTTATTTTCCCAAGGTGTGTG 1268
Db 361 TGAACCAAGCTGTGGGTAGATGTGCAATAGAAATAGCTAAATTTATTTTCCCAAGGTGTGTG 420

QY 1269 CTTTAGGCGTGGGCTGACCAAGCTTCTTCCATCATCTTCTTCCCAAGTATTTCCCTCT 1328
Db 421 CTTTAGGCGTGGGCTGACCAAGCTTCTTCCATCATCTTCTTCCCAAGTATTTCCCTCT 480

QY 1329 GAGCTTGACAGATAGAGGTGTGTGCAATTTGTTCAGCTCCCAAGGCTGTTCACAGCTT 1388
Db 481 GAGCTTGACAGATAGAGGTGTGTGCAATTTGTTCAGCTCCCAAGGCTGTTCACAGCTT 540

QY 1389 CACAGCTGTGTGCTTGGAGAGAGTCAAGCAAGGTTAACTGTGAGAGACAGTTGCCACCCC 1448
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QY 1449 TGTCAGATTTATTTGGCTGCTTGGCTTACCAAGTTGGCAGACAGCCGTTGTCTACATG 1508
Db 601 TGTCAGATTTATTTGGCTGCTTGGCTTACCAAGTTGGCAGACAGCCGTTGTCTACATG 660

QY 1509 GCTTGTATTAATTTGTTGAGGGAGAGATGGAACAATGTGAGTCTCTCTGATTTGGT 1568
Db 661 GCTTGTATTAATTTGTTGAGGGAGAGATGGAACAATGTGAGTCTCTCTGATTTGGT 720

QY 1569 TTTGGGGAAATGTGG-AGAAGATGTCCTGCTTGGCAACATCAACCTGGCAAAATATCA 1627
Db 721 TTTGGGGAAATGTGGAAAGATGTCCTGCTTGGCAACATCAACCTGGCAAAATATCA 780

QY 1628 ACAATGAAATTTTCCACGCA-GTCTTTTCATGGGC--ATAGTAAGCTGTGCTTACG 1684
Db 781 ACAATGAAATTTTCCACGCAAGTCTTTCATGGGCATAGTAAGCTGTGCTTACG 840

QY 1685 TGTGTG--CAGATGAAATGTCTCTTCAACC--TGATTAACATGTGTTAT 1731
Db 841 TGTGTGCAAAATGAATGTCTCTTCAACCCTGGCATTAACCTGGGTTTAT 891

RESULT 27
BO687864 898 bp mRNA linear EST 15-JUL-2002
LOCUS AGENCOURT 8346023 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6250987
DEFINITION 5', mRNA sequence.

ACCESSION
BO687864
VERSION BO687864.1 GI:21813180
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1CM2319 row: o column: 20
High quality sequence stop: 650.

FEATURES
source
1..898
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/mol_type="mRNA"

/db_xref="taxon:9606"
 /clone="IMAGE:6250987"
 /issue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_11b="NIH MG_C 110"
 /note="Organ: pancreas; Vector: pOT37; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGACAGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH MG_C Library."

BASE COUNT 181 a 222 c 267 g 227 t 1 others

ORIGIN

Query Match 31.2%; Score 806.8; DB 13; Length 898;

Best Local Similarity 99.5%; Pred. No. 2,4e-96;

Matches 830; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

Db 849 CCCCTGCCCGTGGAGGGGAGCTTTGCCATGACCCCGGCGGGCTTGGACCTCAGC 908
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RESULT 28
 LOCUS
 DEFINITION

AK013622
 Mus musculus adult male hippocampus cDNA, RIKEN full-length
 enriched library, clone:250036K07 product:dickeopf homolog 3
 (Xenopus laevis), full insert sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AK013622
 AK013622.1 GI:12851055
 HTC; CAP trapper.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS

1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 99279253
 10349636
 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 sequencing pipeline with 384 multiplexed sequencer
 Genome Res. 10 (10), 1617-1630 (2000)
 20499374
 11042159
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagasaka, S., Sasaki, N., Carninci, P.,
 Kono, H., Akiyama, J., Nishi, K., Kitsumaru, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matshiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
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 RIKEN integrated sequence analysis (RISA) system-384-format
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 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 11076861

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS

4
 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
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 Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Butt, C.,
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 Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kontuski, S.
 and Hayashizaki, Y.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409 (6821), 685-690 (2001)
 21085660
 11217851

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS
 TITLE

The PANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs

RESULT 29
LOCUS B0686410
DEFINITION AGENCOURT_8046835 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6209080
5', mRNA sequence.
ACCESSION B0686410
VERSION B0686410.1 GI:21811726
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 879)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@nci.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM2367 row: m column: 17
High quality sequence stop: 614.
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/clone="IMAGE:6209080"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 110"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; CDNA made by oligo-dt priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library." 1 others

BASE COUNT 174 a 219 c 262 g 223 t
ORIGIN

Query Match 30.9%; Score 799.6; DB 13; Length 879;
Best Local Similarity 99.2%; Pred. No. 2.1e-95;
Matches 835; Conservative 0; Mismatches 4; Indels 3; Gaps 3;

QY 849 CCCCTGCCCCGAGGCGAGCTTTGCCATGACCCCGCAGCCGCTTCTGACCTCATC 908
DB 1 CCCTGCCCCGAGGCGAGCTTTGCCATGACCCCGCAGCCGCTTCTGACCTCATC 60

QY 909 ACCTGGAGCTAGAGCTGATGAGCTTGCACCGATGCTTGTGCGAGTGCCTCTC 968
DB 61 ACCTGGAGCTAGAGCTGATGAGCTTGCACCGATGCTTGTGCGAGTGCCTCTC 120

QY 969 TGGCAGCCCAACGACAGCTTGTATGTGTGCAAGCCGCTTGTGGGAGCCGT 1028
DB 121 TGGCAGCCCAACGACAGCTTGTATGTGTGCAAGCCGCTTGTGGGAGCCGT 180

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DB 301 CCGCTGAGGAGAGCTGCGGCTGCGCGCTGACACTGCTGGAGAGGGAAGATTGATC 360

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QY 1389 CACAGCTGTGGTGTGGAGAGTCCAGCAAGGTTAAATGTCAGAGAGAGTTGCAAGCC 1448
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DB 780 CAATGATTTTCCAGCAGTCTTCCATGAGCATAGTAAGCTGTCCTTCAAGCTG 839

QY 1687 TT 1688
DB 840 TT 841

RESULT 30
LOCUS B0688783
DEFINITION AGENCOURT_834454 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6251276
5', mRNA sequence.
ACCESSION B0688783
VERSION B0688783.1 GI:21814099
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 940)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@nci.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM2395 row: k column: 21
High quality sequence stop: 684.
Location/Qualifiers
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/tissue type="ductal carcinoma, cell line"
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/clone lib="NIH_MGC_110"
/notes="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAACGAG(G). Library constructed by
ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."
BASE COUNT      188 a      235 c      275 g      239 t      2 others
ORIGIN
Query Match      30.9%; Score 798.8; DB 13; Length 940;
Best Local Similarity 98.9%; Pred. No. 2.6e-95;
Matches 814; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
QY      849 CCCCTGCCCTGGAGGGCCGACCTTTCATGACCCCGCAGCCGGCTTGGACCTCATC
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61      ACCTGGAGCTAGAGGCTGATGGAGGCTTGACCCGATGCCCTGTCAGTGGACCTCCCTC
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Db
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Db
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Db
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Db
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721      TTTGGGGAATGTGGGAAGAGTGCCTGCTTGCACAAATCAACTGGGCAAAATGA
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DEFINITION
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enriched library, clone:2810409E22 product:dictkopf homolog 3
(Xenopus laevis), full insert sequence.
AK013054
AK013054.2 GI:26105950
HTC; CAP trapper.
Mus musculus (house mouse)
SOURCE
ORGANISM
REFERENCE
AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159
JOURNAL
MEDLINE
PUBMED
AUTHORS
REFERENCE
3
Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kikunishi, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
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Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
JOURNAL
MEDLINE
PUBMED
AUTHORS
REFERENCE
4
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Aizawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S.,
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Quackenbush, J., Schriml, L.M., Staudli, F., Suzuki, R., Tomita, M.,
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Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S.,
and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
JOURNAL
MEDLINE
PUBMED
AUTHORS
REFERENCE
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2303)
JOURNAL
MEDLINE
PUBMED
AUTHORS
REFERENCE

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DEFINITION AGNCOURT.8343875 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6248433
5', mRNA sequence.

ACCESSION BQ689483
VERSION BQ689483.1 GI:21814799
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 867)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished

AUTHORS Contact: Robert Strausberg, Ph.D.
JOURNAL Email: cgabs-r@mail.nih.gov
COMMENT Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Plate: LINC2388 row: e column: 10
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/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library."

BASE COUNT 173 a 218 c 261 g 215 t

ORIGIN

Query Match 30.7%; Score 794.6; DB 13; Length 867;
Best Local Similarity 98.0%; Pired. No. 9.7e-95;
Matches 836; Conservative 0; Mismatches 14; Indels 3; Gaps 3;

QY 849 CCCCTGCCGTGGAGGGCGAGCTTTGCCATGACCCCGCAGCGGCTTCTGGACCTCATC 908
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QY 909 ACCTGGAGCTAGAGCCTGATGGAGCCTTGACCCAGTGCCTTTGTGCCAGTGGCCTCTC 968
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QY 969 TGGCAGCCCGACAGCCAGCAGCTGTGTATGTGTGCAAGCCAGCTTCTGTGGAGGCGCT 1028
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QY 1029 GACCAAGATGGAGATCTCTGTGCCAGAGAGTCCCGATAGATAGATTGGCAGC 1088
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QY 1089 TTATATGAGAGAGTGGCGCAGAGCTGTGAGAGACCTGGAAGAGAGCCTGACTGAAGAAGATG 1148
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QY 1149 GCGCTGGAGGAGAGCTGTGCGCGCTGCAGCTGCTGGAGAGGAGAGATTAGATC 1208
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QY 1329 GCGTTGACAGATGAGAGTGTGTGATTTGTTCAGCTTCCCGCAGGCTGTCTTCCAGGCTT 1388
481 GCGTTGACAGATGAGAGTGTGTGATTTGTTCAGCTTCCCGCAGGCTGTCTTCCAGGCTT 540

QY 1389 CACAGCTGTGCTTGGAGAGACAGCAGGCTTAACTGACAGAGAGATTGGCACTCC 1448
541 CACAGCTGTGCTTGGAGAGACAGCAGGCTTAACTGACAGAGAGATTGGCACTCC 600

QY 1449 TGTCCAGATTATTTGCGTCTTTGCTTACACAGTTGGCAGACAGCGCTTTGTTACATG 1508
601 TGTCCAGATTATTTGCGTCTTTGCTTACACAGTTGGCAGACAGCGCTTTGTTACATG 660

QY 1509 GCTTGAATTAATTTGTTAGGAGAGAGATGAAACAATGTGAGTCTCCCTGATTTGT 1568
661 GCTTGAATTAATTTGTTAGGAGAGAGATGAAACAATGTGAGTCTCCCTGATTTGT 720

QY 1569 TTTGGGAAATGTGAGAGAGATGCTCCTGCTTGCACAAATCAACTGCAAAAATGCAA 1628
721 TTTGGGAAATGTGAGAGAGATGCTCCTGCTTGCACAAATCAACTGCAAAAATGCAA 780

QY 1629 CAATGAA-TTTTCCAGCAGGCTTCTTCCATGGG-CATAGTAAAGCTG-CCTTCAGCT 1685
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QY 1686 GTTCCAGATGAAA 1698
841 GTTCCAGATGAAA 853

Db 841 GTTCCAGATGAAA 853

RESULT 33
AL547689 1182 bp mRNA linear EST 31-MAY-2003
LOCUS AL547689 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CSOD1008YN07 5-PRIME, mRNA sequence.
AL547689
VERSION AL547689.2 GI:31269518
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1182)
L4 M.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 15, 2001 this sequence version replaced gi:12881985.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seq@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6027.r For
more information about this cluster, see
<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSOD1008CG04QPI&cluster=6027.r>. Contact :
Feng Liang Email: liang@lifetech.com URL: <http://fulllength.invitrogen.com/InvitrogenCorporation1600>
Faraday Avenue Genoscope sequence ID: CSOD1008CG04QPI.
Location/Qualifiers
1..1182
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CSOD1008YN07"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

FEATURES
source

QY 1149 GCGGTGGGAGAGCTGGGCTGCGCCGCTGCACTGCTGGAGAGGAGATTGATC 1208
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QY 1269 CTTAGAGCTGGGCTGAGTATGTCATATAGAAATAGCTAATTTATTTCCCAAGTGTG 1328
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QY 1329 GCGTTGACAGCATAGAGTGTGTGCAATTTGTGCACTCCCAAGCTGTGTCAGAGCTT 1388
Db 481 GCGTTGACAGCATAGAGTGTGTGCAATTTGTGCACTCCCAAGCTGTGTCAGAGCTT 540
QY 1389 CACAGTGTGGCTGGGAGAGTACAGAGGTTAACTGACAGAGAGATTGGCCACCC 1448
Db 541 CACAGTGTGGCTGGGAGAGTACAGAGGTTAACTGACAGAGAGATTGGCCACCC 600
QY 1449 TGTCCAGATTATGCTGCTGCTTGTGCTTACAGATTGACAGACCGTTGTGTCATG 1508
Db 601 TGTCCAGATTATGCTGCTGCTTGTGCTTACAGATTGACAGACCGTTGTGTCATG 660
QY 1509 GCTTTGATTAATGTTTGGAGGAGAGATGGAACAATGTGAGTCTCCCTGTGATTGCT 1568
Db 661 GCTTTGATTAATGTTTGGAGGAGAGATGGAACAATGTGAGTCTCCCTGTGATTGCT 720
QY 1569 TTTGGGAAATGTGAGAGAGTCCCTGCTTGGCAACATCAA-CCTGGCAAAATGCA 1627
Db 721 TTTGGGAAATGTGAGAGAGTCCCTGCTTGGCAACATCAA-CCTGGCAAAATGCA 780
QY 1628 ACAATGAATTTTCCAGCGAG-TTCTTTCATGGGCAAT-AGTAACTGTGCTT 1680
Db 781 ACAATGAATTTTCCAGCGAGTTCTTTCATGGGCAATAGGTAAGTGTGCTT 835

RESULT 35
B0897670
LOCUS B0897670 877 bp mRNA linear EST 16-AUG-2002
DEFINITION AGENCOURT_8074427 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:5085740
5', mRNA sequence.
ACCESSION B0897670
VERSION B0897670.1 GI:22289684
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 877)
NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: gsgaps-femail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LNCM219 row: 3 column: 13
High quality sequence stop: 576.
Location/Qualifiers
1..877
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5085740"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"

/clone.lib="NIH_MGC_110"
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACAGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 177 a 220 c 263 g 217 t
ORIGIN

Query Match 30.6%; Score 792.4; DB 13; Length 877;
Best Local Similarity 97.5%; Pred. No. 1.9e-94;
Matches 848; Conservative 0; Mismatches 16; Indels 6; Gaps 4;

QY 849 CCCCTGCCCGTGGAGAGGAGAGCTTTGACATGACCCCGGACCGGCTTGTGACCTCATC 908
Db 1 CCCCTGCCCGTGGAGAGGAGAGCTTTGACATGACCCCGGACCGGCTTGTGACCTCATC 60
QY 909 ACTGGAGCTTAGAGCTGATGAGAGCTTGAACCGATGCCCTTGTGCAATGAGCTCTCTC 968
Db 61 ACTGGAGCTTAGAGCTGATGAGAGCTTGAACCGATGCCCTTGTGCAATGAGCTCTCTC 120
QY 969 TGGCAGCCCCACAGCACAAGCCTGTGTATGTGTGCAAGCCGACCTGTGTGGAGAGCCCT 1028
Db 121 TGGCAGCCCCACAGCACAAGCCTGTGTATGTGTGCAAGCCGACCTGTGTGGAGAGCCCT 180
QY 1029 GACCAAGATGGGGAGATCTCTGCTCCAGAGAGGTCCCGATGATAGTAAGATTGGCAGC 1088
Db 181 GACCAAGATGGGGAGATCTCTGCTCCAGAGAGGTCCCGATGATAGTAAGATTGGCAGC 240
QY 1089 TTCTATGAGAGAGGTGCGCCAGAGCTGAGAGACCTGAGAGAGAGCTTGAAGAGATG 1148
Db 241 TTCTATGAGAGAGGTGCGCCAGAGCTGAGAGACCTGAGAGAGAGCTTGAAGAGATG 300
QY 1149 GCGGTGGGAGAGCTGCGGCTGCGCGCTGCACTGCTGAGAGGAGAGAGATTGATC 1208
Db 301 GCGGTGGGAGAGCTGCGGCTGCGCGCTGCACTGCTGAGAGGAGAGAGATTGATC 360
QY 1209 TGGACCAAGCTGTGGTGTGATGTGCAATAGAAATAGCTAATTTATTTCCCAAGTGTG 1268
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QY 1269 CTTAGAGCTGGGCTGAGTATGTCATATAGAAATAGCTAATTTATTTCCCAAGTGTG 1328
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QY 1329 GCGTTGACAGCATAGAGTGTGTGCAATTTGTGCACTCCCAAGCTGTGTCAGAGCTT 1388
Db 481 GCGTTGACAGCATAGAGTGTGTGCAATTTGTGCACTCCCAAGCTGTGTCAGAGCTT 540
QY 1389 CACAGTGTGGCTGGGAGAGTACAGAGGTTAACTGACAGAGAGATTGGCCACCC 1448
Db 541 CACAGTGTGGCTGGGAGAGTACAGAGGTTAACTGACAGAGAGATTGGCCACCC 600
QY 1449 TGTCCAGATTATGCTGCTGCTTGTGCTTACAGATTGACAGACCGTTGTGTCATG 1508
Db 601 TGTCCAGATTATGCTGCTGCTTGTGCTTACAGATTGACAGACCGTTGTGTCATG 660
QY 1509 GCTTTGATTAATGTTTGGAGGAGAGATGGAACAATGTGAGTCTCCCTGTGATTGCT 1568
Db 661 GCTTTGATTAATGTTTGGAGGAGAGATGGAACAATGTGAGTCTCCCTGTGATTGCT 720
QY 1569 TTTGGGAAATGTGAGAGAGTCCCTGCTTGGCAACATCAA-CCTGGCAAAATGCA 1628
Db 721 TTTGGGAAATGTGAGAGAGTCCCTGCTTGGCAACATCAA-CCTGGCAAAATGCA 780
QY 1629 C-AATGAATTTTCCAGCGAGTCTT---CCATGGGAGATGAGTAAGTGTG-CCTTGA 1683
Db 781 CAAATGAATTTTCCCGAGTCTTCTTTCATGGGAGATAGGTAAGTGTGCTTGA 840
QY 1684 CTGTGAG-ATGAATGTCTGTGACCC 1712

Db 841 CTCCTGACAAATGAATCTTCTTTCACCC 870

RESULT 36
LOCUS BQ897953
DEFINITION AGENCOURT 8061767 NIH_MGC_110 Homo sapiens CDNA clone IMAGE:6208520
ACCESSION BQ897953
VERSION BQ897953.1 GI:22289967
SOURCE EST.
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS 1 (bases 1 to 883)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLCM2366 row: f column: 09
High quality sequence stop: 684.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6208520"
/tissue_type="ductal carcinoma, cell line"
/lab_host="PHIOB (phage-resistant)"
/clone_11b="NIH_MGC_110"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-AT priming. Directionally cloned into EcoRI/XhoI using the following 5' adaptor: GGCACTGAG(9). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

BASE COUNT 178 a 220 c 263 g 222 t

ORIGIN

Query Match 30.6%; Score 791.2; DB 13; Length 883;
Best Local Similarity 99.3%; Pred. No. 2.7e-94;
Matches 816; Conservative 0; Mismatches 3; Indels 3; Gaps 2;

QY 849 CCCCTGCCCTGGAGGGCGAAGCTTTGCCATGACCCGCCAGCCGGCTTGTGACCTCATC 908
Db 1 CCCCTGCCCTGGAGGGCGAAGCTTTGCCATGACCCGCCAGCCGGCTTGTGACCTCATC 60

QY 909 ACCTGGAGAGTGAAGCTGATGAGAGCTTGACCGATGCCCTTGTGCCAGTGGCCCTCC 968
Db 61 ACTGGAGAGTGAAGCTGATGAGAGCTTGACCGATGCCCTTGTGCCAGTGGCCCTCC 120

QY 969 TGGCAGCCCCCAGCAGCAGCCTGTGTATGTGTGTGCAAGCCGACTTGTGTGGAGCCGT 1028
Db 121 TGGCAGCCCCCAGCAGCAGCCTGTGTATGTGTGTGCAAGCCGACTTGTGTGGAGCCGT 180

QY 1029 GACCAAGATGGGGAGATCTGTGCTGCCAGAGAGTCCCGATGAGATGAATTGGCAGC 1088
Db 181 GACCAAGATGGGGAGATCTGTGCTGCCAGAGAGTCCCGATGAGATGAATTGGCAGC 240

QY 1089 TTTCATGAGAGAGTGGCCAGAGAGCTGAGAGACTTGGAGAGAGGCTGATGAAGATG 1148

Db 241 TTTCATGAGAGAGTGGCCAGAGAGCTGAGAGACCTGAGAGAGAGAGCTGACTGAAGATG 300

QY 1149 GCGCTGGGGAGAGCTGTGGCTGCCCGCGCTGCACTGCTGGGAGGGGAGAGATTTGATC 1208

Db 301 GCGCTGGGGAGAGCTGTGGCTGCCCGCGCTGCACTGCTGGGAGGGGAGAGATTTGATC 360

QY 1209 TGAACACAGCTGTGGAGATGTGCAATAGATTAATTAATTTCCACAGTGTG 1268

Db 361 TGAACACAGCTGTGGAGATGTGCAATAGATTAATTAATTTCCACAGTGTG 420

QY 1269 CTTTAGGCGGTGGGCTGACAGGCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1328

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Db 481 GCGCTTACAGATAGAGTGTGTGCAATTTTGTGAGCTCCCGCGCTGCTTCTTCTTCTTCTT 540

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Db 601 TGTCCAGATTAATTTGGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 660

QY 1509 GCTTTGATTAATTTGTGAGGAGAGAGATGAAACATGTGAGTCTCCCTGTGATTTGGT 1568

Db 661 GCTTTGATTAATTTGTGAGGAGAGAGATGAAACATGTGAGTCTCCCTGTGATTTGGT 720

QY 1569 TTTGGGGAATGTGGAGAGAGTCCCTGCTTGTGCAACATGCA - CTTGGCAAAATGCA 1627

Db 721 TTTGGGGAATGTGGAGAGAGTCCCTGCTTGTGCAACATGCA - CTTGGCAAAATGCA 780

QY 1628 ACAATGAATTTTCCAGCAGATT - CTTTCCATGGCATTAG 1667

Db 781 ACAATGAATTTTCCAGCAGATTCTTTTCCATGGCATTAG 822

RESULT 37
BQ889489 892 bp mRNA linear EST 16-AUG-2002
LOCUS BQ889489
DEFINITION AGENCOURT 8061866 NIH_MGC_110 Homo sapiens CDNA clone IMAGE:6208646
ACCESSION BQ889489
VERSION BQ889489.1 GI:22281503
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS 1 (bases 1 to 892)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLCM2366 row: k column: 15
High quality sequence stop: 680.
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1..892
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/tissue_type="ductal carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dt priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC library."

BASE COUNT

179 a 223 c 269 g 221 t

Query Match 30.6%; Score 790.8; DB 13; Length 892;
 Best Local Similarity 99.0%; Pred. No. 36-94;
 Matches 806; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

849 CCCCTGCCGTCGAGGCGAGCTTTCATGACCCCGCAGCCGCTTCTGACCTCATC 908
 1 CCCCTGCCGTCGAGGCGAGCTTTCATGACCCCGCAGCCGCTTCTGACCTCATC 60

909 ACCTGGAGATAGACCTGATGAGAGCTTGGACCACTGCTTGTGCGAGTGGCTCTC 968
 61 ACCTGGAGATAGACCTGATGAGAGCTTGGACCACTGCTTGTGCGAGTGGCTCTC 120

969 TGCCAGCCCGACACGACCTGTGTATGTGTGCAAGCCGACTTGTGCGAGAGCGT 1028
 121 TGCCAGCCCGACACGACCTGTGTATGTGTGCAAGCCGACTTGTGCGAGAGCGT 180

1029 GACCAAGATGGGAGATCTGTCTGCCAGAGAGTCCCGATGATGATGATGAGTTGGCAGC 1088
 181 GACCAAGATGGGAGATCTGTCTGCCAGAGAGTCCCGATGATGATGATGAGTTGGCAGC 240

1089 TTGATGAGAGAGTGTGCGCCAGAGCTGAGAGACCTGAGAGAGAGCTGACTGAAGAAGATG 1148
 241 TTGATGAGAGAGTGTGCGCCAGAGCTGAGAGACCTGAGAGAGAGCTGACTGAAGAAGATG 300

1149 GCGCTGGGGAGGCTGCGGCTGCGGCTGCTGCACTGCTGCGAGGGAGAGATTTAGATC 1208
 301 GCGCTGGGGAGGCTGCGGCTGCGGCTGCTGCACTGCTGCGAGGGAGAGATTTAGATC 360

1209 TGAGACAGGCTGTGGGAGATGTGCAATGAAATAGCTAATTATTTCCCGAGGTGTG 1268
 361 TGAGACAGGCTGTGGGAGATGTGCAATGAAATAGCTAATTATTTCCCGAGGTGTG 420

1269 CTTTAGGCGTGGGCTGACAGAGCTTCTCTACATCTTCTCCAGTAAATTTCCCTCT 1328
 421 CTTTAGGCGTGGGCTGACAGAGCTTCTCTACATCTTCTCCAGTAAATTTCCCTCT 480

1329 GCGTTGACAGAGAGTGTGTGCAATTTGTCAGTCTCCCGAGGTGTCTTCCAGAGCTT 1388
 481 GCGTTGACAGAGAGTGTGTGCAATTTGTCAGTCTCCCGAGGTGTCTTCCAGAGCTT 540

1389 CACAGTGTGTGCTTGGAGAGTCAAGGAGGTTAACTGACAGAGAGTGTGCGACCC 1448
 541 CACAGTGTGTGCTTGGAGAGTCAAGGAGGTTAACTGACAGAGAGTGTGCGACCC 600

1449 TGTCGAGATTTTGGCTGCTTGTCTTACAGTGTGCGAGAGAGCTTGTGTTACATG 1508
 601 TGTCGAGATTTTGGCTGCTTGTCTTACAGTGTGCGAGAGAGCTTGTGTTACATG 660

1509 GCTTTGATATTTTGTGAGGGAGAGATGAAACAATGAGAGTCTCCCTGATGAGT 1568
 661 GCTTTGATATTTTGTGAGGGAGAGATGAAACAATGAGAGTCTCCCTGATGAGT 720

1569 TTTGGGAGAAATGTGGAGAGAGTCCCTGCTTTGCAACATCACTGGCAAAAATGCAA 1628
 721 TTTGGGAGAAATGTGGAGAGAGTCCCTGCTTTGCAACATCACTGGCAAAAATGCAA 780

1629 CAATGATATTTT-CCAGCAGTCTTTTCATGGG 1661
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RESULT 38
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 DEFINITION AGNCOURT 7974830 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6082014
 5' mRNA sequence.
 BUI74805
 VERSION BUI74805.1 GI:22688776
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 841)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: rgs@lel.nhl.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LICM2309 row: c column: 07
 High quality sequence stop: 649.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dt priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC library."

FEATURES

source
 Location/Qualifiers
 1. 841
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6082014"
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 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dt priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC library."

BASE COUNT

168 a 210 c 254 g 209 t

Query Match 30.5%; Score 789.4; DB 13; Length 841;
 Best Local Similarity 98.9%; Pred. No. 4,76-94;
 Matches 826; Conservative 0; Mismatches 6; Indels 3; Gaps 3;

849 CCCCTGCCGTCGAGGCGAGCTTGGCATGACCCCGCAGCCGCTTCTGACCTCATC 908
 1 CCCCTGCCGTCGAGGCGAGCTTGGCATGACCCCGCAGCCGCTTCTGACCTCATC 60

909 ACCTGGAGATAGACCTGATGAGAGCTTGGACCGATGCTTGTGCAATGAGTGGCTCTC 968
 61 ACCTGGAGATAGACCTGATGAGAGCTTGGACCGATGCTTGTGCAATGAGTGGCTCTC 120

969 TGCCAGCCCGACAGCCACAGCTGTGTATGTGTGCAAGCCGACTTGTGCGAGAGCGT 1028
 121 TGCCAGCCCGACAGCCACAGCTGTGTATGTGTGCAAGCCGACTTGTGCGAGAGCGT 180

1029 GACCAAGATGGGAGATCTGTGCTGCGAGAGAGTCTCCGATGATGATGAGTTGGCAGC 1088
 181 GACCAAGATGGGAGATCTGTGCTGCGAGAGAGTCTCCGATGATGATGAGTTGGCAGC 240

1089 TTGATGAGAGAGTGTGCGCCAGAGCTGAGAGACCTGAGAGAGAGCTGACTGAAGAGATG 1148
 241 TTGATGAGAGAGTGTGCGCCAGAGCTGAGAGACCTGAGAGAGAGCTGACTGAAGAGATG 300

1149 GCGCTGGGGAGGCTGCGGCTGCGCGCTGCACTGCTGGAGGGAGAGATTTAGATC 1208

```

Db      301 GGCCTGAGGAGGCTGCGCTGCGCGCTGCACTGCTGGGAGGAAAGATTGATC 360
QY      1209 TGGACAGAGCTGGGGTAGATGTCATAGAAATAGCTATTTATTTCCCGAGTGTG 1268
Db      361 TGGACAGAGCTGGGGTAGATGTCATAGAAATAGCTATTTATTTCCCGAGTGTG 420
QY      1269 CTTTAAAGCTGGGCTGACCAAGGCTTTCTTCATACATTTCTTCCAGTAAATTTCCCTCT 1328
Db      421 CTTTAAAGCTGGGCTGACCAAGGCTTTCTTCATACATTTCTTCCAGTAAATTTCCCTCT 480
QY      1329 GGCCTGACAGCATGAGGTGTGTGTCATTTGTCATGCTCCCGAGGTGTTCCAGGCT 1388
Db      481 GGCCTGACAGCATGAGGTGTGTGTCATTTGTCATGCTCCCGAGGTGTTCCAGGCT 540
QY      1389 CACAGTCTGTGCTGGGAGAGTCAGGACAGGTTAAATGTCAGAGCAATTTGCCACCC 1448
Db      541 CACAGTCTGTGCTGGGAGAGTCAGGACAGGTTAAATGTCAGAGCAATTTGCCACCC 600
QY      1449 TGTCCAGATTAATGCGTGGCTTGGCTCTACAGCTGGGACAGCGCTTGTTCATAG 1508
Db      601 TGTCCAGATTAATGCGTGGCTTGGCTCTACAGCTGGGACAGCGCTTGTTCATAG 660
QY      1509 GCTTTGATTAATGTTTGGAGGAGAGATGAAACATGTGAGTCTCCCTCTGATTTGT 1568
Db      661 GCTTTGATTAATGTTTGGAGGAGAGATGAAACATGTGAGTCTCCCTCTGATTTGT 720
QY      1569 TTTGGGGAATGT-GGAGAAAGATGCTTGTCTTGGCAATCATCACTTGGCAAAATGCA 1627
Db      721 TTTGGGGAATGTGGAGAAAGATGCTTGTCTTGGCAATCATCACTTGGCAAAATGCA 780
QY      1628 ACAATGAATTTTCCAGCGAG-TTCTTCCATGGGCAAT-AGTAAAGCTGTGCTT 1680
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RESULT 39
BO686534      877 bp      mRNA      linear      EST 15-JUL-2002
LOCUS      BO686534
DEFINITION      AGENCOURT 8034689 NIH_MGC_110 Homo sapiens CDNA clone IMAGE:6207169
5', mRNA sequence.
ACCESSION      BO686534
VERSION      BO686534.1 GI:21811850
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 877)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
DNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/BLN at:
http://image.lnl.gov
Plate: LNCM362 row: n column: 02
High quality sequence smp: 692.
Location/Qualifiers
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/mol_type="mRNA"
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/clone="IMAGE:6207169"
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/lab_host="DH10B (phage-resistant)"
/clone_11b="NIH MGC_110"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;"

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FEATURES
source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6207169"
/issue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_11b="NIH MGC_110"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;"

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Site 2: EcorI; CDNA made by oligo-dT priming.
 Directionally cloned into EcorI/XhoI sites using the
 following 5' adaptor: GGACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH-MGC Library. 1 others

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BASE COUNT      179 a      213 c      265 g      219 t
ORIGIN
Query Match      30.5%; Score 788.2; DB 13; Length 877;
Best Local Similarity 99.1%; Pred. No. 6,6e-94;
Matches 814; Conservative 0; Mismatches 3; Indels 4; Gaps 2;
849 CCCCTGCCCTGGAAGGGCGAGCTTTGCGCATGACCCCGCAGCCGGCTTCTGACCTCATC 908
Db      1 CCCCTGCCCTGGAAGGGCGAGCTTTGCGCATGACCCCGCAGCCGGCTTCTGACCTCATC 60
QY      909 ACCGTGGAGCTAGAGCCTGATGAGAGCTTGGACCGATGACCTTGTGCGAGTGGCTCTC 968
Db      61 ACCGTGGAGCTAGAGCCTGATGAGAGCTTGGACCGATGACCTTGTGCGAGTGGCTCTC 120
QY      969 TGCAGCCCCACAGCCACAGCCTGTGTATGTGTGCAAGCCGACTTGTGGGAGCCGT 1028
Db      121 TGCAGCCCCACAGCCACAGCCTGTGTATGTGTGCAAGCCGACTTGTGGGAGCCGT 180
QY      1029 GACCAAGTGGGAGATCTGTCGCCAGAGAGTCCCGATGATGATGAAGTTGGCAGC 1088
Db      181 GACCAAGTGGGAGATCTGTCGCCAGAGAGTCCCGATGATGATGAAGTTGGCAGC 240
QY      1089 TTCATGAGAGAGTGCACGACCTGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1148
Db      241 TTCATGAGAGAGTGCACGACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY      1149 GCGGTGGGGAGCCTGGCGCTGCGCGCTGCACTGCTGGGAGGGAGAGATTAGATC 1208
Db      301 GCGGTGGGGAGCCTGGCGCTGCGCGCTGCACTGCTGGGAGGGAGAGATTAGATC 360
QY      1209 TGAACAGAGCTGTGGTATGATGTCATTAATAATAGCTAAATTTATTTCCAGGTGTG 1268
Db      361 TGAACAGAGCTGTGGTATGATGTCATTAATAATAGCTAAATTTATTTCCAGGTGTG 420
QY      1269 CTTTAAAGCTGGGCTGACCAAGGCTTTCTTCATACATTTCTTCCAGTAAATTTCCCTCT 1328
Db      421 CTTTAAAGCTGGGCTGACCAAGGCTTTCTTCATACATTTCTTCCAGTAAATTTCCCTCT 480
QY      1329 GGCCTGACAGCATGAGGTGTGTGTCATTTGTCATGCTCCCGAGGTGTTCCAGGCT 1388
Db      481 GGCCTGACAGCATGAGGTGTGTGTCATTTGTCATGCTCCCGAGGTGTTCCAGGCT 540
QY      1389 CACAGTCTGTGCTGGGAGAGTCAGGACAGGTTAAATGTCAGAGCAATTTGCCACCC 1448
Db      541 CACAGTCTGTGCTGGGAGAGTCAGGACAGGTTAAATGTCAGAGCAATTTGCCACCC 600
QY      1449 TGTCCAGATTAATGCGTGGCTTGGCTCTACAGCTGGGACAGCGCTTGTTCATAG 1508
Db      601 TGTCCAGATTAATGCGTGGCTTGGCTCTACAGCTGGGACAGCGCTTGTTCATAG 660
QY      1509 GCTTTGATTAATGTTTGGAGGAGAGATGAAACATGTGAGTCTCCCTCTGATTTGT 1568
Db      661 GCTTTGATTAATGTTTGGAGGAGAGATGAAACATGTGAGTCTCCCTCTGATTTGT 720
QY      1569 TTTGGGGAATGT-GGAGAAAGATGCTTGTCTTGGCAATCATCACTTGGCAAAATGCA 1627
Db      721 TTTGGGGAATGTGGAGAAAGATGCTTGTCTTGGCAATCATCACTTGGCAAAATGCA 780
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RESULT 40
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LOCUS B0689208 870 bp mRNA linear EST 15-JUL-2002
 DEFINITION AGENCOURT 8063999 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6207819
 5', mRNA sequence.
 ACCESSION B0689208
 VERSION B0689208.1 GI:21814524
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 870)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgapds-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LNCM364 row: 1 column: 04
 High quality sequence stop: 691.
 Location/Qualifiers
 1..870
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6207819"
 /tissue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
 Site 2: EcoRI; CDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAAGAG(G). Library constructed
 by Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."
 BASE COUNT 170 a 217 c 267 g 216 t
 ORIGIN
 Query Match 30.5%; Score 788; DB 13; Length 870;
 Best Local Similarity 99.4%; Pred. No. 7e-94; 5; Indels 0; Gaps 0;
 Matches 791; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 849 CCCCTGCCCGTGGAGGGGAGCTTGGCATGACCCGCCAGCCGGCTTGTGAGACTTCATC 908
 Db 1 CCCCTGCCCGTGGAGGGGAGCTTGGCATGACCCGCCAGCCGGCTTGTGAGACTTCATC 60
 QY 909 ACCGTGGAGCTAGAGCTGTATGAGAGCTTGGACCGATGACCTTGTGAGAGGCTTCCTC 968
 Db 61 ACCGTGGAGCTAGAGCTGTATGAGAGCTTGGACCGATGACCTTGTGAGAGGCTTCCTC 120
 QY 969 TGCAGAGCCCAAGCCAGAGCTGTATGAGAGCTTGGACCGATGACCTTGTGAGAGGCTTC 1028
 Db 121 TGCAGAGCCCAAGCCAGAGCTGTATGAGAGCTTGGACCGATGACCTTGTGAGAGGCTTC 180
 QY 1029 GACCAAGATGGGGAGATCTGCTGCCAGAGAGTCCCGCATGATGATGAGATTGGAGC 1088
 Db 181 GACCAAGATGGGGAGATCTGCTGCCAGAGAGTCCCGCATGATGATGAGATTGGAGC 240
 QY 1089 TTCAATGAGAGAGTGTGCGCCAGAGAGCTGTGAGAGAGCTGTGAGAGAGCTGTGAGAGATG 1148
 Db 241 TTCAATGAGAGAGTGTGCGCCAGAGAGCTGTGAGAGAGCTGTGAGAGAGCTGTGAGAGATG 300
 QY 1149 GCGGTGGAGAGCTGTGCGCTGCGCGCTGTCACTGTGTGAGAGGAGAGATTATATC 1208
 Db 301 GCGGTGGAGAGCTGTGCGCTGCGCGCTGTCACTGTGTGAGAGGAGAGATTATATC 360

QY 1209 TGGACCAAGCTGTGGGTAGATGTGCATAGAAATAGCTAATTTATTTCCAGGTGTGTG 1268
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 QY 1269 CTTTAGGGGTGGGGAGACAGAGCTTCTCCATACATCTTCCAGTAGTTCCTCCCT 1328
 Db 421 CTTTAGGGGTGGGGAGACAGAGCTTCTCCATACATCTTCCAGTAGTTCCTCCCT 480
 QY 1329 GCGTTGACAGATGAGAGTGTGTGATTTGTTCAGCTCCCGAGGCTTGTCCAGGCTT 1388
 Db 481 GCGTTGACAGATGAGAGTGTGTGATTTGTTCAGCTCCCGAGGCTTGTCCAGGCTT 540
 QY 1389 CACAGTCTGTGCTTGGAGAGATGAGAGAGGAGTTAAATGTGAGAGAGAGTTCACAGCC 1448
 Db 541 CACAGTCTGTGCTTGGAGAGATGAGAGAGGAGTTAAATGTGAGAGAGAGTTCACAGCC 600
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 QY 1509 GCTTTGATTAATTTGTGAGAGGAGAGATGGAACAAATGTGAGCTTCCCTGATTTGT 1568
 Db 661 GCTTTGATTAATTTGTGAGAGGAGAGATGGAACAAATGTGAGCTTCCCTGATTTGT 720
 QY 1569 TTTGGGAAATGTGAGAGAGAGTGCCTGCTTGTGCAACATCAACTGGCAAAATGCA 1628
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 QY 1629 CAATGAAATTTTCCAC 1644
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 DEFINITION AGENCOURT 8063962 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6207793
 5', mRNA sequence.
 ACCESSION B0688234
 VERSION B0688234.1 GI:21813550
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 883)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgapds-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LNCM364 row: 02
 High quality sequence stop: 680.
 Location/Qualifiers
 1..883
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6207793"
 /tissue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
 Site 2: EcoRI; CDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAAGAG(G). Library constructed by

ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 175 a 223 c 269 g 221 t 1 others

Query Match 30.3%; Score 783.4; DB 13; Length 887;
Best Local Similarity 98.4%; Pred. No. 2.8e-93;
Matches 801; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

849 CCCCTGCCGTGAGGCGAGCTTTGTCATGACCCCGCCAGCGGCTTGTGACCTCATC 908
1 CCCCTGCCGTGAGGCGAGCTTTGTCATGACCCCGCCAGCGGCTTGTGACCTCATC 60
QY 909 ACCTGGAGAGTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGA 968
DB 61 ACCTGGAGAGTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGA 120
QY 969 TGCACAGCCCAACAGCAGCTGTGTATGTGTGACAGCCGCTTGTGAGGAGCCGT 1028
DB 121 TGCACAGCCCAACAGCAGCTGTGTATGTGTGACAGCCGCTTGTGAGGAGCCGT 180
QY 1029 GACCAAGATGGGAGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1088
DB 181 GACCAAGATGGGAGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 1089 TTGATGAGAGAGTGGGAGAGCTGAGAGAGCTGAGAGAGCTGAGAGAGCTGAGAGAG 1148
DB 241 TTGATGAGAGAGTGGGAGAGCTGAGAGAGCTGAGAGAGCTGAGAGAGCTGAGAGAG 300
QY 1149 GCGCTGGGAGAGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 1208
DB 301 GCGCTGGGAGAGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 360
QY 1209 TGACACAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGG 1268
DB 361 TGACACAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGG 420
QY 1269 CTTTGGCGGTGGGCTGACAGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1328
DB 421 CTTTGGCGGTGGGCTGACAGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 480
QY 1329 GCGTTCACAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGT 1388
DB 481 GCGTTCACAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGT 540
QY 1389 CACAGTGTGTGCTTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGT 1448
DB 541 CACAGTGTGTGCTTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGT 600
QY 1449 TGTTCAGATTAATGGCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 1508
DB 601 TGTTCAGATTAATGGCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 660
QY 1509 GCTTGTATTAATGGCTTGTGAGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGG 1568
DB 661 GCTTGTATTAATGGCTTGTGAGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGG 720
QY 1569 TTTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGG 1628
DB 721 TTTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGG 780
QY 1629 CAATGAA-TTTTCAGCAGAGTCTTTCATGGG 1661
DB 781 CAATGAA-TTTTCAGCAGAGTCTTTCATGGG 814

RESULT 42
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DEFINITION 5', mRNA sequence.

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VERSION BU191090.1 GI:22705074
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 887)
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: L1CM320 row: f column: 19
High quality sequence stop: 592.
location/Qualifiers
1. 887
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6086034"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lid="NIH_MGC_110"
/note="Organ: pancreas; Vector: pOT7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 179 a 223 c 269 g 216 t
ORIGIN
Query Match 30.3%; Score 783.4; DB 13; Length 887;
Best Local Similarity 97.3%; Pred. No. 2.8e-93;
Matches 807; Conservative 0; Mismatches 21; Indels 1; Gaps 1;
849 CCCCTGCCGTGAGGCGAGCTTTGTCATGACCCCGCCAGCGGCTTGTGACCTCATC 908
1 CCCCTGCCGTGAGGCGAGCTTTGTCATGACCCCGCCAGCGGCTTGTGACCTCATC 60
QY 909 ACCTGGAGAGTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGA 968
DB 1 ACCTGGAGAGTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGA 120
QY 969 TGCACAGCCCAACAGCAGCTGTGTATGTGTGACAGCCGCTTGTGAGGAGCCGT 1028
DB 61 ACCTGGAGAGTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGA 120
QY 969 TGCACAGCCCAACAGCAGCTGTGTATGTGTGACAGCCGCTTGTGAGGAGCCGT 1028
DB 121 TGCACAGCCCAACAGCAGCTGTGTATGTGTGACAGCCGCTTGTGAGGAGCCGT 180
QY 1029 GACCAAGATGGGAGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1088
DB 181 GACCAAGATGGGAGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 1089 TTGATGAGAGAGTGGGAGAGCTGAGAGAGCTGAGAGAGCTGAGAGAGCTGAGAGAG 1148
DB 241 TTGATGAGAGAGTGGGAGAGCTGAGAGAGCTGAGAGAGCTGAGAGAGCTGAGAGAG 300
QY 1149 GCGCTGGGAGAGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 1208
DB 301 GCGCTGGGAGAGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 360
QY 1209 TGACACAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGG 1268
DB 361 TGACACAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGGAGAGTGGG 420

QY 1269 CTTTAAAGCGTGGGCTGACAGGCTTCTTCTACATCTTTTCCAGTAAGTTCCCTCT 1328
 DB 421 CTTTAAAGCGTGGGCTGACAGGCTTCTTCTACATCTTTTCCAGTAAGTTCCCTCT 480
 QY 1329 GGCTTGACAGCATGAGAGTGTGTGATTTGTTGATGCTCCCGAGCTGTCTTCAGAGCTT 1388
 DB 481 GGCTTGACAGCATGAGAGTGTGTGATTTGTTGATGCTCCCGAGCTGTCTTCAGAGCTT 540
 QY 1389 CACAGT 1448
 DB 541 CACAGT 600
 QY 1449 TGTCCAGATTAATGCTGT 1508
 DB 601 TGTCCAGATTAATGCTGT 660
 QY 1509 GCTTTGATTAATGCTGT 1568
 DB 661 GCTTTGATTAATGCTGT 720
 QY 1569 TTTGGGGAATGTGGAGAGAGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1628
 DB 721 TTTGGGGAATGTGGAGAGAGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
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 DB 781 CAATGAAATTTTCCCCCGAGTCTTTCCAGGGGCTTTAGTAACCTTG 829

RESULT 43
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 LOCUS AGENCOURT 6910865 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:5952243
 DEFINITION 5', mRNA sequence.
 ACCESSION BUI96397.1 GI:22710381
 VERSION BUI96397.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1043)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: gsabds-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: ILCM2139 row: P column: 04
 High quality sequence stop: 599.
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 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOT7; Site_1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed
 by Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 207 a 264 c 308 g 263 t 1 others
 ORIGIN
 Query Match 30.3%; Score 783.4; DB 13; Length 1043;
 Best Local Similarity 96.8%; Pred. No. 2,6e-93;
 Matches 842; Conservative 0; Mismatches 22; Indels 6; Gaps 4;

QY 849 CCCCCTGCCGTTGAGAGGCGAGCTTTGTCATGACCCCGCAGCGGCTTGTGACCTCATC 908
 DB 1 CCCCCTGCCGTTGAGAGGCGAGCTTTGTCATGACCCCGCAGCGGCTTGTGACCTCATC 60
 QY 909 ACCTGGAGCTAGAGCTGTATGAGACCTTGGACCGATGCTTGTGTGCACTGCTCTC 968
 DB 61 ACCTGGAGCTAGAGCTGTATGAGACCTTGGACCGATGCTTGTGTGCACTGCTCTC 120
 QY 969 TGGCAGCCCCCAGAGCCAGACCTGTGTATGTGTGCAAGCGGACCTTGTGGGGAGCGT 1028
 DB 121 TGGCAGCCCCCAGAGCCAGACCTGTGTATGTGTGCAAGCGGACCTTGTGGGGAGCGT 180
 QY 1029 GACCAAGATGGGAGATCTGTCTGCCAGAGAGTCCCGATGATGATGAAGTTGGCAGC 1088
 DB 181 GACCAAGATGGGAGATCTGTCTGCCAGAGAGTCCCGATGATGATGAAGTTGGCAGC 240
 QY 1089 TTCAATGAGAGAGTGGCCAGAGACTGGAGACCTGAGAGAGCTTGAATGAAGATG 1148
 DB 241 TTCAATGAGAGAGTGGCCAGAGACTGGAGACCTGAGAGAGCTTGAATGAAGATG 300
 QY 1149 GCGCTGGGGAGAGCTGTGGCTGCCCGCTGCACTGTGGGAGGGAAGATTAGATC 1208
 DB 301 GCGCTGAGGAGAGCTGTGGCTGCCCGCTGCACTGTGGGAGGGAAGATTAGATC 360
 QY 1209 TGAACAGAGCTGTGGGTATGATGTCAATAGAAATAGTAATTTATTTCCAGAGTGTG 1268
 DB 361 TGAACAGAGCTGTGGGTATGATGTCAATAGAAATAGTAATTTATTTCCAGAGTGTG 420
 QY 1269 CTTTAAAGCGTGGGCTGACAGGCTTCTTCTACATCTTTTCCAGTAAGTTCCCTCT 1328
 DB 421 CTTTAAAGCGTGGGCTGACAGGCTTCTTCTACATCTTTTCCAGTAAGTTCCCTCT 480
 QY 1329 GGCTTGACAGCATGAGAGTGTGTGATTTGTTGATGCTCCCGAGCTGTCTTCAGAGCTT 1388
 DB 481 GGCTTGACAGCATGAGAGTGTGTGATTTGTTGATGCTCCCGAGCTGTCTTCAGAGCTT 540
 QY 1389 CACAGT 1448
 DB 541 CACAGT 600
 QY 1449 TGTCCAGATTAATGCTGT 1508
 DB 601 TGTCCAGATTAATGCTGT 660
 QY 1509 GCTTTGATTAATGCTGT 1567
 DB 661 GCTTTGATTAATGCTGT 720
 QY 1569 TTTGGGGAATGTGGAGAGAGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1627
 DB 721 TTTGGGGAATGTGGAGAGAGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
 QY 1628 AC-AAATGAATTTTTCACGAGTCTTTCCATGGGCTAGTAAGTGTG---CCTTGA 1683
 DB 781 AC-AAATGAATTTTTCACGAGTCTTTCCATGGGCTAGTAAGTGTG---CCTTGA 840
 QY 1684 CTG-TTGCAGATGAATGTTCTGTTCACCC 1712
 DB 841 CTGTTTGCAGATGAATGTTCTGTTCACCC 870

RESULT 44
 BUI96397 1201 bp mRNA linear EST 15-MAY-2003
 LOCUS BUI96397.1
 DEFINITION BUI96397.1 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone

ACCESSION	CS0DF010YE05 5-PRIME, mRNA sequence.
VERSION	BX440690
KEYWORDS	BX440690.1 GI:30771871
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 1201)
AUTHORS	Lj.W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	unpublished
COMMENT	Contact: Genoscope

FEATURES

cg1-bam/cluster.cgi?seq=CS0Df010AC03QPL&cluster=6027.r. Contact
Peng Liang Email : fliang@fatech.com URL :
<http://fulllength.invitrogen.com/> INVITROGEN CORPORATION 1600
Faraday Avenue Genoscope sequence ID : CS0Df010AC03QPL.
Location/Qualifiers

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSDF010YE05"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo (dr) primer. Five prime end
enriched. double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
BASE COUNT      248 a      340 c      367 g      198 t      48 others
ORIGIN

```

Query Match	Best Local Similarity	Score	DB	Length
Matches	83%	Conservative	6	Mismatches 17; Indels 8; Gaps 4
QY	1	CGCCGCGCTTC	CGCACCCGCGCCCGCCACCGCGCGCTTCGCGCATCTTGACATCCGCGACG	60
Db	136	CGCCGCGCTTC	CGCACCCGCGCCCGCCACCGCGCGCTTCGCGCATCTTGACATCCGCGACG	195
QY	61	CGCGCGCGCTTC	CGCGCGGAGGAGACATCAGTCCGCGCCGAGCGGACATCCGCGTCA	120
Db	196	CGCGCGCGCTTC	CGCGCGGAGGAGACATCAGTCCGCGCCGAGCGGACATCCGCGTCA	255
QY	121	GTCGCGCGCGCGCTTC	CGCGCGCAGAGCGAGTCAAGCGGCTTGGCGCCACCTGCTGT	180
Db	256	GTCGCGCGCGCGCTTC	CGCGCGCAGAGCGAGTCAAGCGGCTTGGCGCCACCTGCTGT	315
QY	181	GCTGCTGCTGCGCGCGCGCTTC	CGCCCGCGCCCGCGCTTCGACGCGGACCTCGG	240
Db	316	GCTGCTGCTGCGCGCGCGCTTC	CGCCCGCGCCCGCGCTTCGACGCGGACCTCGG	375
QY	241	CTCCAGTCAAGCCCGCGCGCTTC	CAGCTAACCGCAGAGAGGACCACTCATAGAGA	300
Db	376	CTCCAGTCAAGCCCGCGCGCTTC	CAGCTAACCGCAGAGAGGACCACTCATAGAGA	435
QY	301	TGTTCCGCGAGGTTGAGAACTGATGAGAGA	CACGACGACAAATTGCGAGCGCGGTG	360
Db	436	TGTTCCGCGAGGTTGAGAACTGATGAGAGA	CACGACGACAAATTGCGAGCGCGGTG	494
QY	361	AAGAGATGAGGCGAGAAAGAGCTGCTGCTAAAGCATCTCA	TGCAAGTGAACCTGGCAAACT	420
Db	495	AAGAGATGAGGCGAGAAAGAGCTGCTGCTAAAGCATCTCA	TGCAAGTGAACCTGGCAAACT	554

QY	421	TACCTCCACCTATCAAAATGAGACCAACACACAGAGTTGGAAATATATCATCC	480
Db	555	TACCTCCACCTATCAAAATGAGACCAACACACAGAGTTGGAAATATATCATCC	614
QY	481	ATGTGCACCGAAGAAATTCACAGATTAACAACAACGACTCGAACAATGTCTTTTCA	540
Db	615	ATGTGCACCGAAGAAATTCACAGATTAACAACAACGACTCGAACAATGTCTTTTCA	674
QY	541	AGACAGTTATCAATCTGTGGAGACGAAGAAGCAAGAAGCCAGAGTCATACG	600
Db	675	AGACAGTTATCAATCTGTGGAGACGAAGAAGCAAGAAGCCAGAGTCATACG	734
QY	601	ACGAGAGCTGTGGCCCGACATGTACTGCCAGTTTGCAGCTTCAAGTAACCTGCCAGC	660
Db	735	ACGAGAGCTGTGGCCCGACATGTACTGCCAGTTTGCAGCTTCAAGTAACCTGCCAGC	794
QY	661	CATGCCCGGGCCAGAGATGCTCTGCACCCCGGACAGTAGTGCTGTGGAGACCAAGCTGT	720
Db	795	CATGCCCGGGCCAGAGATGCTCTGCACCCCGGACAGTAGTGCTGTGGAGACCAAGCTGT	854
QY	721	GTCGTCGGGGTCACTGCACCAAAATGACCAACGAGGCGACCAATGGACCATCTGTGACA	780
Db	855	GTCGTCGGGGTCACTGCACCAAAATGACCAACGAGGCGACCAATGGACCATCTGTGAC	913
QY	781	ACCAGAGGAACTGCAGCCCGGGGCTGTGCTGTGCTTCCAGAGAGGCTGTGTTCCCTG	840
Db	914	ACCAGAGGAACTGCAGCCCGGGGCTGTGCTGTGCTTCCAGAGAGGCTGTGTTCC	967
QY	841	TGTGACACACCCTGCGCCGTGAGAGGCGC	867
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RESULT 45
B0686811
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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AGNCOURT_9345155 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6250117
5', mRNA sequence.
B0686811
B0686811.1 GI:21812127
EST.
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominiidae, Homo.
1 (bases 1 to 915)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: gga@biml.nih.gov
Tissue Procurement: ATCC
cDNA library Preparation: Rubin Laboratory
cDNA library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: L10CM2392 row: k column: 14
High quality sequence stop: 688.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/dd_xref="taxon:9606"
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/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1b="NIH MGC 110"
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGAG(G). Library constructed

```


Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library."

BASE COUNT 183 a 223 c 273 g 236 t

Query Match 30.2%; Score 779.8; DB 13; Length 915;
Best Local Similarity 99.6%; Pred. No. 8.1e-93;
Matches 792; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

849 CCCCTGCGCGTGAAGGAGAGCTTGGCCATGACCCCGCCAGCCGGCTTGTGACCTCATC 908
1 CCCCTGCGCGTGAAGGAGAGCTTGGCCATGACCCCGCCAGCCGGCTTGTGACCTCATC 60
909 ACCTGGAGAGCTAGAGCTGATGAGCCTTGGACCGATGCTTGTGCGAGTGCCTCTC 968
61 ACCTGGAGAGCTAGAGCTGATGAGCCTTGGACCGATGCTTGTGCGAGTGCCTCTC 120
969 TGGCAGCCCAACAGCCAGCTGTGTATGTGTGCAAGCCGACCTTGTGGGAGAGCGT 1028
121 TGGCAGCCCAACAGCCAGCTGTGTATGTGTGCAAGCCGACCTTGTGGGAGAGCGT 180
1029 GACCAAGATGGGAGATCTCTGCTCCAGAGAGGTCCCGATGATGATGAGTTGGCAGC 1088
181 GACCAAGATGGGAGATCTCTGCTCCAGAGAGGTCCCGATGATGATGAGTTGGCAGC 240
1089 TTCTATGAGAGAGTGGCCCGAGAGACTGGAGAGCTGTGAGAGAGCTGATGAGAGATG 1148
241 TTCTATGAGAGAGTGGCCCGAGAGACTGGAGAGCTGTGAGAGAGCTGATGAGAGATG 300
1149 GCGCTGGGAGAGCTGTGGGAGCTGCGCCGCTGCACTGCTGGGAGGAGAGATTTAGATC 1208
301 GCGCTGGGAGAGCTGTGGGAGCTGCGCCGCTGCACTGCTGGGAGGAGAGATTTAGATC 360
1209 TGGACCAAGCTGTGGGAGAGTGTGCAATAGAAATAGCTAATTTATTTCCCAAGTGTG 1268
361 TGGACCAAGCTGTGGGAGAGTGTGCAATAGAAATAGCTAATTTATTTCCCAAGTGTG 420
1269 CTTTAGAGCGTGGGAGTGAACAGGCTTCTCCATCTTCTCCAGTAATTTCCCTCT 1328
421 CTTTAGAGCGTGGGAGTGAACAGGCTTCTCCATCTTCTCCAGTAATTTCCCTCT 480
1329 GCGCTGACAGCATGAGTGTGTGCAATTTGTTCAAGTCTCCCGAGGCTGTCTCAGGCTT 1388
481 GCGCTGACAGCATGAGTGTGTGCAATTTGTTCAAGTCTCCCGAGGCTGTCTCAGGCTT 540
1389 CACAGTCTGGGAGCTTGGGAGAGTGAAGGAGTTAACTGAGAGAGAGTTGCCACCCC 1448
541 CACAGTCTGGGAGCTTGGGAGAGTGAAGGAGTTAACTGAGAGAGAGTTGCCACCCC 600
1449 TGTCCAGATTAATTTGGCTGCTTGTCTTACCAAGTTGGCAGACAGCCGTTTGTCTCATG 1508
601 TGTCCAGATTAATTTGGCTGCTTGTCTTACCAAGTTGGCAGACAGCCGTTTGTCTCATG 660
1509 GCTTTGATTAATTTGTTTGAAGGAGAGATGAAATGAGTGTGCTGCTGATTTGCT 1568
661 GCTTTGATTAATTTGTTTGAAGGAGAGATGAAATGAGTGTGCTGCTGATTTGCT 720
1569 TTTGGGAGAAATGT-GAGAGAGAGTGCCTGCTTTCGAATCATCAACTGCGCAAAAATGCA 1627
721 TTTGGGAGAAATGTGGGAGAGAGTGCCTGCTTTCGAATCATCAACTGCGCAAAAATGCA 780
1628 ACAATGATTTTCC 1642
781 ACAATGATTTTTC 795

RESULT 46
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LOCUS BO688328
DEFINITION AGENCOURT_8046580 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6209136
5', mRNA sequence.

ACCESSION BO688328
VERSION BO688328.1 GI:21813644
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS NIH-MGC
TITLE NIH-MGC
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaapb-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L10M2367 row: p column: 01
High quality sequence stop: 683.
Location/Qualifiers

FEATURES

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/note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI; Site: 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library."

BASE COUNT 172 a 213 c 260 g 209 t 1 others

Query Match 30.1%; Score 779.4; DB 13; Length 855;
Best Local Similarity 98.8%; Pred. No. 9.5e-93;
Matches 806; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

849 CCCCTGCGCGTGAAGGAGAGCTTGGCCATGACCCCGCCAGCCGGCTTGTGACCTCATC 908
1 CCCCTGCGCGTGAAGGAGAGCTTGGCCATGACCCCGCCAGCCGGCTTGTGACCTCATC 60
909 ACCTGGAGAGCTAGAGCTGATGAGCCTTGGACCGATGCTTGTGCGAGTGCCTCTC 968
61 ACCTGGAGAGCTAGAGCTGATGAGCCTTGGACCGATGCTTGTGCGAGTGCCTCTC 120
969 TGGCAGCCCAACAGCCAGCTGTGTATGTGTGCAAGCCGACCTTGTGGGAGAGCGT 1028
121 TGGCAGCCCAACAGCCAGCTGTGTATGTGTGCAAGCCGACCTTGTGGGAGAGCGT 180
1029 GACCAAGATGGGAGATCTCTGCTCCAGAGAGTCCCGATGATGATGAGTTGGCAGC 1088
181 GACCAAGATGGGAGATCTCTGCTCCAGAGAGTCCCGATGATGATGAGTTGGCAGC 240
1089 TTCTATGAGAGAGTGGCCCGAGAGACTGGAGAGCTGTGAGAGAGCTGATGAGAGATG 1148
241 TTCTATGAGAGAGTGGCCCGAGAGACTGGAGAGCTGTGAGAGAGCTGATGAGAGATG 300
1149 GCGCTGGGAGAGCTGTGGGAGCTGCGCCGCTGCACTGCTGGGAGGAGAAAGATTTAGATC 1208
301 GCGCTGGGAGAGCTGTGGGAGCTGCGCCGCTGCACTGCTGGGAGGAGAAAGATTTAGATC 360
1209 TGGACCAAGCTGTGGGAGAGTGTGCAATAGAAATGCTAATTTATTTCCCAAGTGTG 1268
361 TGGACCAAGCTGTGGGAGAGTGTGCAATAGAAATGCTAATTTATTTCCCAAGTGTG 420

QY 1269 CTTTAGGGCTGGGCTGACCGAGCTTCTTCTACATCTTCTTCCAGTAAGTTCCCTCT 1328
|||||
Db 421 CTTTAGGCTGGGCTGACCGAGCTTCTTCTACATCTTCTTCCAGTAAGTTCCCTCT 480
1329 GGCTTGACAGCATGAGGTGTGTGCAATTGTTCAGCTCCCGAGGCTGTTCACAGGCTT 1388
481 GGCTTGACAGCATGAGGTGTGTGCAATTGTTCAGCTCCCGAGGCTGTTCACAGGCTT 540
QY 1389 CACAGCTGTGTGTGTGAGAGTACAGGAGGTTAACTGACAGGACAGTTGCCACCC 1448
541 CACAGCTGTGTGTGTGAGAGTACAGGAGGTTAACTGACAGGAGTTGCCACCC 600
QY 1449 TGTCCAGATTATATGCTGTGCTTGTCTTACAGATTGACAGAGGCTTGTCTACATG 1508
601 TGTCCAGATTATATGCTGTGCTTGTCTTACAGATTGACAGAGGCTTGTCTACATG 660
QY 1509 GCTTTGATTAATTTGTTGAGGGAGAGATGAAACAATGTGAGTCTCCTCTGATTGGT 1568
661 GCTTTGATTAATTTGTTGAGGGAGAGATGAAACAATGTGAGTCTCCTCTGATTGGT 720
QY 1569 TTGGGGAAATGTGAGAGAGTGC-CCTGCTTTGCAACATCACTGACAAATGCA 1627
721 TTGGGGAAATGTGAGAGAGTGC-CCTGCTTTGCAACATCACTGACAAATGCA 780
QY 1628 ACAATGAA-TTTTCCACGAGTCTTTCATGGG 1661
781 ACAATGAAATTTTCCACGAGTCTTTCATGGG 816

RESULT 47
LOCUS BUI49760 921 bp mRNA linear EST 03-SEP-2002
DEFINITION AGENCOURT_8074878 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6086248
5', mRNA sequence.
ACCESSION BUI49760
VERSION BUI49760.1 GI:22663292
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2320 row: 0 column: 17
High quality sequence stop: 647.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 110"
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

FEATURES
source

BASE COUNT 183 a 231 c 278 g 229 t
ORIGIN
Note: this is a NIH_MGC Library."

Query Match 30.1%; Score 778.2; DB 13; Length 921;
Best Local Similarity 98.8%; Pred. No. 1.3e-92;
Matches 805; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

QY 849 CCCCCTGCGGTGAGAGGCGAGCTTTCGATGACCCCGCAGAGCGGCTTGTGACCTCATC 908
1 CCCCCTGCGGTGAGAGGCGAGCTTTCGATGACCCCGCAGAGCGGCTTGTGACCTCATC 60
Db 909 ACCTGGAGCTTAAGCCTGTATGAGAGCCTTGTGACAGTCCCTTGTGACAGTCCCTC 968
61 ACCTGGAGCTTAAGCCTGTATGAGAGCCTTGTGACAGTCCCTTGTGACAGTCCCTC 120
QY 969 TGCAGGCCCAAGCCACAGCAGCTGTATGATGTGTGAGAGCCGACCTTGTGAGAGCCGT 1028
121 TGCAGGCCCAAGCCACAGCAGCTGTATGATGTGTGAGAGCCGACCTTGTGAGAGCCGT 180
QY 1029 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGTCCCGATAGATAGTAAGTTGGCAGC 1088
181 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGTCCCGATAGATAGTAAGTTGGCAGC 240
QY 1089 TTCTATGAGAGAGTGGCCCGAGAGCTGTGAGAGACCTGTGAGAGAGCTGTGAGAGAGT 1148
241 TTCTATGAGAGAGTGGCCCGAGAGCTGTGAGAGACCTGTGAGAGAGCTGTGAGAGAGT 300
QY 1149 GCGCTGGGGAGAGCCTGCGAGCTGCGCGCTGACCTGCTGAGAGAGGAGATTATGATC 1208
301 GCGCTGGGGAGAGCCTGCGAGCTGCGCGCTGACCTGCTGAGAGAGGAGATTATGATC 360
QY 1209 TGAACACAGGCTGTGGAGTATGTGCAATAGAAATAGCTAATTTATTTCCACAGTGTG 1268
361 TGAACACAGGCTGTGGAGTATGTGCAATAGAAATAGCTAATTTATTTCCACAGTGTG 420
QY 1269 CTTTAGGCGTGGGCTGACAGAGCTTCTCTCAATCTTCTTCCAGTAAGTTCCCTCT 1328
421 CTTTAGGCGTGGGCTGACAGAGCTTCTCTCAATCTTCTTCCAGTAAGTTCCCTCT 480
QY 1329 GGCTTGACAGCATGAGGTGTGTGCAATTGTTCAGCTCCCGAGGCTGTTCACAGGCTT 1388
481 GGCTTGACAGCATGAGGTGTGTGCAATTGTTCAGCTCCCGAGGCTGTTCACAGGCTT 540
QY 1389 CACAGCTGTGTGTGTGAGAGTACAGGAGGTTAACTGACAGGAGCTTGTGCCACCC 1448
541 CACAGCTGTGTGTGTGAGAGTACAGGAGGTTAACTGACAGGAGCTTGTGCCACCC 600
QY 1449 TGTCCAGATTATATGCTGTGCTTGTCTTACAGATTGACAGAGGCTTGTCTACATG 1508
601 TGTCCAGATTATATGCTGTGCTTGTCTTACAGATTGACAGAGGCTTGTCTACATG 660
QY 1509 GCTTTGATTAATTTGTTGAGGGAGAGATGAAACAATGTGAGTCTCCTCTGATTGGT 1568
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QY 1569 TTGGGGAAATGTGAGAGAGTGC-CCTGCTTTGCAACATCACTGACAAATGCA 1626
721 TTGGGGAAATGTGAGAGAGTGC-CCTGCTTTGCAACATCACTGACAAATGCA 780
QY 1627 AACCAATGAAATTTTCCACGAGTCTTTCATGGG 1661
781 AACCAATGAAATTTTCCACGAGTCTTTCATGGG 815

RESULT 48
LOCUS B0685185 879 bp mRNA linear EST 15-JUL-2002
DEFINITION AGENCOURT_8343820 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6248669
5', mRNA sequence.
ACCESSION B0685185
VERSION B0685185.1 GI:21810501
KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 879)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: csapbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LICM2388 row: 0 column: 06
 High quality sequence stop: 649.
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 /organism="Homo sapiens"
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 /clone="IMAGE:6248669"
 /tissue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOTB7; Site:1: XhoI;
 Site 2: EcoRI; CDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAACAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library." 3 others

BASE COUNT 176 a 220 c 263 g 217 t

ORIGIN

Query March 30.0%; Score 774.8; DB 13; Length 879;
 Best Local Similarity 99.3%; Pred. No. 3.7e-97;
 Matches 809; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

QY 849 CCCCTGCCGTGAGGGGCGAGCTTTGCCATGACCCCGCAGCCGCTTGTGACCTCATT 908
 1 CCCCTGCCGTGAGGGGCGAGCTTTGCCATGACCCCGCAGCCGCTTGTGACCTCATT 60

DB 909 ACCGTGGAGCTAGAGCTGTGATGAGCCTTGAGACCGCTTGTGCGAGTGGCTCTC 968
 61 ACCGTGGAGCTAGAGCTGTGATGAGCCTTGAGACCGCTTGTGCGAGTGGCTCTC 120

QY 969 TGGCAGCCCAACAGCCAGCCTTGATGTGTGCAAGCCGACCTTCGTGGAGAACCGT 1028
 121 TGGCAGCCCAACAGCCTTGATGTGTGCAAGCCGACCTTCGTGGAGAACCGT 180

DB 1029 GACCAAAATGGGAGATCTGCTGCCCAAGAGAGTCCCGCATGATGATGAGTTGGCAGC 1088
 181 GACCAAAATGGGAGATCTGCTGCCCAAGAGAGTCCCGCATGATGATGAGTTGGCAGC 240

QY 1089 TTCTAGAGAGAGTGGCCAGAGAGCTGAGAGAGCTGAGAGAGAGCTGACTGAGAGATG 1148
 241 TTCTAGAGAGAGTGGCCAGAGAGCTGAGAGAGCTGAGAGAGAGCTGACTGAGAGATG 300

DB 1149 GCGCTGGGGAGAGCTGGCGCTGCCCGCTGCACTGCTGGAGAGGAGAGATTTAGATC 1208
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DB 421 CTTAGCGGTGGGCTGACCAAGGCTTTCTTCTAATCTTTCTCCAGTAAGTTCCCTCT 480

QY 1329 GCGCTGACAGCATGAGAGTGTGTGATTTGTCATTTGTCAGTCCCGCAGGCTGTTCAGGCTT 1388
 DB 481 GCGCTGACAGCATGAGAGTGTGTGATTTGTCATTTGTCAGTCCCGCAGGCTGTTCAGGCTT 540

QY 1389 CACAGTCTGGTGTGCTGGAGAGTCAAGCAGGCTTAACTGAGAGAGAGTGTGCAACCC 1448
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QY 1449 TGTCAGATTAATTTGGCTGCTTGGCTCTACAGTTGGCAGACAGCCGTTGTTTACATG 1508
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QY 1509 GCTTGTATTAATTTGTTGA-GGGAGAGAGATGAAACATGTGAGAGTCTCCCTCGATTGG 1567
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QY 1568 TTTTGGGGAAT-GTGGAGAGAGAGGCGCTGCTTGGCAAAATCATCACTGGCAAAATGC 1626
 DB 721 TTTTGGGGAATGTGGAGAGAGAGTGCCTGCTTGGCAAAATCATCACTGGCAAAATGC 780

QY 1627 AACAAATGA-ATTTTCCAGCAGATTCTTTCATG 1660
 DB 781 AACAAATGATTTTTCACAGCAGATTCTTTCATG 815

RESULT 49
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 LOCUS AGENCOURT 7974356 NIH_MGC_110 Homo sapiens CDNA clone IMAGE:6082897
 DEFINITION 5', mRNA sequence.
 ACCESSION BU196968
 VERSION BU196968.1 GI:22710952
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 905)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: csapbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LICM2312 row: d column: 02
 High quality sequence stop: 571.
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 /db_xref="taxon:9606"
 /clone="IMAGE:6082897"
 /tissue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOTB7; Site:1: XhoI;
 Site 2: EcoRI; CDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAACAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

BASE COUNT 189 a 223 c 271 g 222 t

ORIGIN

Query Match 30.0%; Score 774.6; DB 13; Length 905;
Best Local Similarity 97.8%; Pred. No. 3.9e-92;
Matches 807; Conservative 0; Mismatches 14; Indels 4; Gaps 2;

849 CCCCTGCGGTGGAGGCGAGCTTTGTCATGACCCCGCAGCCGCTTGTGACCTCATC
1 CCCCTGCGGTGGAGGCGAGCTTTGTCATGACCCCGCAGCCGCTTGTGACCTCATC 60
909 ACCGTGGAGCTTAAGCTGATGAGAGCTTGGACCATGCTTGTGACAGTGGCTCTC 968
61 ACCGTGGAGCTTAAGCTGATGAGAGCTTGGACCATGCTTGTGACAGTGGCTCTC 120
969 TGGCAGCCCGCAGCAGCAGCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1028
121 TGGCAGCCCGCAGCAGCAGCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
1029 GACCAAGATGGGAGATCTCTGCTGCGCCAGAGAGTCCCGAGATGATGAAATTGGCAGC 1088
181 GACCAAGATGGGAGATCTCTGCTGCGCCAGAGAGTCCCGAGATGATGAAATTGGCAGC 240
1089 TTTCATGAGAGAGGTGGCGCAGAGAGCTGAGAGACCTGAGAGAGCCTGATGAAGATG 1148
241 TTTCATGAGAGAGGTGGCGCAGAGAGCTGAGAGACCTGAGAGAGCCTGATGAAGATG 300
1149 GCGCTGGGAGAGCTTGGCGCTGCGCGCTGCACTGTGTGTGTGTGTGTGTGTGTGT 1208
301 GCGCTGGGAGAGCTTGGCGCTGCGCGCTGCACTGTGTGTGTGTGTGTGTGTGTGT 360
1209 TGGACAGAGCTGGGAGATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 1268
361 TGGACAGAGCTGGGAGATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 420
1269 CTTTAAAGCGTGGCTGACAGAGCTTCTTCCATCTTCTTCCAGTAAAGTTCCCTCT 1328
421 CTTTAAAGCGTGGCTGACAGAGCTTCTTCCATCTTCTTCCAGTAAAGTTCCCTCT 480
1329 GCGTTTACAGAGAGGT 1388
481 GCGTTTACAGAGAGGT 540
1389 CACAGTCTGGTGTGGAGAGTCAAGAGAGGTTAACTGACAGAGCAGTTTGCACCCC 1448
541 CACAGTCTGGTGTGGAGAGTCAAGAGAGGTTAACTGACAGAGCAGTTTGCACCCC 600
1449 TGTCCAGATTATGTGCTGCTTGTGCTTGTACAGTTTGGCAGACAGCCGTTTGTCTA 1508
601 TGTCCAGATTATGTGCTGCTTGTGCTTGTACAGTTTGGCAGACAGCCGTTTGTCTA 660
1509 GCTTATATATTTTGTGAGGGAGAGATGAAACAATGTGAGTCCCTCTGATGGT 1568
661 GCTTATATATTTTGTGAGGGAGAGATGAAACAATGTGAGTCCCTCTGATGGT- 719
1569 TTTGGGGAAATGTGAGAGAGTGCCTGCTTGTGCAAACTCAACTGGCAAAATGCA 1628
720 TTTGGGGAAATGTGAGAGAGTGCCTGCTTGTGCAAACTCAACTGGCAAAATGCA 779
1629 CAATGAAATTTTCCAGC--AGTTCTTCCATGGCATAGTAA 1670
780 CAATGAAATTTTCCAGCAGGTTCTTCCATGGCATAGGAA 824

RESULT 50
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LOCUS AGENCYCOURT 7546543 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:6025929
DEFINITION 5', mRNA Sequence.
ACCESSION BQ230977
VERSION BQ230977.1 GI:20412377
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 853)
AUTHORS NIH-MGC
TITLE NIH-MGC
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strauberg, Ph.D.
Email: rstraub@nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:
http://image.llnl.gov
Plate: LIML3238 row: n column: 10
High quality sequence stop: 658.

FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6025929"
/tissue_type="epithelioid carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_70"
/note="Organ: pancreas; Vector: pCMV-Sport6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.1 kb. Library constructed by Life Technologies."

BASE COUNT 226 a 179 c 188 g 260 t
ORIGIN

Query Match 29.9%; Score 772.6; DB 13; Length 853;
Best Local Similarity 99.1%; Pred. No. 7.3e-92;
Matches 806; Conservative 0; Mismatches 3; Indels 4; Gaps 3;

1769 GGGCAGATTTTCATATCC-AAGTCAATCCCTC-TCTCAGCAGAGCTGGGAGGAG 1826
837 GGGCAGATTTTCATATCCAAAGATCAATTCCTTCTTCAAGCAGAGCTGGGAGGAG 778
1827 TCATTGTCTCTCTGTCATCAGAGATCTCAGAGCTCAGAGCTGAGAGCTGCTTGGCC 1886
777 TCATTGTCTCTCTGTCATCAGAGATCTCAGAGCTCAGAGCTGAGAGCTGCTTGGCC 718
1887 AAGTCAAGCTAGTAAAGACAGAGAGAGTTCATCTGTTGACTTAAGCTCAGTG 1946
717 AAGTCAAGCTAGTAAAGACAGAGAGAGTTCATCTGTTGACTTAAGCTCAGTG 658
1947 CTCTCTCACTACCCACACAGAGCTTGTGTCACCAAAAGTCTCTCCCAAAAGAGGA 2006
657 CTCTCTCACTACCCACACAGAGCTTGTGTCACCAAAAGTCTCTCCCAAAAGAGGA 598
2007 GAATGGAGATTTTC--TTGAGGAGATGACATCTGAATTAAGTCAAACTAATTTTCACA 2064
597 GAATGGAGATTTTC--TTGAGGAGATGACATCTGAATTAAGTCAAACTAATTTTCACA 538
2065 TCCCTCTAAAGTAACTACTGTAGGAGACAGAGTGTCTCAAGTGGGAGAGCGT 2124
537 TCCCTCTAAAGTAACTACTGTAGGAGACAGAGTGTCTCAAGTGGGAGAGCGT 478
2125 CCTCTCTAAGAGCATGATTTGACAGTGCCTCTTGGAGTGGCATTAAGTAACTT 2184
477 CCTCTCTAAGAGCATGATTTGACAGTGCCTCTTGGAGTGGCATTAAGTAACTT 418
2185 TGAAGGATATGACTGAGGCTAGCATATAGTTAACTTCAGAGAAACAGTAACTAGTAA 2244
417 TGAAGGATATGACTGAGGCTAGCATATAGTTAACTTCAGAGAAACAGTAACTAGTAA 358
2245 TTGTAGGGCCAGAGTTTAAATGAAATTTTGCAGAAATCTTACAGAGAACTGAAGCAAT 2304
357 TTGTAGGGCCAGAGTTTAAATGAAATTTTGCAGAAATCTTACAGAGAACTGAAGCAAT 236
2305 TATCAACACAGTGGAGAAATCAACCGAGAGGCTGTGTGAAACATGTTGTAATATG 2364

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Db      297 TATCAACCAAGTGAAGAAATCAACCGAGAGGCTGTGAAACATGTTGTAATATG 238
QY      2365 CGACTGCGAACTGTAAGTCTAGCGCACTCCACAAATGATGTTTCAGGTGATGACT 2424
Db      237 CGACTGCGAACTGTAAGTCTAGCGCACTCCACAAATGATGTTTCAGGTGATGACT 178
QY      2425 GTTGCACCATGATCATCCAGAGTTCTTAAGTTAAGTGCACATGTTATAG 2484
Db      177 GTTGCACCATGATCATCCAGAGTTCTTAAGTTAAGTGCACATGTTATAG 118
QY      2485 CATGCTTCTTGTAGTTTAATTATGATTAACATAGTGCATTAGAAATCAAGCAT 2544
Db      117 CATGCTTCTTGTAGTTTAATTATGATTAACATAGTGCATTAGAAATCAAGCAT 58
QY      2545 AAATCACTTCACTGCAAAAAAAAAAAAAA 2577
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Search completed: February 20, 2004, 01:31:06
Job time : 5357 secs

Db 361 AACAGAGCTGAGCAATGCTTTTTCAGAGACATGATACATCTGTGGAGACGAGAA 420
QY 573 GCGAGAGAGGCGACAGAGTCATGATCGACGAGAGCTGTGGGCGCAGATGATCGCCAG 632
Db 421 GCGAGAGAGGCGACAGAGTCATGATCGACGAGAGCTGTGGGCGCAGATGATCGCCAG 480
QY 633 TTTCAGAGCTTCCAGTACCTGTCCAGCCATGCGCGGCGCAGAGATGCTGTGACCCGG 692
Db 481 TTTCAGAGCTTCCAGTACCTGTCCAGCCATGCGCGGCGCAGAGATGCTGTGACCCGG 540
QY 693 GACAGTGAAGTGTGTGAGACCGACGCTGTGTCTGTGGGCTCACTGACCAAAATGGCCAC 752
Db 541 GACAGTGAAGTGTGTGAGACCGACGCTGTGTCTGTGGGCTCACTGACCAAAATGGCCAC 600
QY 753 AGGGGAGAGCAATGGAGCACTGTGTGCAACAGAGAGGAGCTGCGAGCGGGGCTGTGCTGT 812
Db 601 AGGGGAGAGCAATGGAGCACTGTGTGCAACAGAGAGGAGCTGCGAGCGGGGCTGTGCTGT 660
QY 813 GCGTTCCAGAGAGGCGCTGTGTTCCCTGTGTGTGCAACCCCTGCGGTGGAGGCGAGCTT 872
Db 661 GCGTTCCAGAGAGGCGCTGTGTTCCCTGTGTGTGCAACCCCTGCGGTGGAGGCGAGCTT 720
QY 873 TGGCATGACCCCGCGCAGCGGCTTGTGACCTCATCACTGTGGAGCTAGAGCTGATGGA 932
Db 721 TGGCATGACCCCGCGCAGCGGCTTGTGACCTCATCACTGTGGAGCTAGAGCTGATGGA 780
QY 933 GCGTTGGAGCCGATGCCCTTGTGTGCAAGTGGGCTCTCTGTGCGAGCCCGACACCGCAGCTGT 992
Db 781 GCGTTGGAGCCGATGCCCTTGTGTGCAAGTGGGCTCTCTGTGCGAGCCCGACACCGCAGCTGT 840
QY 993 GTGTATGTGTGCAAGCGACCTTGTGTGTGGGAGCGGTGACCAAGATGGGAGATCTGTGCTG 1052
Db 841 GTGTATGTGTGCAAGCGACCTTGTGTGTGGGAGCGGTGACCAAGATGGGAGATCTGTGCTG 900
QY 1053 CCCAGAGAGTCCCGATGATGATGAAATTGGAGAGCTTCAATGAGAGGTGCGCCAGAGAG 1112
Db 901 CCCAGAGAGTCCCGATGATGATGAAATTGGAGAGCTTCAATGAGAGGTGCGCCAGAGAG 960
QY 1113 CTGGAGAGACTGGAGAGAGAGCTGACTGAAGAAGATGGGCTGTGGGAGGCTGTGCTGCC 1172
Db 961 CTGGAGAGACTGGAGAGAGAGCTGACTGAAGAAGATGGGCTGTGGGAGGCTGTGCTGCC 1020
QY 1173 GCGGCTGCACTGCTGGAGAGGAGAGATTTAG 1205
Db 1021 GCGGCTGCACTGCTGGAGAGGAGAGATTTAG 1053

RESULT 2
US-09-161-241-1
/ Sequence 1, Application US/09161241
/ Patent No. 6344541
/ GENERAL INFORMATION:
/ APPLICANT: Baas, Michael B
/ APPLICANT: Sullivan, John K
/ APPLICANT: Theill, Lars E
/ APPLICANT: Wang, Daquan
/ TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
/ FILE REFERENCE: A-548
/ CURRENT APPLICATION NUMBER: US/09/161,241
/ CURRENT FILING DATE: 1998-09-25
/ NUMBER OF SEQ ID NOS: 78
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 1050
/ TYPE: DNA
/ ORGANISM: Mouse
US-09-161-241-1

Query Match 29.8%; Score 769.8; DB 4; Length 1050;
Best Local Similarity 83.9%; Pred. No. 2.8e-175;
Matches 883; Conservative 0; Mismatches 167; Indels 3; Gaps 1;

QY 153 ATGACGAGCTGTGGGCGACCCCTGTGTGCTGTGCTGTGCGGCGGCGGTCCCGACGCGC 212
Db 1 ATGACGAGGCGCTCGGGGGGTATTTTGTGTGTACATGCTGTGGCGGCGGCGGTCCCGACCTGCGT 60
QY 213 CCGGCGCGCGCTCGGAGGCGACCTGTGGCTTCCAGTCAAGCCCGGCGCGCTCTCACTAC 272
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QY 273 CCGGAGAGAGGCGACCCCTCAATGAGATGTTCCGCGAGGTTGAGGAACTGATGAGAGAC 332
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QY 333 ACGGAGCAAAATTTGGCGACGCGGTGTGAAGAATGAGAGGCAAAAGCTGTCTTAA 392
Db 181 ACTGAGCAAACTGGCGCACTGTGCGAGAGATGAGAGCGGGAAGCGAGCTGTCTTAA 240
QY 393 GCATCATCAGAGTGAACCTGTGCAAACTTACCTCCAGCTTATGACATGAGACCAACACA 452
Db 241 ACGTCTCTGAGGTGAACCTGTGCAAACTTACCTCCAGCTTATGACATGAGACCAACACA 300
QY 453 GACACGAGGTTGAAATTAATACATTCATGTGTGACCGAGAAATTGCAAGATTAACCAAC 512
Db 301 GAGACGAGGTTGAAATTAATACATTCATGTGTGACCGAGAAATTGCAAGATTAACCAAC 360
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QY 573 GCGAGAGAGGCGACGAGTGCATTCATGACGAGAGCTGTGGGCGCAGCATGTGCTGAC 632
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QY 1113 CTGGAGAGACTGGAGAGAGAGCTGACTGAAGAAGTGGGCTGTGGGAGGCTGTGCGCTGCC 1172
Db 961 CTGGAGAGACTGGAGAGAGAGCTGACTGAAGAAGTGGGCTGTGGGAGGCTGTGCGCTGCC 1017
QY 1173 GCGGCTGCACTGCTGGAGAGGAGAGATTTAG 1205
Db 1018 GTGAGTCACTAGCGGAGAGAGAGATTTAG 1050


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OTHER INFORMATION: region 36.167
OTHER INFORMATION: id HUM137D01B
FEATURE:
NAME/KEY: other
LOCATION: 12.142
IDENTIFICATION METHOD: biasn
OTHER INFORMATION: identity 99
OTHER INFORMATION: region 143.273
OTHER INFORMATION: id AA155928
FEATURE:
NAME/KEY: other
LOCATION: 12.141
IDENTIFICATION METHOD: biasn
OTHER INFORMATION: identity 99
OTHER INFORMATION: region 115.244
OTHER INFORMATION: id W39572
OTHER INFORMATION: est
FEATURE:
NAME/KEY: other
LOCATION: complement(12.135)
IDENTIFICATION METHOD: biasn
OTHER INFORMATION: identity 95
OTHER INFORMATION: region 1.124
OTHER INFORMATION: id M78698
OTHER INFORMATION: est
FEATURE:
NAME/KEY: other
LOCATION: complement(32.151)
IDENTIFICATION METHOD: biasn
OTHER INFORMATION: identity 98
OTHER INFORMATION: region 346.465
OTHER INFORMATION: id H99266
OTHER INFORMATION: est
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 67.114
IDENTIFICATION METHOD: Von Heljne matrix
OTHER INFORMATION: score 5.9
OTHER INFORMATION: seq MULTISFSCIS/NF
US-08-905-223-215

Query Match
Best Local Similarity 5.3%; Score 137; DB 3; Length 150;
Matches 137; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2077 TAAACTAGTTAGGAACAGAGCTGTTCTCAGAGTGGGAGCGGCTCTTAATGAA 2136
DB 12 TAACTACTGTTAGGAACAGAGCTGTTCTCAGAGTGGGAGCGGCTCTTAATGAA 71
QY 2137 GACAAATGATATATGACACTGTCTCTTGGCAGTTGATTAAGTAAAGTAAAT 2196
DB 72 GACAAATGATATATGACACTGTCTCTTGGCAGTTGATTAAGTAAAGTAAAT 131
QY 2197 GACTGAGCGTAGCATACAG 2215
DB 132 GACTGAGCGTAGCATACAG 150

RESULT 5
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
```

```
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMWU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ9pt-F15
US-08-232-463-14

Query Match
Best Local Similarity 2.9%; Score 52.4; DB 1; Length 7218;
Matches 11; Conservative 216; Mismatches 147; Indels 0; Gaps 0;

QY 277 AGGAGAGGCCACCTCATGATGATGTTCCGCGAGTTGAGAGACTGATGAGACAGC 336
DB 1422 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1363
QY 337 AGCAAAATGCGCAGCGCGGTGGAAGATGAGAGAGAGAGAGAGCTGCTTAAGCAT 396
DB 1362 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1303
QY 397 CATCAGAGTGAACCTGCAACTTACCTCCAGCTATCACAATGAGACCAACAGACA 456
DB 1302 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1243
QY 457 CGAAGTTGGAATATATACATCATGTCACCGAGAAATTCACAAGATACCAACACC 516
DB 1242 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1183
QY 517 AGACTGACAAATGTTCTTTTCAAGACAGTTATCATCTGTGGAGACGAAAGGCA 576
DB 1182 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1123
QY 577 GAAGAGCCACAGAGTGCATATGACAGAGACTGTGGGCCACAGATATATGCAAGTTG 636
DB 1122 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1063
QY 637 CCAGCTTCAGTAC 650
DB 1062 CAAGCTCCCTGCAC 1049

RESULT 6
US-09-461-325-118
; Sequence 118, Application US/09461325A
; Patent No. 6475753
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GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 94 Human Secreted Proteins
FILE REFERENCE: P2029P1
CURRENT APPLICATION NUMBER: US/09/461,325A
CURRENT FILING DATE: 1999-12-14
EARLIER APPLICATION NUMBER: PCT/US99/13418
EARLIER FILING DATE: 1999-06-15
EARLIER APPLICATION NUMBER: 60/089,507
EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/089,508
EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/089,509
EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/089,510
EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/090,112
EARLIER FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: 60/090,113
EARLIER FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 532
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 118
LENGTH: 882
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (117)
OTHER INFORMATION: n equals a,t,g, or c
US-09-461-325-118

Query Match
Best Local Similarity 55.8%; Pred. No. 0.0065;
Matches 96; Conservative 1; Mismatches 75; Indels 0; Gaps 0;

2.0%; Score 51.6; DB 4; Length 882;
US-09-128-155-16

RESULT 7
US-09-128-155-16
Sequence 16, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 152331
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(152331)

Db 406 TGAACCTGGCAAACTTACCTCCAGCTATCAATGAGACACACAGACAGAGAGTTG 465
362 TGGCTTCCTCCGGGCTCTCCGGAACTACCAAGAGGAGGAGGAGGAGGAGGAGGAG 421
466 GAAATATACCATCATCATGTCACCGAGAAATTCACAAATTAACCAACCAAGACTGAGC 525
422 GGAACAACACCTCTCCAGCCACTTCAGATCGAAGATGACCGACCAACAGAGGAG 481
QY 526 AATGTCCTTTTCAGAGACAGTTATCATCTGTGGAGACGAAAGAGGAG 577
482 AGGTGCTGATCTCCGAGAAATGTGTGGATTCATTCACCAAGGAGGAGGAG 533
Db

OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

Query Match
Best Local Similarity 48.6%; Pred. No. 0.078;
Matches 141; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

2.0%; Score 51.6; DB 3; Length 152331;
US-08-665-259-19

RESULT 8
US-08-665-259-19
Sequence 19, Application US/08665259
Patent No. 6028173
GENERAL INFORMATION:
APPLICANT: Landes, Gregory M.
APPLICANT: Burn, Timothy C.
APPLICANT: Connors, Timothy D.
APPLICANT: Dackowski, William R.
APPLICANT: Van Raay, Terence J.
TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESSES:
ADDRESSEE: GENZYME CORPORATION
STREET: One Mountain Road
CITY: Framingham
STATE: Massachusetts
COUNTRY: United States of America
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,259
FILING DATE: 17-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dugan, Deborah A.
REGISTRATION NUMBER: 37,315
REFERENCE/DOCKET NUMBER: 1G5-9.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 872-8400
TELEFAX: (508) 872-5415
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 6803 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-665-259-19

Db 4 CGGCTCCCGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 63
21931 CC 21990
QY 64 GCGGCTCCCGGCGGAGCGAGCGAGCATTCAGTCCGCGCGGCGGCGGCGGCGGCGGCGG 123
21991 CCGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 22050
QY 124 GGGGCGGCGGCTGGGGCGGCGAGCGAGATTCAGCGGCTTGGGGCGGCGGCGGCGGCGG 183
22051 CCGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 22110
Db 184 TGCTGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 243
22111 CGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 22170
QY 244 CAGTCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 293
22171 CGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 22220
Db

Query Match 1.9%; Score 49; DB 3; Length 6803;
Best Local Similarity 49.8%; Pred. No. 0.073;
Matches 155; Conservative 0; Mismatches 150; Indels 6; Gaps 1;
Molecule Type: DNA (genomic)
US-08-762-500-19

17 CCGCGGCGCCCGCCACCGCCGCTCCCGATCTGACCCCGAGCCCGCGGCGCTCCCGGC 76
2746 CTGCACCCCGAGAGAGAGCGCGCGCGCTGACACCGAGCGCCCGCCCGCCACCGCGCTTC 2805

QY 77 GGGAGCGAGCATCCAGTCCGCGCCCGAGCCCACTCGCTCAATCGGCGGCGGCGCTG 136
DB 2806 CCGGAGCGCGAGAGACCTGCTCCCGCGGCTGAGTGGCGAGCGCGCGGCTG 2865

QY 137 CCGGCGCGAGCGAGATGAGCGGCTTGGGCGCACCTGCTGCTGCTGCTGCGCGC 196
DB 2866 GGGCGCTCCGCGCGCGAGAGACCGGAGCGGCGGCGAGCGCGCTGATCGCTTAAGCCCA 2925

QY 197 GCGCGTCCCGACCGCGCCCGCGCGCTCGACGCGGACCTGGCTCCAGTCAAGCCCG 256
DB 2926 GCGGGA-----GGACGCGCGCAACATCCCGCTGCTGCTGCGCGCGCGCTGCGC 2979

QY 257 CCGGCGCTCAGCTACCGCGAGAGAGCGCACCTCAATGAGATGTTCCGCGAGGTTGA 316
DB 2980 CGCTGCTCCACCTCTGCGCGCGCGCTGGGCGCGCGCGCGCGCGCTGCTGCGCATTCG 3039

QY 317 GGAAGTGAATG 327
DB 3040 GGGCGTGTGG 3050

RESULT 9
US-08-762-500-19
Sequence 19, Application US/08762500
Patent No. 6030806
GENERAL INFORMATION:
APPLICANT: Landes, Gregory M.
APPLICANT: Burn, Timothy C.
APPLICANT: Connors, Timothy D.
APPLICANT: Dackowski, William R.
APPLICANT: Van Raay, Terence J.
APPLICANT: Klingner, Katherine W.
TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: One Mountain Road
CITY: Framingham
STATE: Massachusetts
COUNTRY: United States of America
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,500
FILING DATE: 09-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,259
FILING DATE: 17-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10469
FILING DATE: 17-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Dugan, Deborah A.
REGISTRATION NUMBER: 37,315
REFERENCE/DOCKET NUMBER: 165-9.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 872-8400
TELEFAX: (508) 872-5415

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 6803 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-762-500-19

Query Match 1.9%; Score 49; DB 3; Length 6803;
Best Local Similarity 49.8%; Pred. No. 0.073;
Matches 155; Conservative 0; Mismatches 150; Indels 6; Gaps 1;
Molecule Type: DNA (genomic)
US-07-751-891B-24/C

17 CCGGCGCGCCCGCCACCGCGCTCCCGATCTGACCCCGAGCCCGCGGCGCTCCCGGC 76
2746 CTGCACCCCGAGAGAGCGCGCGCGCTGACACCGAGCGCCCGCCCGCCACCGCGCTTC 2805

QY 77 GGGAGCGAGCATCCAGTCCGCGCCCGAGCCCACTCGCTCAATCGGCGGCGGCGCTG 136
DB 2806 CCGGAGCGCGAGAGACCTGCTCCCGCGGCTGAGTGGCGAGCGCGCGGCTG 2865

QY 137 CCGGCGCGAGCGAGATGAGCGGCTTGGGCGCACCTGCTGCTGCTGCTGCGCGC 196
DB 2866 GGGCGCTCCGCGCGCGAGAGACCGGAGCGGCGGCGAGCGCGCTGCTGCTGCGCGCA 2925

QY 197 GCGCGTCCCGACCGCGCCCGCGCGCTCGACGCGGAGCGGACCTGCGCTCAATGAGATGTTCCGCGAGGTTGA 316
DB 2926 GCGGGA-----GGACGCGCGCAACATCCCGCTGCTGCTGCGCGCGCGCTGCGC 2979

QY 257 CCGGCGCTCAGCTACCGCGAGAGAGCGCACCTCAATGAGATGTTCCGCGAGGTTGA 316
DB 2980 CGCTGCTCCACCTCTGCGCGCGCGCTGGGCGCGCGCGCGCGCGCTGCTGCGCATTCG 3039

QY 317 GGAAGTGAATG 327
DB 3040 GGGCGTGTGG 3050

RESULT 10
US-07-751-891B-24/C
Sequence 24, Application US/07751891B
Patent No. 6180337
GENERAL INFORMATION:
APPLICANT: Caskey, C. T.
APPLICANT: Nelson, David L.
APPLICANT: Pieretti, Maurea
APPLICANT: Warren, Stephen T.
APPLICANT: Costra, Ben A.
TITLE OF INVENTION: Diagnosis of the Fragile X Syndrome
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas D. Paul
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/751,891B
FILING DATE: 29-AUG-1991
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5350
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325

TELEFAX: 713/651-5246
TELEX: 762829
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1026 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 24:

US-07-751-891B-24
Query Match 1.9%; Score 48.4; DB 3; Length 1026;
Best Local Similarity 47.9%; Pred. No. 0.041;
Matches 139; Conservative 0; Mismatches 151; Indels 0; Gaps 0;
QY 2 GCGGCGCTCCCGACCCGCGGCGCCCGCCACCGCGCGCTCCGATCTGCACCCGAGCC 61
DB 555 GCGCGGCTCCCGACCCGCGGCGCCCGCCACCGCGCGCTCCGATCTGCACCCGAGCC 496
QY 62 CGGCGGCTCCCGGCGGAGCGAGCAGATCCAGTCCGCGCCCGAGCGCACTCGGTCCAG 121
DB 495 CCGCGCGGAGAGGTGGGCTGGCGGCGCTCGAGGCCACCGCGCGCGCGCGCGCG 436
QY 122 TCGGGGCGGCGGCTGGCGGCGCAGAGCGGAGATGACGCGGCTTGGGGCCACCTGCTGTG 181
DB 435 CCGCGCGGCGGCGGCGGCGCGCGCGCGCGCGCTGCGCGACGCGCGCGCGCTCC 376
QY 182 CCGCTGCTGGCGGCGGCGGCTCCCGAGCGCGCGCGCGCGCGCTCGAGCGGAGCGCGG 241
DB 375 GTACCGCGCGCGCGCGCGCTGCGCTGCGCGCGCGCGCGCGCGCGCTCGAGCGGCGG 316
QY 242 TCCAGTCAAGCGCGCGCGCGCTCTCACTACCGCGAGAGAGGCCACCC 291
DB 315 CGGAGGTGAACCGAAGCGAGCTGAGCGCGCTGACTAGGCGCGAAGCCCGC 266

RESULT 11
US-07-751-891B-23/C
Sequence 23, Application US/0751891B
Patent No. 6180337
GENERAL INFORMATION:
APPLICANT: Caskey, C. T.
Nelson, David L.
Pieretti, Maura T.
Warren, Stephen T.
Costra, Ben A.
Fu, Ying-hui
TITLE OF INVENTION: Diagnosis of the Fragile X Syndrome
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: Thomas D. Paul
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/751,891B
FILING DATE: 29-Aug-1991
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5350
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246

TELEX: 762829
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 5222 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-07-751-891B-23

Query Match 1.9%; Score 48.4; DB 3; Length 5222;
Best Local Similarity 47.9%; Pred. No. 0.09;
Matches 139; Conservative 0; Mismatches 151; Indels 0; Gaps 0;
QY 2 GCGGCGCTCCCGACCCGCGGCGCCCGCCACCGCGCGCTCCGATCTGCACCCGAGCC 61
DB 2866 GCGCGGCTCCCGACCCGCGGCGCCCGCCACCGCGCGCTCCGATCTGCACCCGAGCC 2807
QY 62 CGGCGGCTCCCGGCGGAGCGAGCAGATCCAGTCCGCGCCCGAGCGCACTCGGTCCAG 121
DB 2806 CCGCGCGGAGAGGTGGGCTGGCGGCGCTCGAGGCCACCGCGCGCGCGCGCGCG 2747
QY 122 TCGGGGCGGCGGCTGGCGGCGCAGAGCGAGATGACGCGGCTTGGGGCCACCTGCTGTG 181
DB 2746 CCGCGCGGCGGCGGCGGCGCGCGCGCGCGCTGCGCGACGCGCGCGCGCTCC 2687
QY 182 CCGCTGCTGGCGGCGGCGGCTCCCGAGCGCGCGCGCGCGCTCGAGCGGAGCGCGG 241
DB 2686 GTACCGCGCGCGCGCGCGCTGCGCTGCGCGCGCGCGCGCGCGCTCGAGCGGCGG 2627
QY 242 TCCAGTCAAGCGCGCGCGCGCTCTCACTACCGCGAGAGAGGCCACCC 291
DB 2626 CGGAGGTGAACCGAAGCGAGCTGAGCGCGCTGACTAGGCGCGAAGCCCGC 2577

RESULT 12
US-09-252-991A-9441
Sequence 9441, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107136.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 9441
LENGTH: 1269
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9441

Query Match 1.8%; Score 47.4; DB 4; Length 1269;
Best Local Similarity 51.8%; Pred. No. 0.079;
Matches 131; Conservative 0; Mismatches 121; Indels 1; Gaps 1;
QY 64 GCGGCTCCCGGCGGAGCGAGCAGATCCAGTCCGCGCCCGAGCGCACTCGGTCCAGTC 123
DB 831 GCGGCGCGGCTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 890
QY 124 GGGGCGGCGGCTGGCGGCGGAGCGGAGATGACGCGGCTTGGGGCCACCTGCTGTGCC 183
DB 891 GGGCGGCGGAGGTAGTGTGCTG-GAGCTGACGCTGAGAGAAAGCGCGCGGAGTGA 949
QY 184 TGCTGTGGCGGCGGCGGCTCCCGAGCGCGCGCGCGCGCTCGGAGCGGAGCTCGGCTC 243
DB 950 CGGTGCGGCGGAGAGCGGCTTCCCGCGCTTGC-CGGGCGAGGCTGCGAGCGGTGCGCGGCGG 1009

QY 244 CAGTCAAGCCCGCCCGGCTTCACTACCCGAGAGAGAGCCCACTCTCATGATGT 303
DB 1010 CGGCGCCCGCCGAGCGGCTGCGCGCCCGCGGTAAAGCCCACTCTGAGAGC 1069
QY 304 TCCGCGAGGTGA 316
DB 1070 TGGTCCAGGTGA 1082

RESULT 13
US-09-252-991A-9392/c
Sequence 9392, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 9392
LENGTH: 1890
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9392

Query Match 1.8%; Score 47.4; DB 4; Length 1890;
Best Local Similarity 51.8%; Pred. No. 0.096;
Matches 111; Conservative 0; Mismatches 121; Indels 1; Gaps 1;

QY 64 GGGGCTCTCCCGCGGAGAGAGATCCAGTCCGCGCCGCGAGCCCACTCGGTCAATC 123
DB 502 GCGGGGCGCGTCTCTGCGCGCGCCGCGCCATCGCGCGCTATCGAGGCCCTGT 443
QY 124 GCGGCGCGCGCTGCGCGCGCAGAGCGAGATGACGCGCTTGCGGCGCACTGTGTGCC 183
DB 442 GCGCGCGCGCGCTCAAGTCTG-GAGCTGAGCTGGAAGAACCCCGCGGAGGTGA 384
QY 184 TCGTGTGCGCGCGCGGTCCCAAGCGCCCGCGCTCCGAGCGCACTGTGGTCC 243
DB 383 CGGTGCGCGCGCGCGGTCCCAAGCGCCCGCGCTCCGAGCGCACTGTGGTCC 324
QY 244 CAGTCAAGCCCGCCCGGCTCTCAGTCAACCGAGAGAGAGCCCACTCATGATGT 303
DB 323 CGGCGCGCGCGCGAGCGGCGGCGCGCGGTAAAGCCCACTCTGAGAGC 264
QY 304 TCCGCGAGGTGA 316
DB 263 TGGTCCAGGTGA 251

RESULT 14
US-08-469-526A-21
Sequence 21, Application US/08469526A
Patent No. 5792849
GENERAL INFORMATION:
APPLICANT: Gooddearl, Andrew
APPLICANT: Strobant, Paul
APPLICANT: Minshetti, Luisa
APPLICANT: Waterfield, Michael
APPLICANT: Marchionni, Mark
APPLICANT: Chen, Miao Su
APPLICANT: Hiles, Ian
TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
PREPARATION AND USE
NUMBER OF SEQUENCES: 187
CORRESPONDENCE ADDRESS:

ADDRESSEE: Clark & Elding LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,526A
FILING DATE: 06 June 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/036,555
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
APPLICATION NUMBER: 07/907,138
FILING DATE: 03-JUN-1992
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
APPLICATION NUMBER: U.K. 91 07566.3
FILING DATE: 10-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bleker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 04585/00200A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-7045
TELEFAX: 617-428-0200
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 2003
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: N in positions 31 and 32 could be
either A or G.
US-08-469-526A-21

Query Match 1.8%; Score 47; DB 1; Length 2003;
Best Local Similarity 47.5%; Pred. No. 0.12;
Matches 140; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 94 GTCGCGCGCGCGCACTCGGTCCAGTCCGCGCGCGCGCTGCGGCGGAGAGCGAGA 153
DB 299 GTCCCG 358
QY 154 TCGAGCGGCTTGAGCGCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 213
DB 359 TCGTGCACACTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 418
QY 214 CCGGCGCGCGCTCGAGAGCGCACTTGGCTTCAGTCAAGCGCGCGCGCGCTTCAGTACC 273
DB 419 ACGAGGCGGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 478
QY 274 CCGAGAGAGAGCGCACCTTCATGATGATGATGATGATGATGATGATGATGATGAT 333
DB 479 TCGAGGAGTAGTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 538
QY 334 CCGAGCAAAATTGCGCAAGCGCGGTGGAAGATGAGCAAGAAAGTCTGCG 388
DB 539 GCGAGCAGGCGGCACTCGACAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 593

RESULT 15
US-08-734-591A-21

Sequence 21, Application US/08734591A
Patent No. 5854220
GENERAL INFORMATION:
APPLICANT: Goodheart, Andrew
APPLICANT: Stroobant, Paul
APPLICANT: Minghetti, Luisa
APPLICANT: Waterfield, Michael
APPLICANT: Hiles, Ian
APPLICANT: Marchionni, Mark
TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
NUMBER OF SEQUENCES: 187
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Biring LLP
STREET: 176 Federal Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible Pentium
OPERATING SYSTEM: Windows95
SOFTWARE: WordPerfect (Version 7.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/734,591A
FILING DATE: 22-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/470,335
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/036,555
FILING DATE: 03-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 91 07566.3
FILING DATE: 10-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 04585/00200P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 428-0200
TELEFAX: (617) 428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 2003
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: N in positions 31 and 32 could be
OTHER INFORMATION: either A or G.
US-08-734-591A-21
Query Match 1.88; Score 47; DB 2; Length 2003;
Best Local Similarity 47.5%; Pred. No. 0.12;
Matches 140; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

Oy 94 GTCCGCGCCCGCAGCGCACTCGGTCAGTCGCGCGCGGCTGCGGCGCAGAGCCGAGA 153
Db 299 GTCCCGGCCCCCGGCCCCCAGCGCCCCCGGCTCCGCCCCGCTGTCGCGCGCGCTGCCGC 358
Oy 154 TGCAGCGGCTTGGGGCCACCTGCTGTGCTGTGCTGCGCGGGGTCCCAAGGCC 213
Db 359 TGTGCTCACTACTGCTGCTGCTGCTGCGGACCCGCGCCCTGCGCGCGGGCGCGCGGCA 418
Oy 214 CCGGCGCCGCTCGAGCGGCGAGCCTCGGCTCCAGTCAAGCCCGCGGCTCTCAGCTACG 273
Db 419 ACGAGCGGCTCCCGCGGGGCTTCGCTGCTACTGCTCCCGCCAGGCTGGATCGG 478
Oy 274 CGCAGAGGAGGCGCACCTCAATGATGTTCCGCGAGGTTGAGGAACTGATGAGGACA 333
Db 479 TGCAGGAGTAGTCAAGCGCGCGCGGTGCTCATCGAGGAGAAAGTGCACCCGACGCGC 538
Oy 334 CGCAGCACAATTTGCGAGCGCGGTGGAAGATGAGGAGGAGAGAGCTGCTGC 388
Db 539 GGCAGCGGGGCACTGACAGAGAGAGCGCGCGCGCGCGGCGAGGCAAGGGGC 593

Search completed: February 19, 2004, 21:20:51
Job time : 161 secs

PN	WO9827933-A2.
XX	
PD	02-JUL-1998.
XX	
PF	18-DEC-1997; 97WO-US23518.
XX	
PR	20-DEC-1996; 96US-0033870.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC
XX	
PI	Ruben SM, Soppet DR;
XX	

DR MPI: 1998-377366/32.
 DR N-PSDB; AAY38798.
 XX
 PT New isolated cerebellum and embryo specific polypeptide - used to
 PT develop products for treating e.g. coronary stenosis, myocardial
 PT infarction, heart disease and artery or venous thrombosis
 XX
 PS Claim 17; Fig 1; 77pp; English.
 CC The sequence is that of cerebellum and embryo specific protein
 CC (CBSP). CBSP is involved in: (i) the regulation of collateral
 CC circulation (particularly in the heart), coronary artery stenosis
 CC following a revascularisation procedure, apoptosis in myocytes; (ii) the
 CC modulation of myocyte development in the developing heart; (iii)
 CC regulation of circulating blood volume, vascular tone, blood pressure and
 CC cardiac output, diuresis, natriuresis; (iv) facilitation of transudation
 CC of plasma water to the interstitium, and (iv) inhibition of the release
 CC or action of hormones such as aldosterone, angiotensin II, endothelin,
 CC renin and vasopressin. The products can be used in the diagnosis and
 CC treatment of CBSP related disorders, e.g. coronary stenosis following
 CC coronary revascularisation, coronary artery thrombus or occlusion,
 CC myocardial infarction, atrial and/or ventricular arrhythmias, heart
 CC block, hereditary medial necrosis of small coronary arteries,
 CC cardiomyopathy, arrhythmogenic right ventricular dysplasia, athero-
 CC sclerotic heart disease, venous thrombosis or Reynaud's syndrome.
 XX
 SQ Sequence 350 AA;
 Query Match 100.0%; Score 1880; DB 19; Length 350;
 Best Local Similarity 100.0%; Pred. No. 6.5e-149;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQRIGATLCLLLAAVPTAPAPATATAPKPGPALSTPQEBATLNMREVELEMD 60
 DB 1 MQRIGATLCLLLAAVPTAPAPATATAPKPGPALSTPQEBATLNMREVELEMD 60
 QY 61 TQHKRSAYEMEAEEAAKASEVNLALPPSYHNETNTDKVANTTIHVAREIHKITN 120
 DB 61 TQHKRSAYEMEAEEAAKASEVNLALPPSYHNETNTDKVANTTIHVAREIHKITN 120
 QY 121 NOTGVVFSEVTITSGDEGRSHSECTIDEDCGSNVQSPSFQYTCQPCGQMLCTR 180
 DB 121 NOTGVVFSEVTITSGDEGRSHSECTIDEDCGSNVQSPSFQYTCQPCGQMLCTR 180
 QY 181 DSECCDQLCVMGCHCTKMATRGNGTICDNQDCQPGALCCAFQGLFLFVCTPLFVEGEL 240
 DB 181 DSECCDQLCVMGCHCTKMATRGNGTICDNQDCQPGALCCAFQGLFLFVCTPLFVEGEL 240
 QY 241 CHDPASRLDLITWLEPDPGALDRCPASGLICQPHSHSLVYVCKPTFVGRDQGEILL 300
 DB 241 CHDPASRLDLITWLEPDPGALDRCPASGLICQPHSHSLVYVCKPTFVGRDQGEILL 300
 QY 301 PRFVPEVEYEGSMEEVROELFELSLTEEMALGPAAALAAALGGEEI 350
 DB 301 PRFVPEVEYEGSMEEVROELFELSLTEEMALGPAAALAAALGGEEI 350

RESULT 2
 ID AAY92070 standard; Protein; 350 AA.
 XX
 AC AAY92070;
 XX
 DT 01-AUG-2000 (first entry);
 XX
 DE Human DKR-3.
 XX
 KM DKR-3: human rig-like 7-1 mRNA; chicken lens fiber protein; c1feet 4;
 KM dkk-1; dickkopf-1; antagonist; wnt-8 signaling; morphogenesis;
 KM growth factor; cytoskeletal; sonic hedgehog; tissue differentiation.
 XX
 OS Homo sapiens.
 XX

FN Key Location/Qualifiers
 FT Peptide 1..20
 FT /label= "signal_peptide"
 FT /note= "putative"
 FT Peptide 1..21
 FT /label= "signal_peptide"
 FT /note= "putative"
 FT Cleavage-site 16..17
 FT /note= "putative endogenous processing site"
 FT Region 21..145
 FT /note= "alpha helical region and region of N-linked glycosylation"
 FT Cleavage-site 22..23
 FT /note= "putative endogenous processing site"
 FT Cleavage-site 32..33
 FT /note= "putative endogenous processing site"
 FT Cleavage-site 41..42
 FT /note= "putative endogenous processing site"
 FT Modified-site 96
 FT /note= "N-glycosylated"
 FT Modified-site 106
 FT /note= "N-glycosylated"
 FT Modified-site 121
 FT /note= "N-glycosylated"
 FT Modified-site 204
 FT /note= "N-glycosylated"
 FT Region 300..350
 FT /note= "alpha helical region"
 FN W020018914-A2.
 XX
 XX 06-Apr-2000.
 XX
 XX 17-SEP-1999; 99MO-US21647.
 XX
 XX 25-SEP-1998; 98US-0161241.
 XX
 XX (AMGE-) AMGEN INC.
 XX
 XX Baas MB, Sullivan JK, Theill LE, Wang D;
 DR MPI: 2000-229153/25.
 DR N-PSDB; AAA08839.
 XX
 PT New nucleic acid molecule encoding a biologically active DKR
 PT polypeptide, useful in treatment of cancer, e.g. mammary tumors and
 PT stem cell tumors
 XX
 PS Claim 18; Page 126-127; 143pp; English.
 XX
 XX AAY92069-75 are novel mouse and human DKR polypeptides.
 XX The human DKR-3 open reading frame has homology to human rig-like 7-1
 XX mRNA and to chicken lens fiber protein c1feet 4 gene. Human DKR-3
 XX appears to be secreted, with a signal peptide cleavage site after either
 XX amino acid 20 or 21.
 CC DKR-1 is a human ortholog of dkk-1 (dickkopf-1), a novel gene identified
 CC in Xenopus and mouse, purportedly an antagonist of wnt-8 signaling.
 CC DKR-2, -3 and -4 are each related to DKR-1 by their cysteine pattern,
 CC therefore a growth factor, by inference DKR polypeptides are also
 CC growth factors. The DKR polypeptides are useful for treating cancer,
 CC e.g. mammary tumors, stem cell tumors, or other cancers in which the wnt
 CC and/or sonic hedgehog (shh) signal transduction pathways are activated.
 CC They can also be used to enhance tissue differentiation, such as bone
 CC formation and hematopoietic cell formation.
 XX
 SQ Sequence 350 AA;
 Query Match 100.0%; Score 1880; DB 21; Length 350;
 Best Local Similarity 100.0%; Pred. No. 6.5e-149;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQRIGATLCLLLAAVPTAPAPATATAPKPGPALSTPQEBATLNMREVELEMD 60


```

Db      1 MQLGATLCLLLAAVPTAPAPATATSAVPKGPALSYQEBATINEMFREVEELMED 60
QY      61 TQKLSAVEEMEAEEAAKASSEVNLANLPSPYHNENTDTKVGNNTHVHREIHKITN 120
Db      61 TQKLSAVEEMEAEEAAKASSEVNLANLPSPYHNENTDTKVGNNTHVHREIHKITN 120
QY      121 NOTGQWVFSEVTITVSVDDEGRSHSECTIDEDCGPSMYCQFASFOYTCQPCRGQRLCTR 180
Db      121 NOTGQWVFSEVTITVSVDDEGRSHSECTIDEDCGPSMYCQFASFOYTCQPCRGQRLCTR 180
QY      121 NOTGQWVFSEVTITVSVDDEGRSHSECTIDEDCGPSMYCQFASFOYTCQPCRGQRLCTR 180
Db      121 NOTGQWVFSEVTITVSVDDEGRSHSECTIDEDCGPSMYCQFASFOYTCQPCRGQRLCTR 180
QY      181 DSECCGQQLCWGHCTKMATRGSGNGTICDNQRCQPGLCQAFQRLFPVCTPLPVEGEL 240
Db      181 DSECCGQQLCWGHCTKMATRGSGNGTICDNQRCQPGLCQAFQRLFPVCTPLPVEGEL 240
QY      241 CHDPASRLDLITWELEPDGALDRCPGASGLCQPHSHSLVYVCKPTFVGSRDQDEILL 300
Db      241 CHDPASRLDLITWELEPDGALDRCPGASGLCQPHSHSLVYVCKPTFVGSRDQDEILL 300
QY      301 PREVPDEYEVGSFMEVROELEDLERSLITEMALGEPAAAAALLGGEEI 350
Db      301 PREVPDEYEVGSFMEVROELEDLERSLITEMALGEPAAAAALLGGEEI 350

RESULT 3
AAG80271 ID AAG80271 standard; Protein: 350 AA.
AC AAG80271;
DT 11-FEB-2002 (first entry)
XX
DE Human DKK-3 protein.
XX
KM DKK-3; detection; schizophrenia; neuroleptic; vaccine; gene therapy;
KW neuroleptic defect; neuropsychiatric disorder; human.
XX
OS Homo sapiens.
XX
PN MO200163295-A2.
PD 30-AUG-2001.
PF 26-FEB-2001; 2001WO-1B00259.
PR 24-FEB-2000; 2000GB-0004412.
PR 15-MAR-2000; 2000GB-0004415.
PR 24-NOV-2000; 2000GB-0028734.
PR 28-NOV-2000; 2000US-0724391.
PR 08-DEC-2000; 2000GB-0030050.
PR 12-DEC-2000; 2000US-0254830.
PR 28-DEC-2000; 2000US-0750395.
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAc, Parekh RB, Rohlf C, Patel TP;
XX
DR WPI; 2001-570652/64.
XX
DR N-PSDB; AAI69309.
XX
PT Diagnosing and monitoring Schizophrenia by detecting the presence of
PT Schizophrenia Associated Features and Schizophrenia Associated Protein
PT isoforms in samples of cerebrospinal fluid -
XX
PS Claim 1a; Fig 1; 91p; English.
XX
CC This invention describes a novel method for detecting the presence of
CC schizophrenia associated features (SfEs) and schizophrenia associated
CC protein isoforms (SPIs) in samples, e.g. by electrophoresis, immunoassay
CC or hybridisation assay, for diagnosing and monitoring schizophrenia,
CC studying the effectiveness of treatments and for identifying potential
CC therapeutic agents. The products of the invention have neuroleptic

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CC activity and can be used in vaccines or for gene therapy. The method (1)
CC is used: (1) for screening or diagnosis of schizophrenia and the relative
CC abundance of at least 1 chosen feature correlates with the presence or
CC absence of schizophrenia and for monitoring the effect of therapy
CC administered to a subject with schizophrenia and the relative abundance
CC of at least 1 chosen feature which correlates with the severity of
CC schizophrenia. The expression and activity of the SfEs, SPIs and related
CC molecules (e.g. secondary messengers) are studied to diagnose
CC schizophrenia, monitor the progress of the disorder and the effectiveness
CC of treatment and as targets to identify and produce potential therapeutic
CC agents for the treatment of schizophrenia. The paucity of detectable
CC neuroleptic defects distinguishes neuropsychiatric disorders such as
CC schizophrenia from neurological disorders, where manifestations of
CC anatomical and biochemical changes have been identified in many cases.
CC Consequently the identification and characterisation of cellular and/or
CC molecular causative defects and neuropathies are necessary for improved
CC treatment of neuropsychiatric disorders. This sequence represents the
CC human DKK-3 protein described in the method of the invention.
XX
SQ Sequence 350 AA:
Query Match 100.0%; Score 1880; DB 22; Length 350;
Best Local Similarity 100.0%; Pred. No. 6.5e-149;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQLGATLCLLLAAVPTAPAPATATSAVPKGPALSYQEBATINEMFREVEELMED 60
Db 1 MQLGATLCLLLAAVPTAPAPATATSAVPKGPALSYQEBATINEMFREVEELMED 60
QY 61 TQKLSAVEEMEAEEAAKASSEVNLANLPSPYHNENTDTKVGNNTHVHREIHKITN 120
Db 61 TQKLSAVEEMEAEEAAKASSEVNLANLPSPYHNENTDTKVGNNTHVHREIHKITN 120
QY 121 NOTGQWVFSEVTITVSVDDEGRSHSECTIDEDCGPSMYCQFASFOYTCQPCRGQRLCTR 180
Db 121 NOTGQWVFSEVTITVSVDDEGRSHSECTIDEDCGPSMYCQFASFOYTCQPCRGQRLCTR 180
QY 121 NOTGQWVFSEVTITVSVDDEGRSHSECTIDEDCGPSMYCQFASFOYTCQPCRGQRLCTR 180
Db 121 NOTGQWVFSEVTITVSVDDEGRSHSECTIDEDCGPSMYCQFASFOYTCQPCRGQRLCTR 180
QY 181 DSECCGQQLCWGHCTKMATRGSGNGTICDNQRCQPGLCQAFQRLFPVCTPLPVEGEL 240
Db 181 DSECCGQQLCWGHCTKMATRGSGNGTICDNQRCQPGLCQAFQRLFPVCTPLPVEGEL 240
QY 241 CHDPASRLDLITWELEPDGALDRCPGASGLCQPHSHSLVYVCKPTFVGSRDQDEILL 300
Db 241 CHDPASRLDLITWELEPDGALDRCPGASGLCQPHSHSLVYVCKPTFVGSRDQDEILL 300
QY 301 PREVPDEYEVGSFMEVROELEDLERSLITEMALGEPAAAAALLGGEEI 350
Db 301 PREVPDEYEVGSFMEVROELEDLERSLITEMALGEPAAAAALLGGEEI 350

RESULT 4
AAG62468 ID AAG62468 standard; Protein: 350 AA.
AC AAG62468;
DT 10-SEP-2001 (first entry)
XX
DE Human reduced expression in immortalised cells protein.
XX
KM REIC; reduced expression in immortalised cells; cancer; tumour;
KW proliferation inhibitor; viral infection; human.
XX
OS Homo sapiens.
XX
PN WO200138528-A1.
PD 31-MAY-2001.
PF 30-AUG-2000; 2000WO-JP05879.
PR 19-NOV-1999; 99JP-0330604.
XX

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PA (HISM) HISAMITSU PHARM CO LTD.
 XX Namba M, Tsuji T;
 XX WPI; 2001-367688/38.
 DR N-PSDB; AAA45489, AAA45490, AAA45491.
 XX
 PT Cell proliferation inhibiting protein REIC and polynucleotide encoding
 PT it for diagnosis and therapy of cancer and as an antiviral agent -
 PS Claim 2; Page 56-57; 66pp; Japanese.
 XX
 CC This invention relates to a protein designated REIC (reduced expression
 CC in immortalised cells) which inhibits proliferation. REIC shows reduced
 CC or suppressed expression in immortalised cells such as cancer cells. The
 CC invention includes DNA and protein sequences for REIC. The protein is
 CC useful for the treatment and diagnosis of a wide range of benign and
 CC malignant tumours and of viral infections (including HIV, influenza,
 CC hepatitis and Epstein-Barr virus). The present sequence represents REIC.
 XX
 SQ Sequence 350 AA;
 Query Match 100.0%; Score 1880; DB 22; Length 350;
 Best Local Similarity 100.0%; Pred. No. 6.5e-149;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MORGATLCLILAAVPTAPAPATSAVYKPGPALSTPOEATLNEMFREVEBELMED 60
 DB 1 MORGATLCLILAAVPTAPAPATSAVYKPGPALSTPOEATLNEMFREVEBELMED 60
 QY 61 TOHKLRSAYEEMAEBAKASSEVNLANLPSTYHNETNTDTKVGNNITHVREIHKITT 120
 DB 61 TOHKLRSAYEEMAEBAKASSEVNLANLPSTYHNETNTDTKVGNNITHVREIHKITT 120
 QY 121 NOTGQVFSSTVITVSVDDEGRSHCEIIDDCGSPMYCQFASFOYTCQPCRCQRMCTR 180
 DB 121 NOTGQVFSSTVITVSVDDEGRSHCEIIDDCGSPMYCQFASFOYTCQPCRCQRMCTR 180
 QY 121 NOTGQVFSSTVITVSVDDEGRSHCEIIDDCGSPMYCQFASFOYTCQPCRCQRMCTR 180
 DB 121 NOTGQVFSSTVITVSVDDEGRSHCEIIDDCGSPMYCQFASFOYTCQPCRCQRMCTR 180
 QY 181 DSECCGDLQVWGHCTKMAKTRGNGTICNORDCQGLCCAFRGILLFPVCTPLPYEGEL 240
 DB 181 DSECCGDLQVWGHCTKMAKTRGNGTICNORDCQGLCCAFRGILLFPVCTPLPYEGEL 240
 QY 241 CHDPASRLDLITWELPDGALDRCPASGLLCQPHSHSLVYVCKPTFVGRDQDEIILL 300
 DB 241 CHDPASRLDLITWELPDGALDRCPASGLLCQPHSHSLVYVCKPTFVGRDQDEIILL 300
 QY 301 PREVPDEYEVGSFMEYRQELDLERSLTETMALGEPAAAAALLGGEEL 350
 DB 301 PREVPDEYEVGSFMEYRQELDLERSLTETMALGEPAAAAALLGGEEL 350
 RESULT 5
 AAB87529 standard; Protein; 350 AA.
 XX ID AAB87529;
 XX AC AAB87529;
 XX
 XX 15-MAY-2001 (first entry)
 XX
 XX Human PRO295.
 XX
 XX Human; PRO protein; mapping.
 XX
 XX Homo sapiens.
 XX
 XX WO200116318-A2.
 XX
 XX 08-MAR-2001.
 XX
 XX 24-AUG-2000; 2000MO-US23328.
 XX
 XX 01-SEP-1999; 99WO-US20111.
 XX
 XX 15-SEP-1999; 99WO-US21090.
 PR

PR 07-DEC-1999; 99US-0169495.
 PR 09-DEC-1999; 99US-0170262.
 PR 11-JAN-2000; 2000US-0175481.
 PR 18-FEB-2000; 2000MO-US04341.
 PR 18-FEB-2000; 2000MO-US04342.
 PR 22-FEB-2000; 2000MO-US04414.
 PR 01-MAR-2000; 2000MO-US05601.
 PR 03-MAR-2000; 2000US-0187202.
 PR 25-APR-2000; 2000US-0199397.
 PR 22-MAY-2000; 2000MO-US14042.
 PR 05-JUN-2000; 2000US-0209832.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
 XX WPI; 2001-183260/18.
 DR N-PSDB; AAF92061.
 XX
 XX Eighty four nucleic acids encoding PRO polypeptides, useful in
 PT molecular biology, including use as hybridization probes, and in
 PT chromosome and gene mapping. -
 XX
 PS Claim 12; Fig 8; 278pp; English.
 XX
 CC The present sequence is a human PRO polypeptide (secreted and
 CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
 CC anti-PRO antibodies are useful for preparation of a medicament useful in
 CC the treatment of a condition which is responsive to the PRO protein,
 CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
 CC employed as molecular weight markers for protein electrophoresis. The PRO
 CC coding sequence has applications in molecular biology, including use as
 CC hybridisation probes, and in chromosome and gene mapping.
 XX
 SQ Sequence 350 AA;
 Query Match 100.0%; Score 1880; DB 22; Length 350;
 Best Local Similarity 100.0%; Pred. No. 6.5e-149;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MORGATLCLILAAVPTAPAPATSAVYKPGPALSTPOEATLNEMFREVEBELMED 60
 DB 1 MORGATLCLILAAVPTAPAPATSAVYKPGPALSTPOEATLNEMFREVEBELMED 60
 QY 61 TOHKLRSAYEEMAEBAKASSEVNLANLPSTYHNETNTDTKVGNNITHVREIHKITT 120
 DB 61 TOHKLRSAYEEMAEBAKASSEVNLANLPSTYHNETNTDTKVGNNITHVREIHKITT 120
 QY 61 TOHKLRSAYEEMAEBAKASSEVNLANLPSTYHNETNTDTKVGNNITHVREIHKITT 120
 DB 61 TOHKLRSAYEEMAEBAKASSEVNLANLPSTYHNETNTDTKVGNNITHVREIHKITT 120
 QY 121 NOTGQVFSSTVITVSVDDEGRSHCEIIDDCGSPMYCQFASFOYTCQPCRCQRMCTR 180
 DB 121 NOTGQVFSSTVITVSVDDEGRSHCEIIDDCGSPMYCQFASFOYTCQPCRCQRMCTR 180
 QY 121 NOTGQVFSSTVITVSVDDEGRSHCEIIDDCGSPMYCQFASFOYTCQPCRCQRMCTR 180
 DB 121 NOTGQVFSSTVITVSVDDEGRSHCEIIDDCGSPMYCQFASFOYTCQPCRCQRMCTR 180
 QY 181 DSECCGDLQVWGHCTKMAKTRGNGTICNORDCQGLCCAFRGILLFPVCTPLPYEGEL 240
 DB 181 DSECCGDLQVWGHCTKMAKTRGNGTICNORDCQGLCCAFRGILLFPVCTPLPYEGEL 240
 QY 241 CHDPASRLDLITWELPDGALDRCPASGLLCQPHSHSLVYVCKPTFVGRDQDEIILL 300
 DB 241 CHDPASRLDLITWELPDGALDRCPASGLLCQPHSHSLVYVCKPTFVGRDQDEIILL 300
 QY 301 PREVPDEYEVGSFMEYRQELDLERSLTETMALGEPAAAAALLGGEEL 350
 DB 301 PREVPDEYEVGSFMEYRQELDLERSLTETMALGEPAAAAALLGGEEL 350
 RESULT 6
 AAB80252 standard; Protein; 350 AA.
 XX ID AAB80252;
 XX AC AAB80252;
 XX
 XX 24-APR-2001 (first entry)
 DT

DE Human PRO295 protein.

KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
XX antiparkinsonian neurotropic; neuroprotective; vulnerary; cardiant;
KW antineurogenic; vasotrophic; antisthmatic; antineutritic; cancer;
KW antiarthritic; antineutritic; antidiabetic; antiviral; diabetes;
KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
XX ischaemia; inflammation.

OS Homo sapiens.

PN WO2001:04311-A1.

PD 18-JAN-2001.

PF 22-FEB-2000; 2000WO-US04414.

XX 07-JUL-1999; 99US-0143046.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 05-JAN-2000; 99WO-US00219.

XX (GENTH) GENENTECH INC.

PI Ashkenazi AJ, Botstein D, Desnovers L, Baton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy WA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;

DR WPI: 2001-08:051/09.
DR N-PSDB: AAF72413.

XX Sixty one nucleic acids encoding PRO polypeptides which are useful in
PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung
PT squamous cell carcinoma) and neurodegenerative diseases (e.g.
PT Alzheimer's disease) -

XX Claim 1; Fig 84; 393pp; English.

XX The present sequence is one of sixty one novel secreted and
CC transmembrane PRO polypeptides. The PRO polypeptides are
CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung
CC squamous cell carcinoma), gastrointestinal disorders (e.g.
CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,
CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.
CC endometrial bleeding angiogenesis), ischaemias such as coronary
CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,
CC rheumatoid arthritis, multiple sclerosis), infertility, AIDS and
CC diabetes and retinal disorders such as retinitis pigmentosa.
CC The PRO nucleic acids have applications in molecular biology, including
CC use as hybridization probes, and in chromosome and gene mapping.

XX Sequence 350 AA;

Query Match 100.0%; Score 1880; DB 22; Length 350;
Best Local Similarity 100.0%; Pred. No. 6,5e-149;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

1 MORGATLCTLLAAVTPAPAPATASAPKPGPAISPYOEEXTLNMREVVELMED 60
1 MORGATLCTLLAAVTPAPAPATASAPKPGPAISPYOEEXTLNMREVVELMED 60

QY		6TQHX.RSAVEEHEAEAAAXXSSENVLANLPSPYHETNTDTKGNNTIHVREIHKITN	120
Dd		61TQH.KRSANVEEHEAEAAAXXSSENVLANLPSPYHETNTDTKGNNTIHVREIHKITN	120
QY		121NOTGVMFSEIVITSVGBEGRRSHCEIIDDCGSPMYCCOPAFQYTCOPCRGMCTR	180
Dd		121NOTGVMFSEIVITSVGBEGRRSHCEIIDDCGSPMYCCOPAFQYTCOPCRGMCTR	180
QY		181DSKCCGDOLCWGHCTKMATRGSNGTICDNQRDOPGLCAFORGLLFPCTPLPVEGEL	240
Dd		181DSKCCGDOLCWGHCTKMATRGSNGTICDNQRDOPGLCAFORGLLFPCTPLPVEGEL	240
QY		241CHDPASRLDLITWLEBPDALDRCPASGLLCQPHSHSLVYCKPTFVGSRDGELL	300
Dd		241CHDPASRLDLITWLEBPDALDRCPASGLLCQPHSHSLVYCKPTFVGSRDGELL	300
QY		301PREVPPEYVSGFMEEVRQOELEDERSLTTEEMALGEPAAAAALLGGEI	350
Dd		301PREVPPEYVSGFMEEVRQOELEDERSLTTEEMALGEPAAAAALLGGEI	350
RESULT 7			
ABG95854	ID	ABG95854 standard; Protein; 350 AA.	
AC		ABG95854;	
XX			
DT		10-DEC-2002 (first entry)	
XX			
DE		Human secreted/transmembrane protein PRO295.	
XX			
KM		Human; secreted protein; transmembrane protein; antirheumatic;	
KW		antiarthritic; osteopathic; sports-related joint problem;	
KW		articular cartilage defect; osteoarthritis; rheumatoid arthritis.	
XX			
OS		Homo sapiens.	
XX			
PN		US200219130-A1.	
PD			
XX		29-AUG-2002.	
PF			
XX		06-DEC-2001; 2001US-0006867.	
XX			
PR		29-OCT-1997; 97US-063435P.	
PR		29-OCT-1997; 97US-064215P.	
PR		22-APR-1998; 98US-082797P.	
PR		29-APR-1998; 98US-083465P.	
PR		15-MAY-1998; 98US-085579P.	
PR		10-JUN-1998; 98US-088811P.	
PR		10-JUN-1998; 98US-088824P.	
PR		10-JUN-1998; 98US-088633P.	
PR		11-JUN-1998; 98US-089105P.	
PR		12-JUN-1998; 98US-089514P.	
PR		16-SEP-1998; 98MO-US19330.	
PR		08-MAR-1999; 99MO-US03028.	
PR		14-MAY-1999; 99MO-US10733.	
PR		02-JUN-1999; 99MO-US12452.	
PR		01-SEP-1999; 99MO-US20111.	
PR		15-SEP-1999; 99MO-US21090.	
PR		15-SEP-1999; 99MO-US21994.	
PR		22-DEC-1999; 99MO-US30720.	
PR		18-FEB-2000; 2000MO-US04341.	
PR		18-FEB-2000; 2000MO-US04342.	
PR		30-MAR-2000; 2000MO-US08439.	
PR		22-MAY-2000; 2000MO-US14042.	
PR		02-JUN-2000; 2000MO-US15264.	
PR		23-AUG-2000; 2000MO-US23522.	
PR		24-AUG-2000; 2000MO-US23238.	
PR		10-NOV-2000; 2000MO-US30873.	
PR		01-DEC-2000; 2000MO-US32378.	
PR		20-DEC-2000; 2000MO-US34956.	

PR 26-FEB-2001; 2001MO-US06520.
 PR 20-JUN-2001; 2001MO-US19692.
 PR 29-JUN-2001; 2001MO-US21066.
 PR 09-JUL-2001; 2001MO-US21735.
 XX
 PA (GENTH) GENENTECH INC.
 PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ,
 PI Grimaldi JC, Gurney AL, Matanabe CK, Wood WI,
 XX
 DR WPI; 2002-731348/79.
 DR N-PSDB; ABB514381.
 XX
 PT New isolated secreted and transmembrane PRO polypeptide useful for
 PT modulating biological activity of a cell, or for treating
 PT sports-related joint problems, osteoarthritis or rheumatoid arthritis
 PS Claim 20; Fig 8; 399pp; English.
 XX
 CC The invention relates to an isolated secreted and transmembrane PRO
 CC polypeptide having 80 % sequence identity to a sequence appearing
 CC as ABG5851-ABG5534 or their associated signal peptide, or a sequence of
 CC an extracellular domain of the proteins with their associated signal
 CC peptide, or lacking its associated signal peptide. Also included are
 CC the nucleic acids encoding the proteins, vectors, host cells,
 CC fusion proteins and antibodies which specifically bind to the proteins.
 CC The proteins are useful for detecting a polypeptide designated as A, B, C
 CC or D in a sample suspected of containing an A, B, C or D polypeptide,
 CC by contacting the sample with a polypeptide designated as E, F, G, H or
 CC I (or vice versa) and determining the formation of a A/E, B/F, B/G, C/H
 CC or D/I polypeptide conjugate in the sample, where the formation of C/H
 CC conjugate is indicative of the presence of an A, B, C or D polypeptide
 CC in the sample, where A is a PRO10272 polypeptide, B is a PRO20110
 CC polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide,
 CC E is a PRO5801 polypeptide, F is a PRO1 polypeptide, G is a PRO20040
 CC polypeptide, H is a PRO20233 polypeptide and I is a PRO1890
 CC polypeptide. The sample comprises a cell suspected of expressing the A,
 CC B, C or D polypeptide. The E, F, G, H or I polypeptide is labeled with
 CC a detectable label or is attached to a solid support. The proteins are
 CC useful for linking a bioactive molecule to a cell expressing a
 CC polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive
 CC molecule is a toxin, a radiolabel or an antibody. The bioactive molecule
 CC causes death of the cell. A, B, C, D, E, F, G, H, or I, or antibodies
 CC against them are useful for modulating a biological activity of a cell
 CC expressing a polypeptide designated as A, B, C or D or E, F, G, H, or
 CC I. The cell is killed. The proteins are useful for identifying
 CC agonists or antagonists, for the preparation of a medicament useful in
 CC the treatment of a condition which is responsive to the proteins, as
 CC molecular weight markers for protein electrophoresis purposes, and as
 CC therapeutic agents for treating sports-related joint problems, and as
 CC articular cartilage defects, osteoarthritis or rheumatoid arthritis.
 CC Nucleic acids encoding the proteins are useful as hybridization probes,
 CC in chromosome and gene mapping, in the generation of anti-sense RNA and
 CC DNA, for the preparation of the proteins, to generate transgenic or
 CC knockout animals which are useful in the development and screening of
 CC therapeutic useful reagents, for chromosome identification, and in gene
 CC therapy. The antibody is useful as a therapeutic agent, in a diagnostic
 CC assay and for affinity purification of the protein from recombinant
 CC cell culture natural sources. The present sequence represents a novel
 CC secreted or transmembrane protein of the invention.
 XX
 XX Sequence 350 AA;
 SQ
 Query Match 100.0%; Score 1880; DB 23; Length 350;
 Best Local Similarity 100.0%; Pred. No. 6-5e-149;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MORIGATLLCLLLAAVTPAPAPATSAVPKPGALSTPQREATLNMFRVLELMD 60
 1 MORLGATLLCLLLAAVTPAPAPATSAVPKPGALSTPQREATLNMFRVLELMD 60
 DB 1 MORLGATLLCLLLAAVTPAPAPATSAVPKPGALSTPQREATLNMFRVLELMD 60
 QY 61 TOKKLSAVEMEAEAAKASSEVNLANLPSYHNETNTDTKVGNNTHVREIHKTN 120
 61 TOKKLSAVEMEAEAAKASSEVNLANLPSYHNETNTDTKVGNNTHVREIHKTN 120

DB 61 TOKKLSAVEMEAEAAKASSEVNLANLPSYHNETNTDTKVGNNTHVREIHKTN 120
 QY 121 NOTGQWFSEETVITVSVDDEGRSRSHCEIIDEDCGSPMYCQFASFOYTCPCRCQRMLCR 180
 DB 121 NOTGQWFSEETVITVSVDDEGRSRSHCEIIDEDCGSPMYCQFASFOYTCPCRCQRMLCR 180
 QY 181 DSECCGQCLCVMGHCCTKMATRGNSNGTICDNQRCQGLCCAFQRLGLFPYCTPLPYEGEL 240
 DB 181 DSECCGQCLCVMGHCCTKMATRGNSNGTICDNQRCQGLCCAFQRLGLFPYCTPLPYEGEL 240
 QY 241 CHDPASRLDLITWLEFPDGLDRCPASGLLCQPHSHSLVYVCKPTFGSRDQDEILL 300
 DB 241 CHDPASRLDLITWLEFPDGLDRCPASGLLCQPHSHSLVYVCKPTFGSRDQDEILL 300
 QY 301 PREVPDEYGVSGFMEEYRQELDLERSLTFEMALGEPAAAAALLGGEEL 350
 DB 301 PREVPDEYGVSGFMEEYRQELDLERSLTFEMALGEPAAAAALLGGEEL 350
 DB 301 PREVPDEYGVSGFMEEYRQELDLERSLTFEMALGEPAAAAALLGGEEL 350
 RESULT 8
 ABB95447
 ID ABB95447 standard; Protein; 350 AA.
 AC ABB95447;
 DT 19-JUN-2002 (first entry)
 XX Human angiogenesis related protein PRO295 SEQ ID NO: 50.
 DE Human: angiogenesis; PRO protein; cardiovascularization; wound; cancer;
 XX atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiatic; cytosolatic; antiangiogenic; hypotensive; vulnerary;
 KW antiarteriosclerotic.
 XX Homo sapiens.
 OS WO200208284-A2.
 PV 31-JAN-2002.
 PD 09-JUL-2001; 2001MO-US21735.
 PF 20-JUN-2000; 2000US-219556P.
 XX 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220644P.
 PR 28-JUL-2000; 2000MO-US20710.
 PR 02-AUG-2000; 2000US-222695P.
 PR 17-AUG-2000; 2000US-0643657.
 PR 23-AUG-2000; 2000MO-US23352.
 PR 24-AUG-2000; 2000MO-US23328.
 PR 07-SEP-2000; 2000US-230978P.
 PR 15-SEP-2000; 2000US-000000P.
 PR 18-SEP-2000; 2000US-064610.
 PR 18-SEP-2000; 2000US-066350.
 PR 24-OCT-2000; 2000US-242922P.
 PR 08-NOV-2000; 2000US-0709238.
 PR 08-NOV-2000; 2000MO-US30952.
 PR 10-NOV-2000; 2000MO-US30873.
 PR 01-DEC-2000; 2000MO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000MO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001MO-US06520.
 PR 01-MAR-2001; 2001MO-US06666.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0806869.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.

[illegible]

Db	301	PREPDEYEVGSEMEVRCLELDERSLTEEMALGEPAAAAAALGGEI	350
XX	RESULT_9		
XX	ABB90735		
XX	ABB90735 standard; Protein; 350 AA.		
XX	ABB90735;		
XX	30-MAY-2002 (first entry)		
XX	Human Tumour Endothelial Marker polypeptide seq ID NO 202.		
XX	Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic; normal endothelial marker; pan-endothelial marker; immunostimulant; antiangiogenic; tumour; neovascularisation; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis; psoriasis.		
XX	Homo sapiens.		
XX	WO200210217-A2.		
XX	07-FEB-2002.		
XX	01-AUG-2001; 2001WO-US24031.		
XX	02-AUG-2000; 2000US-222599P.		
XX	11-AUG-2000; 2000US-224360P.		
XX	11-APR-2001; 2001US-282850P.		
XX	(UYUO) UNIV JOHNS HOPKINS.		
XX	St Croix B, Kinzler KM, Vogelstein B;		
XX	WPI; 2002-291856/33.		
XX	N-PSDB; ABL92089.		
XX	An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth -		
XX	Claim 54; Page 156-157; 331pp; English.		
XX	The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumor growth, neovascularisation in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences; tumour endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers (PEM) ABL91903-ABL91995.		
XX	Sequence 350 AA;		
XX	Query Match 100.0%; Score 1880; DB 23; Length 350;		
XX	Best Local Similarity 100.0%; Pred. No. 6.5e-149;		
XX	Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
XX	1 MORIGATLCLILAAVPTAPAPATASAVKQGPALSYQDEBATINEMREVELMED 60		
XX	1 MORIGATLCLILAAVPTAPAPATASAVKQGPALSYQDEBATINEMREVELMED 60		
XX	1 TORHRSAAVEEMAEBAAKASSEVNLANLPPSYHNENITDTKYGNNTIHYHREIHKTN 120		
XX	1 TORHRSAAVEEMAEBAAKASSEVNLANLPPSYHNENITDTKYGNNTIHYHREIHKTN 120		

XX 05-JUN-2003 (first entry)
 XX Novel human secreted and transmembrane protein PRO295.
 DE
 XX Human, secreted and transmembrane protein; gene therapy; psoriasis;
 KW enterocolitis; gastrointestinal ulceration; skin disease;
 KW keratinocyte differentiation; epithelial cancer; Alzheimer's disease;
 KW squamous cell carcinoma; Parkinson's disease; inflammatory disease;
 KW amyotrophic lateral sclerosis; rheumatoid arthritis; asthma;
 KW multiple sclerosis; organ failure; atherosclerosis; cardiac injury;
 KW infertility; birth defect; premature aging; AIDS; cancer;
 KW diabetic complication; wound repair; tissue re-growth.
 XX Homo sapiens.
 OS
 PN US2003017463-A1.
 XX
 PD 23-JAN-2003.
 XX
 PF 11-JUL-2001; 2001US-0903640.
 XX
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19177.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 01-DEC-1998; 98WO-US25108.
 PR 06-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 11-FEB-2000; 2000WO-US03555.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 02-MAY-2000; 2000WO-US14042.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 17-SEP-1997; 97US-059113P.
 PR 17-SEP-1997; 97US-059115P.
 PR 17-SEP-1997; 97US-059117P.
 PR 17-SEP-1997; 97US-059119P.
 PR 17-SEP-1997; 97US-059121P.
 PR 17-SEP-1997; 97US-059122P.
 PR 17-SEP-1997; 97US-059124P.
 PR 18-SEP-1997; 97US-059263P.
 PR 18-SEP-1997; 97US-059266P.
 PR 15-OCT-1997; 97US-062125P.
 PR 17-OCT-1997; 97US-062285P.
 PR 17-OCT-1997; 97US-062287P.
 PR 21-OCT-1997; 97US-063486P.
 PR 24-OCT-1997; 97US-062814P.
 PR 24-OCT-1997; 97US-062816P.
 PR 24-OCT-1997; 97US-063045P.
 PR 24-OCT-1997; 97US-063120P.
 PR 24-OCT-1997; 97US-063121P.
 PR 24-OCT-1997; 97US-063127P.
 PR 24-OCT-1997; 97US-063128P.
 PR 27-OCT-1997; 97US-063327P.
 PR 27-OCT-1997; 97US-063329P.

PR 28-OCT-1997; 97US-063541P.
 PR 28-OCT-1997; 97US-063542P.
 PR 28-OCT-1997; 97US-063544P.
 PR 28-OCT-1997; 97US-063549P.
 PR 28-OCT-1997; 97US-063550P.
 PR 28-OCT-1997; 97US-063564P.
 PR 29-OCT-1997; 97US-063335P.
 PR 29-OCT-1997; 97US-063704P.
 PR 29-OCT-1997; 97US-063732P.
 PR 29-OCT-1997; 97US-063734P.
 PR 29-OCT-1997; 97US-063735P.
 PR 29-OCT-1997; 97US-063738P.
 PR 29-OCT-1997; 97US-064215P.
 PR 31-OCT-1997; 97US-063870P.
 PR 31-OCT-1997; 97US-064103P.
 PR 03-NOV-1997; 97US-064248P.
 PR 07-NOV-1997; 97US-064609P.
 PR 12-NOV-1997; 97US-065186P.
 PR 17-NOV-1997; 97US-065846P.
 PR 18-NOV-1997; 97US-065693P.
 PR 21-NOV-1997; 97US-065120P.
 PR 21-NOV-1997; 97US-06364P.
 PR 24-NOV-1997; 97US-066453P.
 PR 24-NOV-1997; 97US-066466P.
 PR 24-NOV-1997; 97US-066511P.
 PR 24-NOV-1997; 97US-066770P.
 PR 25-NOV-1997; 97US-066772P.
 PR 25-NOV-1997; 97US-066840P.
 PR 12-DEC-1997; 97US-069425P.
 PR 04-JUN-1998; 98US-088026P.
 PR 10-SEP-1998; 98US-099603P.
 PR 14-SEP-1998; 98US-100262P.
 PR 17-SEP-1998; 98US-100858P.
 PR 13-OCT-1998; 98US-104080P.
 PR 20-NOV-1998; 98US-109304P.
 PR 22-DEC-1998; 98US-113296P.
 PR 07-JUL-1999; 99US-143048P.
 PR 26-JUL-1999; 99US-145698P.
 PR 28-JUL-1999; 99US-146222P.
 PR 18-SEP-2000; 2000US-0665350.
 XX
 PA (GENT) GENENTECH INC.
 XX
 PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
 PI Filvarski E, Fong S, Gao W, Gerber H, Gerltzen WE, Goddard A;
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PM, Wood WI;
 XX
 DR WPI, 2003-341586/32.
 DR N-PSDB, ACAS5002.
 XX
 PT New PRO polypeptides and nucleic acid molecules, useful in diagnosing
 PT or treating inflammatory diseases, organ failure, atherosclerosis,
 PT cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or
 PT Parkinson's disease -
 XX
 PS Claim 12, Fig 84, 473pp; English.
 XX
 CC The invention describes sixty one nucleic acids encoding PRO polypeptides
 CC (secreted and transmembrane). The PRO polypeptides and nucleic acids are
 CC useful in diagnosing or treating enterocolitis, gastrointestinal
 CC ulceration, skin diseases associated with abnormal keratinocyte
 CC differentiation, e.g. psoriasis or epithelial cancers such as squamous
 CC cell carcinoma, Alzheimer's disease, Parkinson's disease, amyotrophic
 CC lateral sclerosis, inflammatory diseases, e.g. rheumatoid arthritis,
 CC asthma or multiple sclerosis, organ failure, atherosclerosis, cardiac
 CC injury, infertility, birth defects, premature aging, AIDS, cancer,
 CC diabetic complications, or mutations in general. The polypeptides are
 CC also useful for wound repair and associated therapies concerned with
 CC re-growth of tissue. The PRO polypeptides and nucleic acid molecules
 CC are also useful in gene therapy, and as molecular weight markers for
 CC protein electrophoresis purposes. The anti-PRO antibodies may be used

CC in diagnostic assays for PRO, or for the affinity purification of PRO
 CC from recombinant cell culture or natural sources. This is the amino
 CC acid sequence of a novel human PRO polypeptide.

XX Sequence 350 AA;

Query Match: 100.0%; Score 1880; DB 24; Length 350;
 Best Local Similarity 100.0%; Pred. No. 6.5e-149;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORGATLLCLLLAAVPTAPAPAPATSAVPKPGPALSYPOEATLNMEREVEELMED 60
 DB 1 MORGATLLCLLLAAVPTAPAPAPATSAVPKPGPALSYPOEATLNMEREVEELMED 60
 QY 61 TQHKRSAAVEEMEAFAAKASSEVNLALPPSYHNETNDTKVGNNTIHVREIHKITN 120
 DB 61 TQHKRSAAVEEMEAFAAKASSEVNLALPPSYHNETNDTKVGNNTIHVREIHKITN 120
 QY 121 NOTGQVFESEVITVSVDDEGRGRSHCEIIDEDCGPSMYCQFASFOYTCQPCRGRLCTR 180
 DB 121 NOTGQVFESEVITVSVDDEGRGRSHCEIIDEDCGPSMYCQFASFOYTCQPCRGRLCTR 180
 QY 181 DSECCGDLQVWGCHCTKMATRGSNGTICDNQRCQPGLCARQGLLPVCTPLPYEGEL 240
 DB 181 DSECCGDLQVWGCHCTKMATRGSNGTICDNQRCQPGLCARQGLLPVCTPLPYEGEL 240
 QY 241 CHDPASRLDLITWLEPDPGALDRCPASGLLCOFPHSHLVYCKPFTVGSRDDGELL 300
 DB 241 CHDPASRLDLITWLEPDPGALDRCPASGLLCOFPHSHLVYCKPFTVGSRDDGELL 300
 QY 301 PRVPEPEYEVGSFMEVROQLBDELSLTBEMALGSPAAAAALLGGEET 350
 DB 301 PRVPEPEYEVGSFMEVROQLBDELSLTBEMALGSPAAAAALLGGEET 350

RESULT 12
 ID ABU71485 standard; Protein; 350 AA.

XX ABU71485;
 XX AC
 XX 10-JUN-2003 (first entry)
 XX DT
 XX DE Human PRO polypeptide #41.
 XX KM Human; secreted and transmembrane protein; PRO polypeptide; cancer;
 XX KM Alzheimer's disease; ischemia; cytosolic; noctropic; vasotropic;
 XX KM neuroprotective.
 XX OS Homo sapiens.
 XX PN US2002192659-A1.
 XX PD 19-DEC-2002.
 XX PF 10-JUL-2001; 2001US-0902853.
 XX PR 10-SEP-1998; 98WO-US18824.
 XX PR 14-SEP-1998; 98WO-US19177.
 XX PR 16-SEP-1998; 98WO-US19310.
 XX PR 17-SEP-1998; 98WO-US19437.
 XX PR 01-DEC-1998; 98WO-US25108.
 XX PR 08-SEP-1999; 99WO-US20594.
 XX PR 13-SEP-1999; 99WO-US20944.
 XX PR 15-SEP-1999; 99WO-US21090.
 XX PR 15-SEP-1999; 99WO-US21547.
 XX PR 05-OCT-1999; 99WO-US23089.
 XX PR 01-DEC-1999; 99WO-US28301.
 XX PR 02-DEC-1999; 99WO-US28564.
 XX PR 02-DEC-1999; 99WO-US28565.
 XX PR 16-DEC-1999; 99WO-US30095.
 XX PR 20-DEC-1999; 99WO-US30911.
 XX PR 20-DEC-1999; 99WO-US30999.

PR 05-JAN-2000; 2000WO-US00219.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 17-SEP-1997; 97US-059113P.
 PR 17-SEP-1997; 97US-059115P.
 PR 17-SEP-1997; 97US-059117P.
 PR 18-SEP-1997; 97US-059266P.
 PR 15-OCT-1997; 97US-062125P.
 PR 17-OCT-1997; 97US-062285P.
 PR 17-OCT-1997; 97US-062287P.
 PR 21-OCT-1997; 97US-063486P.
 PR 24-OCT-1997; 97US-062814P.
 PR 24-OCT-1997; 97US-062816P.

(GETH) GENENTECH INC.

XX Ashkenazi A, Botstein D, Desnoyers I, Eaton Di, Ferrara N;
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PM, Wood WI;
 XX WPI; 2003-361832/34.
 DR N-PSDB; ACAS8487.

PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or
 PT PRO1868, useful in molecular biology, chromosome and gene mapping, in
 PT generating antisense RNA and DNA, and in gene therapy
 XX Claim 12; Fig 84; 474bp; English.

XX The present invention relates to the isolation of novel human secreted
 CC and transmembrane proteins (PRO polypeptides), and the polynucleotide
 CC sequences encoding them. The polynucleotide sequences are useful in
 CC molecular biology, as hybridisation probes, in chromosome and gene
 CC mapping, in generating antisense RNA and DNA, and in gene therapy. The
 CC polynucleotide sequences may also be used in preparing PRO polypeptides
 CC by recombinant techniques, and in generating either transgenic animals
 CC or knock-out animals which, in turn, are useful in the development and
 CC screening of therapeutically useful reagents. The PRO polypeptides or
 CC their antibodies are useful in preparing a medicament for treating a
 CC condition responsive to the polypeptide or antibody, such as cancer,
 CC Alzheimer's disease or ischemia, and in various diagnostic assays.
 CC ABU71445-ABU71505 represent human PRO polypeptides of the invention.

XX Sequence 350 AA;

Query Match: 100.0%; Score 1880; DB 24; Length 350;
 Best Local Similarity 100.0%; Pred. No. 6.5e-149;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORGATLLCLLLAAVPTAPAPATSAVPKPGPALSYPOEATLNMEREVEELMED 60
 DB 1 MORGATLLCLLLAAVPTAPAPATSAVPKPGPALSYPOEATLNMEREVEELMED 60
 QY 61 TQHKRSAAVEEMEAFAAKASSEVNLALPPSYHNETNDTKVGNNTIHVREIHKITN 120
 DB 61 TQHKRSAAVEEMEAFAAKASSEVNLALPPSYHNETNDTKVGNNTIHVREIHKITN 120
 QY 121 NOTGQVFESEVITVSVDDEGRGRSHCEIIDEDCGPSMYCQFASFOYTCQPCRGRLCTR 180
 DB 121 NOTGQVFESEVITVSVDDEGRGRSHCEIIDEDCGPSMYCQFASFOYTCQPCRGRLCTR 180
 QY 181 DSECCGDLQVWGCHCTKMATRGSNGTICDNQRCQPGLCARQGLLPVCTPLPYEGEL 240
 DB 181 DSECCGDLQVWGCHCTKMATRGSNGTICDNQRCQPGLCARQGLLPVCTPLPYEGEL 240
 QY 241 CHDPASRLDLITWLEPDPGALDRCPASGLLCOFPHSHLVYCKPFTVGSRDDGELL 300
 DB 241 CHDPASRLDLITWLEPDPGALDRCPASGLLCOFPHSHLVYCKPFTVGSRDDGELL 300

QY 301 PREVPDEYVGSFMEVRQELDLERSLTEMALGEPAAAAALLGGEI 350
 DB 301 PREVPDEYVGSFMEVRQELDLERSLTEMALGEPAAAAALLGGEI 350

RESULT 13

ID ABU71509 standard; Protein; 350 AA.

AC ABU71509;

DT 10-JUN-2003 (first entry)

DE Human secreted polypeptide PRO295.

KW Human; gene therapy; tumour; cancer.

OS Homo sapiens.

PN US2003013855-A1.

PD 16-JAN-2003.

PF 03-MAY-2002; 2002US-0063616.

PR 30-DEC-1999; 98KR-0062142.

PR 08-MAR-1999; 99MO-US05028.

PR 14-MAY-1999; 99MO-US10733.

PR 30-DEC-1999; 99MO-US11274.

PR 18-FEB-2000; 2000MO-US04341.

PR 01-MAR-2000; 2000MO-US05601.

PR 02-MAR-2000; 2000MO-US05841.

PR 21-MAR-2000; 2000MO-US07532.

PR 22-MAY-2000; 2000MO-US114042.

PR 02-JUN-2000; 2000MO-US15264.

PR 24-AUG-2000; 2000MO-US23328.

PR 10-NOV-2000; 2000MO-US30873.

PR 01-DEC-2000; 2000MO-US32678.

PR 20-DEC-2000; 2000MO-US34956.

PR 28-FEB-2001; 2001MO-US06550.

PR 01-JUN-2001; 2001MO-US117800.

PR 14-MAY-1999; 99US-0311832.

PR 25-AUG-1999; 99US-0380137.

PR 25-AUG-1999; 99US-0380138.

PR 25-AUG-1999; 99US-0380139.

PR 15-SEP-1999; 99US-0397342.

PR 18-OCT-1999; 99US-0403297.

PR 12-NOV-1999; 99US-0423844.

PR 22-AUG-2000; 2000US-0644848.

PR 18-SEP-2000; 2000US-0646410.

PR 18-SEP-2000; 2000US-0665350.

PR 08-NOV-2000; 2000US-0709238.

PR 20-DEC-2000; 2000US-0747259.

PR 22-MAR-2001; 2001US-0816744.

PR 10-MAY-2001; 2001US-0854280.

PR 10-MAY-2001; 2001US-0854280.

PR 30-MAY-2001; 2001US-0870574.

PR 05-JUN-2001; 2001US-0874503.

PR 29-JUN-2001; 2001US-0869599.

PR 18-JUL-2001; 2001US-0908827.

PR 06-DEC-2001; 2001US-0006867.

(GETH) GENENTECH INC.

XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ,

PI Grimaldi JC, Gurney AL, Matarabe CK, Wood WI;

XX WPI; 2003-330485/31.

DR N-PSDB; ACAS8613.

PT New isolated antibody specifically binding a PRO polypeptide, useful for the preparation of a medicament for treating disorders with the

PT aberrant expression or activity of the PRO polypeptide, such as tumor conditions and cancer -

PS Example 17; Page 73; 406pp; English.

CC The invention relates to an antibody that binds to a polypeptide with a fully defined sequence given in the specification. The methods and compositions (containing antibodies that specifically bind a PRO polypeptide) of the present invention are useful for the preparation of a medicament for the treatment of disorders associated with the aberrant expression or activity of the PRO polypeptide, such as tumor conditions and cancer. They can also be used to generate transgenic or knockout animals useful in the development and screening of therapeutically useful reagents. The PRO polypeptides and encoding nucleic acids can be used as molecular weight markers for protein electrophoresis; chromosome identification and tissue typing. The PRO polypeptides are useful to induce angiogenesis e.g wound healing; in the treatment of sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis; diabetes; hyperinsulinaemia and hypoinsulinaemia. The antibodies may be used in various diagnostic, competitive binding and/or immunoprecipitation assays. The present sequence represents the amino acid sequence of a PRO polypeptide of the invention.

CC Sequence 350 AA;

Query Match 100.0%; Score 1880; DB 24; Length 350;
 Best Local Similarity 100.0%; Pred. No. 6, 5e-149;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORGATLLCLLLAAVPTAPAPATSAVVKPGPALSTPOEATLNEMFREVEELMED 60

DB 1 MORGATLLCLLLAAVPTAPAPATSAVVKPGPALSTPOEATLNEMFREVEELMED 60

QY 61 TQHKLRSAVEEMAEBAKASSEVNLANLPSSYHNETNDTKYNNNTIHYRREIHKTN 120

DB 61 TQHKLRSAVEEMAEBAKASSEVNLANLPSSYHNETNDTKYNNNTIHYRREIHKTN 120

QY 121 NOTQGMVSEFTVTSVGBEGRRSHCEIIDCGPSMYCQFASFQYTCQPCRGRLCTR 180

DB 121 NOTQGMVSEFTVTSVGBEGRRSHCEIIDCGPSMYCQFASFQYTCQPCRGRLCTR 180

QY 121 NOTQGMVSEFTVTSVGBEGRRSHCEIIDCGPSMYCQFASFQYTCQPCRGRLCTR 180

DB 121 NOTQGMVSEFTVTSVGBEGRRSHCEIIDCGPSMYCQFASFQYTCQPCRGRLCTR 180

QY 181 DSECCGGDLCTWGHCTKATGNSGTICDNORDCPGLCAFGGLPVCPTLPVGEGL 240

DB 181 DSECCGGDLCTWGHCTKATGNSGTICDNORDCPGLCAFGGLPVCPTLPVGEGL 240

QY 241 CHDPASRLDLITTELEPDGALDRCPASGLLCPHSHSLVYVCKPTFVSGRDDGELL 300

DB 241 CHDPASRLDLITTELEPDGALDRCPASGLLCPHSHSLVYVCKPTFVSGRDDGELL 300

QY 301 PREVPDEYVGSFMEVRQELDLERSLTEMALGEPAAAAALLGGEI 350

DB 301 PREVPDEYVGSFMEVRQELDLERSLTEMALGEPAAAAALLGGEI 350

RESULT 14

ID ABU71931 standard; Protein; 350 AA.

AC ABU71931;

DT 12-JUN-2003 (first entry)

DE Human secreted/transmembrane protein PRO295.

KW Human; secreted protein; transmembrane protein; PRO;

OS Homo sapiens.

PN US2003003530-A1.

PD 02-JAN-2003.

QY 181 DSECCGDLQVWGHCTKMATRSGNGTICDNQDCQPGILCAFORGLLPVCTPLPVEGEL 240
 DB 181 DSECCGDLQVWGHCTKMATRSGNGTICDNQDCQPGILCAFORGLLPVCTPLPVEGEL 240
 QY 241 CHDPASRLDLITWELPBDGALDRCPGASGLLQCPHSHSLVYCKPTFVGSRRDDGETLL 300
 DB 241 CHDPASRLDLITWELPBDGALDRCPGASGLLQCPHSHSLVYCKPTFVGSRRDDGETLL 300
 QY 301 PREVPDEYEVGSFMEYVRQELDLERSLITEMALGEPAAAAALLGGEI 350
 DB 301 PREVPDEYEVGSFMEYVRQELDLERSLITEMALGEPAAAAALLGGEI 350
 RESULT 15
 ID ABU71955 standard; Protein; 350 AA.
 XX ABU71955;
 AC ABU71955;
 XX 11-JUN-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO295.
 XX
 KW Human; secreted and transmembrane polypeptide;
 KW chromosome mapping; gene mapping; transgenic animal; knockout animal;
 KW therapeutic agent screening; chromosome identification; tissue typing;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN US2003018183-A1.
 XX
 PD 23-JAN-2003.
 XX
 PF 01-MAY-2002; 2002US-0063512.
 XX
 PR 06-DEC-2001; 2001US-0006867.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX WPI; 2003-330984/31.
 DR N-PSDB; ACA60366.
 XX
 PT New secreted and transmembrane PRO polypeptides and nucleic acid
 PT molecules encoding the polypeptides, useful in gene therapy or
 PT preparing a medicament for treating a condition that is responsive to
 PT the PRO polypeptide or antibody -
 XX
 PS Claim 1; Fig 8; 409pp; English.
 XX
 CC The invention describes novel isolated PRO polypeptides. The PRO
 CC polypeptides or anti-PRO antibodies are useful in preparing a medicament
 CC for treating a condition that is responsive to the PRO polypeptide or
 CC antibody. The PRO nucleotide sequences may be used as hybridisation
 CC probes in chromosome and gene mapping, or in generating antisense RNA
 CC and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides,
 CC in assays to identify other proteins or molecules involved in binding
 CC reaction, to generate transgenic animals or knockout animals, which in
 CC turn are useful in the development and screening of therapeutically
 CC useful reagents, for chromosome identification, and tissue typing. The
 CC PRO polypeptides and nucleic acid molecules are also useful in gene
 CC therapy, and as molecular weight markers for protein electrophoresis
 CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
 CC PRO, or for the affinity purification of PRO from recombinant cell
 CC culture or natural sources. This is the amino acid sequence of a novel
 CC human secreted and transmembrane PRO polypeptide.
 XX
 SQ Sequence 350 AA;

Query Match 100.0%; Score 1880; DB 24; Length 350;
 Best Local Similarity 100.0%; Pred. No. 6,5e-149;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MORLGATILLCILLAAVPTAPAPATASAPVKPGPALSYQEEATINEMRREYEEIMED 60
 DB 1 MORLGATILLCILLAAVPTAPAPATASAPVKPGPALSYQEEATINEMRREYEEIMED 60
 QY 61 TOHKLRSAVEEMEAEEAAKASSEVNLANLPSSYHNETNTDTKVGNNTIHVHREIHKITN 120
 DB 61 TOHKLRSAVEEMEAEEAAKASSEVNLANLPSSYHNETNTDTKVGNNTIHVHREIHKITN 120
 QY 121 NOTGQWVSEIVITSVGDEGRSHSECTIDEDCGPSMYCOPASFQYTCOPRGQRMCTR 180
 DB 121 NOTGQWVSEIVITSVGDEGRSHSECTIDEDCGPSMYCOPASFQYTCOPRGQRMCTR 180
 QY 181 DSECCGDLQVWGHCTKMATRSGNGTICDNQDCQPGILCAFORGLLPVCTPLPVEGEL 240
 DB 181 DSECCGDLQVWGHCTKMATRSGNGTICDNQDCQPGILCAFORGLLPVCTPLPVEGEL 240
 QY 241 CHDPASRLDLITWELPBDGALDRCPGASGLLQCPHSHSLVYCKPTFVGSRRDDGETLL 300
 DB 241 CHDPASRLDLITWELPBDGALDRCPGASGLLQCPHSHSLVYCKPTFVGSRRDDGETLL 300
 QY 301 PREVPDEYEVGSFMEYVRQELDLERSLITEMALGEPAAAAALLGGEI 350
 DB 301 PREVPDEYEVGSFMEYVRQELDLERSLITEMALGEPAAAAALLGGEI 350

Search completed: February 20, 2004, 18:49:00
 Job time : 79 secs

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OM protein - protein search, using sw model

Run on: February 20, 2004, 18:26:02 ; Search time 38 Seconds
(without alignments)
885.764 Million cell updates/sec

Title: US-10-063-671-8

Perfect score: 1880

Sequence: 1 MQRIGATLILCLILAAVPTA.....EMALGEPAAAAALLGGEI 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1873	99.6	350	2 UC7188	REIC protein - hum
2	138	7.3	577	2 B37057	integrin beta-6 ch
3	131.5	7.0	676	1 KXHU5	plasma protein S p
4	128	6.8	1620	2 T27283	hypothetical prote
5	126	6.7	788	2 A37057	integrin beta-6 ch
6	126	6.7	1394	2 A35626	transforming growt
7	126	6.7	1748	1 UN0786	integrin beta-4 ch
8	123	6.5	1170	2 A53612	laminin B1x chain
9	119	6.3	2318	2 A45306	notch 3 protein -
10	117.5	6.2	996	2 JE0237	apolipoprotein B r
11	117	6.2	3712	2 S18253	laminin alpha-1 ch
12	116	6.2	788	2 S15130	integrin beta-3 su
13	116	6.2	1251	2 A57293	latent transformin
14	116	6.2	2139	2 A35672	crumbs protein - f
15	115	6.1	1807	2 UC6319	integrin beta-4 ch
16	113	6.0	3562	2 A47171	chondroitin sulfat
17	111.5	5.9	1188	2 D86236	protein F1AN23.5 l
18	111.5	5.9	1820	2 A55494	latent transformin
19	110.5	5.9	293	2 B26637	neurogenic repetit
20	110.5	5.9	862	1 ORMSUD	IDL receptor precu
21	110	5.9	2524	2 A35844	notch protein - Af
22	109.5	5.8	656	2 UC2005	integrin beta-5 ch
23	109.5	5.8	799	2 A38308	integrin beta-5 ch
24	109.5	5.8	964	2 UC5545	integrin beta-4 pr
25	109.5	5.8	1712	2 A38261	masking protein pr
26	109.5	5.8	1875	2 A36429	integrin beta-4 ch
27	109.5	5.8	2531	2 T31070	notch homolog - se
28	109	5.8	1168	2 S16985	kalinin B1 - mouse
29	109	5.8	1348	2 S27812	probable epidermal

30	109	5.8	1574	2 T13954	MEGF6 protein - ra
31	108.5	5.8	852	2 A34373	histidine-rich cal
32	108.5	5.8	2195	2 T34264	hypothetical prote
33	108	5.7	1170	1 TSHU01	thrombospondin 1 p
34	108	5.7	2111	2 T15390	hypothetical prote
35	107	5.7	755	2 A44315	cartilage oligomer
36	106	5.6	227	1 LNRZ	lectin oligomer
37	106	5.6	1221	2 A49457	fibulin-2 precursor
38	106	5.6	2945	2 T15840	hypothetical prote
39	105.5	5.6	585	2 S43572	CO5B5.5 protein (c
40	105.5	5.6	585	2 S88571	protein CO5B5.5 (l
41	105.5	5.6	753	2 B36268	platelet glycoprot
42	105.5	5.6	778	2 A60798	platelet glycoprot
43	105.5	5.6	788	2 A26547	platelet glycoprot
44	105.5	5.6	788	2 I77349	platelet glycoprot
45	105.5	5.6	1469	2 B36665	salt protein 2 pre

ALIGNMENTS

RESULT 1					
UC7188	REIC protein - human				
C/Species: Homo sapiens (man)					
C/Date: 04-Mar-2000	#sequence	revision	04-Mar-2000	#text	change 11-May-2000
C/Accession: UC7188					
R/Tsugi, T.; Miyazaki, M.; Sakaguchi, M.; Inoue, Y.; Namba, M.					
Biochem. Biophys. Res. Commun. 268, 20-24, 2000					
A/Title: A REIC gene shows down-regulation in human immortalized cells and human tumor-de					
A/Reference number: UC7188; MUID:201109095; PMID:10652205					
A/Accession: UC7188					
A/Molecule type: mRNA					
A/Residues: 1-350 <TSU>					
A/Cross-references: DBJ:AB034203					
A/Experimental source: heart					
C/Comment: This protein is a secreted glycoprotein for head induction in amphibian embryo					
C/Keywords: cardiac muscle; coiled coil; glycoprotein; heart; tumor					
C/Genetics:					
A/Name: reic					
C/Superfamily: human REIC protein					
Query Match	99.6%	Score	1873	DB 2	Length 350
Best Local Similarity	99.7%	Pred. No.	1e-126		
Matches	349	Conservative	0	Mismatches	1
				Indels	0
				Gaps	0
QY	1 MQRIGATLILCLILAAVPTAPAPATATSAVKGAPALSYQEBXTLNEMREVEELMED 60				
DB	1 MQRIGATLILCLILAAVPTAPAPATATSAVKGAPALSYQEBXTLNEMREVEELMED 60				
QY	61 TOHKRSAYEEMEAEEAAXASSEVNLANTLPPSYHNETNTDTKVGNNTHYHREIKITN 120				
DB	61 TOHKRSAYEEMEAEEAAXASSEVNLANTLPPSYHNETNTDTKVGNNTHYHREIKITN 120				
QY	121 NOTGQVTFSEVITVSVDSEGRSHSECTIDDCGSMYCOFASFOYTQCPRGQMLCTR 180				
DB	121 NOTGQVTFSEVITVSVDSEGRSHSECTIDDCGSMYCOFASFOYTQCPRGQMLCTR 180				
QY	122 NOTGQVTFSEVITVSVDSEGRSHSECTIDDCGSMYCOFASFOYTQCPRGQMLCTR 180				
DB	122 NOTGQVTFSEVITVSVDSEGRSHSECTIDDCGSMYCOFASFOYTQCPRGQMLCTR 180				
QY	181 DSECCGDDLCVWGHTCKATGNSNGTICDNORDCOPGCAFORGLFPVCTPLPVEGEL 240				
DB	181 DSECCGDDLCVWGHTCKATGNSNGTICDNORDCOPGCAFORGLFPVCTPLPVEGEL 240				
QY	241 CHDPASRLDLITWELPDPGALDRCPGASGLICOPHSHSLVYVCKPTFVGRDDDEILL 300				
DB	241 CHDPASRLDLITWELPDPGALDRCPGASGLICOPHSHSLVYVCKPTFVGRDDDEILL 300				
QY	301 PREVPDEYVGSFMEVYVQELDLERSLTHEMALGEPAAAAALLGGEI 350				
DB	301 PREVPDEYVGSFMEVYVQELDLERSLTHEMALGEPAAAAALLGGEI 350				
RESULT 2					
B37057					

Integrin beta-6 chain - guinea pig (fragment)
 C/Species: Cavia porcellus (guinea pig)
 C/Date: 15-Feb-1991 #sequence_revision 13-Sep-1991 #ext_change 20-Aug-1999
 C/Accession: B37057
 R/Sheppard, D.; Rozzo, C.; Starr, L.; Quaranta, V.; Erle, D.J.; Pytela, R.
 J. Biol. Chem. 265, 11502-11507, 1990
 A/Title: Complete amino acid sequence of a novel integrin beta subunit (beta6) identified
 A/Reference number: A37057; MUID:90307659; PMID:2265683
 A/Accession: B37057
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-577 <SHE>
 A/Cross-references: GB:J05522; NID:9191277; PIDN:AAA37043.1; PID:9553845
 A/Note: the authors translated the codon AAA for residue 88 as Asn, AAC for residue 97 as
 as Pro, ACG for residue 355 as Met, GAG for residue 363 as Thr, ACG for residue 364 as A
 Gly
 C/Superfamily: Integrin beta chain; laminin-type EGF-like homology
 C/Keywords: cell adhesion; cytoskeleton; transmembrane protein

Query Match 7.3%; Score 138; DB 2; Length 577;
 Best Local Similarity 26.4%; Pred. No. 0.026;
 Matches 46; Conservative 22; Mismatches 66; Indels 40; Gaps 10;

QY 154 GSEMYCCPASFQYTCQPCRGQRLCTRDSEC-CGDDLCVWG-----HCTKATR--GSN 204
 DB 393 GP--YCCQDNF--SC--VVRKGLICGNDGCEGECVCRSGWTEGXCNTTSTDTICISD 446
 QY 205 GTICDNDQDQPGPLCAFGRLFPVCTPLPVEGELCHDPASRLDLITWLEPDG---- 260
 DB 447 GTICSGRGDCVCKVCYCTNPGASGPTCERPT---CSPPCNSKRCICHLSDQPG 502
 QY 261 -AIDRCPA-----SGLICQPHSHSLVYCKPTFGSGDDQGEILL 300
 DB 503 ECVDKCKLAQVITISKADPFKDSVSCSLQGEN---ECILFPLISDNGKXII 553

RESULT 3
 KXHS
 Plasma protein S precursor - human
 N/Alternate names: vitamin K-dependent protein S
 C/Species: Homo sapiens (man)
 C/Date: 21-Sep-1990 #sequence_revision 26-Jan-1996 #ext_change 16-Jul-1999
 C/Accession: A35610; A35611; A26157; A25691; A35612; A60903; S02424; S09519
 R/Schmid, D.K.; Tatro, A.V.; Phelps, L.G.; Tomczak, J.A.; Long, G.L.
 Biochemistry 29, 7845-7852, 1990
 A/Title: Organization of the human protein S gene.
 A/Reference number: A35610; MUID:91084444; PMID:2148110
 A/Accession: A35610
 A/Molecule type: DNA
 A/Residues: 1-676 <SCCH>
 A/Cross-references: GB:M57853; NID:9190547; PIDN:AAA60357.1; PID:9190549; GB:J02917
 A/Note: the authors translated the codon TTT for residue 26 as Leu
 R/Ploos van Amstel, H.K.; Reitsma, P.H.; van der Logt, C.P.E.; Bertina, R.M.
 Biochemistry 29, 7853-7861, 1990
 A/Title: Intron-exon organization of the active human protein S gene Psalpa and its pse
 A/Reference number: A35611; MUID:91084445; PMID:2148111
 A/Accession: A35611
 A/Molecule type: DNA
 A/Residues: 1-25 <PL3>
 A/Cross-references: GB:J02918
 R/Hoskins, J.; Norman, D.K.; Beckmann, R.J.; Long, G.L.
 Proc. Natl. Acad. Sci. U.S.A. 84, 349-353, 1987
 A/Title: Cloning and characterization of human liver cDNA encoding a protein S precursor
 A/Reference number: A26157; MUID:87092407; PMID:3467362
 A/Accession: A26157
 A/Molecule type: mRNA
 A/Residues: 1-10, 'P', 12-25, 'L', 27-676 <HOS>
 A/Cross-references: GB:M15036; NID:9190288; PIDN:AAA36479.1; PID:9190289
 R/Lundwall, A.; Dackowski, W.; Cohen, E.; Shaffer, M.; Nahr, A.; Dahlback, B.; Stenflo,
 Proc. Natl. Acad. Sci. U.S.A. 83, 6756-6760, 1986
 A/Title: Isolation and sequence of the cDNA for human protein S, a regulator of blood co
 A/Reference number: A25691; MUID:86313649; PMID:2944113
 A/Accession: A25691

A/Molecule type: mRNA
 A/Residues: 27-220, 'U', 222-262, 'H', 264-344, 'Y', 346-676 <LUN>
 A/Cross-references: GB:M4338; NID:9190448; PIDN:AAA60181.1; PID:9190449
 A/Note: part of this sequence, including the amino end of the mature protein, was determi
 R/Edenbrandt, C.M.; Lundwall, A.; Wyder, R.; Stenflo, J.
 Biochemistry 29, 7861-7868, 1990
 A/Title: Molecular analysis of the gene for vitamin K dependent protein S and its pseudoc
 A/Reference number: A35612; MUID:9108446; PMID:2148112
 A/Accession: A35612
 A/Status: not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 284-676 <EDE>
 A/Cross-references: GB:J02919
 R/Ploos van Amstel, J.K.; van der Zanden, A.L.; Bakker, E.; Reitsma, P.H.; Bertina, R.M.
 Thromb. Haemost. 58, 982-987, 1987
 A/Title: Two genes homologous with human protein S cDNA are located on chromosome 3.
 A/Reference number: A60903; MUID:88178564; PMID:2895503
 A/Accession: A60903
 A/Molecule type: mRNA
 A/Residues: 351-676 <PLO>
 R/Ploos van Amstel, H.K.; van der Zanden, A.L.; Reitsma, P.H.; Bertina, R.M.
 FEBS Lett. 222, 186-190, 1987
 A/Title: Human protein S cDNA encodes Phe-16 and Tyr 222 in consensus sequences for the I
 A/Reference number: S02424; MUID:88005138; PMID:2820795
 A/Accession: S02424
 A/Molecule type: mRNA
 A/Residues: 1-676 <PL2>
 A/Cross-references: EMBL:Y00692; NID:936578; PIDN:CAA68687.1; PID:936579
 C/Genetics:
 A/Genes: GDB:PROS1; PROS
 A/Cross-references: GDB:120721; OMIM:176880
 A/Map position: 3p11.1-3p11.2
 A/Introns: 26/1; 78/3; 87/1; 116/1; 157/1; 201/1; 243/1; 283/3; 322/2; 385/3; 441/3; 498/
 C/Complex: in plasma forms a complex with C4b binding protein
 C/Function:
 A/Description: a cofactor for activated protein C (EC 3.4.21.69); thrombin cleavage dest
 C/Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
 C/Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; blood coagulation; carboxy
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-41/Domain: signal sequence #status predicted <SIG>
 F:42-85/Domain: Gla domain homology <GLA>
 F:42-676/Product: plasma protein S #status predicted <MAT>
 F:121-154/Domain: EGF homology <EG1>
 F:121-159/Domain: EGF homology <EG2>
 F:205-241/Domain: EGF homology <EG3>
 F:247-282/Domain: EGF homology <EG4>
 F:315-667/Domain: sex hormone-binding globulin homology <SHB>
 F:325-478/Domain: laminin G repeat homology <LGR>
 F:47-48,55,57,60,61,66,67,70,73,77/Modified site: gamma-carboxyglutamic acid (Glu) #statu
 F:58-63,88-113,121-134,126-143,145-154,151-175,171-184,186-199,205-217,212-226,228-241,24
 F:111-112/Cleavage site: Arg-Ser (thrombin) #status predicted
 F:113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F:177,219,258/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
 F:499,509,550/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match 7.0%; Score 131.5; DB 1; Length 676;
 Best Local Similarity 24.0%; Pred. No. 0.091;
 Matches 83; Conservative 43; Mismatches 129; Indels 91; Gaps 21;

QY 3 RLGATLCTLLAAVPTAPAPATATSPYKPGALSYPOEATLNMFEVLELMDTQ 62
 DB 7 RGALLACLLIV-----LPSEANFLSKQASQVLVK--RANSLLESTK 50
 QY 63 --HKLSAVEEMEAEEAAKASSEVNTANLPPSYHNETNTDTKVGNTTIVHREIKITN 120
 DB 51 QGNLEKECIEELCKNEAREV-----FENPEPD-----VEYPKLVGLRS 91
 QY 121 NOTGQMVSEVIVISVGBEGRSHCECIDEDGCP-----SMYCO--FASFOYTCOP- 170
 DB 92 FQTGTFTNARSTAYNP--LRSQVNAIPDQCPPLCNEGYSKCDGRASFCTCKPG 148
 QY 171 CRGQMLCTRDSECCGDDLCVWGHTKMA--TRGS-----NG-TICDNDRC----- 214

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OM protein - protein search, using sw model

Run on: February 20, 2004, 18:04:23 ; Search time 85 seconds

(without alignments)
1062.570 Million cell updates/sec

Title: US-10-063-671-8

Perfect score: 1880

Sequence: 1 MORIGATLTLTLAAVPTA.....EMALGPAAALALGGEI 350

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPTRMBL_23:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_virus:*
17: sp_bacteriophage:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1217	64.7	277	11	Q9ES33
2	876	46.6	171	4	Q43532
3	703.5	37.4	215	4	Q8N234
4	182.5	9.7	221	11	Q8VEJ3
5	175	9.3	259	13	Q57464
6	170	9.0	255	13	Q9DDA4
7	165	8.8	240	13	Q9PMH3
8	157	8.4	241	13	Q9WED9
9	156	8.3	259	11	Q8BFW0
10	143	7.6	420	5	Q81459
11	132.5	7.0	230	11	Q9BQT4
12	129.5	6.9	128	11	Q9ERW0
13	129.5	6.9	230	11	Q9ERW1
14	128.5	6.8	788	6	Q8SCB8
15	124.5	6.6	1664	5	Q9TVQ2
16	119	6.3	969	4	Q96KG6

17	119	6.3	1168	11	Q91V90	Q91V90 mus musculu
18	118.5	6.3	96	13	Q8UDX3	Q8UDX3 gallus gall
19	117.5	6.2	996	6	Q924X6	Q924X6 mus musculu
20	117	6.2	420	6	Q9XS50	Q9XS50 bos taurus
21	117	6.2	3712	5	Q9VRW0	Q9VRW0 drosophila
22	116	6.2	788	13	Q07012	Q07012 xenopus lae
23	116	6.2	836	13	Q8AW87	Q8AW87 cynops pyr
24	116	6.2	870	11	Q921B6	Q921B6 mus musculu
25	116	6.2	1253	11	Q61810	Q61810 mus musculu
26	116	6.2	2146	5	Q9VC97	Q9VC97 drosophila
27	115	6.1	2376	5	Q9V5J0	Q9V5J0 drosophila
28	115	6.1	2376	5	Q966V1	Q966V1 drosophila
29	114.5	6.1	96	13	Q8JFX8	Q8JFX8 bombina max
30	114.5	6.1	746	4	Q9EBH9	Q9EBH9 homo sapien
31	114.5	6.1	1256	4	Q9NS15	Q9NS15 homo sapien
32	114.5	6.1	1382	4	Q9H7K2	Q9H7K2 homo sapien
33	114	6.1	755	11	Q9R0G6	Q9R0G6 mus musculu
34	114	6.1	755	11	Q8V1S4	Q8V1S4 mus musculu
35	114	6.1	1713	11	Q88349	Q88349 mus musculu
36	113.5	6.0	421	5	Q9NKE1	Q9NKE1 drosophila
37	113.5	6.0	817	4	Q14592	Q14592 homo sapien
38	112	6.0	963	4	Q14114	Q14114 homo sapien
39	112	6.0	1389	11	Q8CG18	Q8CG18 mus musculu
40	112	6.0	1713	11	Q8CG19	Q8CG19 mus musculu
41	111.5	5.9	96	13	Q8JFX9	Q8JFX9 bombina max
42	111.5	5.9	96	13	Q8JFX0	Q8JFX0 bombina max
43	111.5	5.9	96	13	Q8JFE6	Q8JFE6 bombina max
44	111.5	5.9	487	5	Q8MSX5	Q8MSX5 drosophila
45	111.5	5.9	1188	10	Q9SV59	Q9SV59 arabidopsis

ALIGNMENTS

RESULT 1	Q9ES33	PRELIMINARY	PRT:	277 AA.
ID	Q9ES33	Q9ES33		
AC	Q9ES33	Q9ES33		
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Substrate binding subunit of type II 5'-deiodinase Dp29.			
OS	Rattus norvegicus (Rat)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Sprague-Dawley; TISSUE=Brain;			
RX	MEDLINE=20400444; PubMed=10829019;			
RA	Leonard D.M., Stacherek S.T., Saffran M., Farwell A.P., Kowalik T.F.,			
RA	Leonard J.W.;			
RT	"Cloning, expression, and functional characterization of the substrate			
RT	binding subunit of rat type II iodothyronine 5'-deiodinase";			
RL	J. Biol. Chem. 275:25194-25201 (2000).			
DR	EMBL; AF245040; AAG15890.1; -			
DR	InterPro; IPR006796; dckkopf_N.			
DR	Ffam; PF04706; dckkopf_N; 1.			
DR	SEQUENCE 277 AA; 30763 MW; 8025F66DFE4C205E CRC64;			
QY	Query Match	64.7%; Score 1217; DB 11; Length 277;		
QY	Best Local Similarity	78.1%; Pred. No. 2.5e-98;		
QY	Matches 218; Conservative 26; Mismatches 33; Indels 2; Gaps 1;			
DB	72 MAEEBAKASSEVLANLPSPYHNETNTDVKVGNTHVREIKRINNOGQWVFSET 131			
QY	1 MAEEBAKASSEVLANLPSPYHNETNTDVKVGNTHVREIKRINNOGQWVFSET 60			
DB	132 VITSVDEBGRSRSHCCIDEDCGPSPMYCQFASFOYTCPCGQRMCTRDSBCCGDDQICV 191			
QY	61 VITSVDEBGRSRSHCCIDEDCGPSPMYCQFASFOYTCPCGQRMCTRDSBCCGDDQICV 120			
DB	192 WCHCKRMATRGNSNGRTICNQRDCQGLCCAFQRLGLFVCPPLPVEBGLCHDPARLLDL 251			

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DB 121 WGCCTOKATGNSGTTICDNRDCCPGICCAFQGLLFPVCTPLPVEGELCHDPTSGMDL 180
QY 252 ITTELBPDGLDPCASGILGCPHSHSLVYVCKPFPVSGRDDGILLPREVPPEYVG 311
DB 181 ITTELBPDGLDPCASGILGCPHSHSLVYVCKPFPVSGRDDGILLPREVPPEYVG 240
QY 312 SFMEVROLEDELESTITTEMALGEPAPAAAALLGGEI 350
DB 241 GFICEVROLEDELESTITTEMALGEPAPAAAALLGGEI 277

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RESULT 2

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ID 043532 PRELIMINARY; PRT; 171 AA.
AC 043532;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE RIG-like 7.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SOURCE FROM N.A.
RC TISSUE=Brain;
RA Ligon A.H., Peirhouse M.A., Jasser S., Hong Y.K., Yung W.K.A.,
RA Steck P.A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034208; AAB92664.1; -
DR InterPro; IPR006796; dickleof_N.
DR InterPro; IPR005805; Rleske
DR Pfam; PF04706; dickleof_N.1.
DR PROSITE; PS00200; RLESKE_2; 1.
SQ SEQUENCE 171 AA; 19283 MW; B890E38F873D0562 CRC64;

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Query Match 46.6%; Score 876; DB 4; Length 171;
Best Local Similarity 96.8%; Pred. No. 9.2e-69;
Matches 151; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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QY 157 MYCQFASFOYTCQPCRGRLCTRDSECCDOLCWHGCTKATRSNGTICDNRDCCP 216
DB 1 MYCQFASFOYTCQPCRGRLCTRDSECCDOLCWHGCTKATRSNGTICDNRDCCP 60
QY 217 GLCCAFQGLLFPVCTPLPVEGELCHDPAARLLDITTELBPDGLDPCASGILGCPH 276
DB 61 GLCCAFQGLLFPVCTPLPVEGELCHDPAARLLDITTELBPDGLDPCASGILGCPH 120
QY 277 SHSLVYVCKPFPVSGRDDGILLPREVPPEYVG 312
DB 121 SHSLVYVCKPFPVSGRDDGILLPREVPPEYVG 156

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RESULT 3

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ID 08N294 PRELIMINARY; PRT; 215 AA.
AC 08N294;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein FLJ3633.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Amalgam;
RA Niinomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto C., Isono Y.,

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RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kasehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isegai T.,
RT "NEO human cDNA sequencing project";
RT Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK090952; BAC03555.1; -
KW Hypothetical protein.
SQ SEQUENCE 215 AA; 23904 MW; 2D9DEABCAFAB80B0 CRC64;

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Query Match 37.4%; Score 703.5; DB 4; Length 215;
Best Local Similarity 92.5%; Pred. No. 1.5e-53;
Matches 136; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

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QY 25 PTATAPYKP-GPALSYPOEBATINEMFREVEIMEDTQKLSAVEEMEAEEAATAASS 83
DB 69 FCASGLGCPHSHSLSYPOEBATINEMFREVEIMEDTQKLSAVEEMEAEEAATAASS 128
QY 84 EVNLANI-PPSYHNETNTDTKVGNTIHYHREIKHTINNOTGOMVSETVITSVDEGR 143
DB 129 EVNLANI-PPSYHNETNTDTKVGNTIHYHREIKHTINNOTGOMVSETVITSVDEGR 188
QY 144 SHECIIDECGSPMYCQFASFOYTCOP 170
DB 189 SHECIIDECGSPMYCQFASFOYTCOP 215

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RESULT 4

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ID 08VEJ3 PRELIMINARY; PRT; 221 AA.
AC 08VEJ3;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Similar to dickleof (Xenopus laevis) homolog 4.
GN DK4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018400; AAH18400.1; -
DR MGD; MGI:2385239; Dk4.
SQ SEQUENCE 221 AA; 24260 MW; 670AD9F750BF1715 CRC64;

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Query Match 9.7%; Score 182.5; DB 11; Length 221;
Best Local Similarity 24.3%; Pred. No. 6.3e-08;
Matches 50; Conservative 20; Mismatches 71; Indels 65; Gaps 7;

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QY 133 ITSVDSEGR-RSHECIIDECGSPMYC-QFASFOYTCOPCGQRLCTRDSECCDOLC 190
DB 26 IKSSADYVQAGKGLCASDRDCSEGRCLAFHDERSPCATCRVRRRCQGRSAVCCPVC 85
QY 191 VMGHT-----KATRSNGTIC 208
DB 86 VNDVCTAVEDTRPYMDNRDQDQAVAEGLTKWAEENRPGKSTKSSQSSQGBGSC 145
QY 209 DNRDCCGGLCCAFQGLLFPVCTPLPVEGELC-----HDPASRLDITTELBPDGLD 264
DB 146 LRTSDCGPGLCA--RHWTICKPVAREGVCSRGKHDTAQAPEI-----FOR 193
QY 265 CPCASGLGCP-----SHSLVYVCK 285
DB 194 CDCGPGILGRSQVTSNRQHSRLVCO 219

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RESULT 5

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ID 057464 PRELIMINARY; PRT; 259 AA.
AC 057464;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 20, 2004, 18:47:56 ; Search time 28 Seconds

(without alignments)
528.886 Million cell updates/sec

Title: US-10-063-671-8

Perfect score: 1880

Sequence: 1 MORLGATLLCLLAAAVPTA.....EMALGPAAAAALGGEET 350

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.dep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.dep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.dep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.dep.*
5: /cgn2_6/ptodata/2/1aa/PTCUS.COMB.dep.*
6: /cgn2_6/ptodata/2/1aa/backfile1.dep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1880	100.0	350	4	US-09-161-241-9 Sequence 9, Appl
2	1589	84.5	349	4	US-09-161-241-8 Sequence 8, Appl
3	214.5	11.4	224	4	US-09-161-241-14 Sequence 14, Appl
4	174.5	9.3	266	4	US-09-161-241-10 Sequence 10, Appl
5	169	9.0	207	4	US-09-161-241-13 Sequence 13, Appl
6	162	8.6	259	4	US-09-161-241-12 Sequence 12, Appl
7	156	8.3	259	4	US-09-161-241-11 Sequence 11, Appl
8	138	7.3	577	2	US-07-728-215-29 Sequence 29, Appl
9	138	7.3	577	4	US-08-938-085A-29 Sequence 29, Appl
10	138	7.3	577	4	US-10-072-844-29 Sequence 29, Appl
11	132.5	7.0	676	1	US-08-435-434-3 Sequence 3, Appl
12	131.5	7.0	676	1	US-08-435-434-3 Sequence 3, Appl
13	131.5	7.0	676	1	US-08-435-434-3 Sequence 3, Appl
14	131.5	7.0	676	2	US-08-438-863-3 Sequence 3, Appl
15	131.5	7.0	676	2	US-08-438-864-3 Sequence 3, Appl
16	131.5	7.0	676	3	US-08-438-862-3 Sequence 3, Appl
17	131.5	7.0	676	3	US-08-628-747-3 Sequence 3, Appl
18	131.5	7.0	676	3	US-08-402-253-3 Sequence 3, Appl
19	131.5	7.0	676	3	US-08-443-866B-3 Sequence 3, Appl
20	126	6.7	788	2	US-07-728-215-27 Sequence 27, Appl
21	126	6.7	788	4	US-08-938-085A-27 Sequence 27, Appl
22	126	6.7	788	4	US-10-072-844-27 Sequence 27, Appl
23	126	6.7	1394	6	5177197-30 Patent No. 5177197
24	116	6.2	1251	1	PCT-US95-02251-3 Sequence 3, Appl
25	116	6.2	1251	1	US-08-199-780-3 Sequence 3, Appl
26	116	6.2	1252	2	US-08-316-650-3 Sequence 3, Appl
27	116	6.2	1253	3	US-08-479-722B-4 Sequence 4, Appl

28	110.5	5.9	1147	1	US-08-144-121-3 Sequence 3, Appl
29	110.5	5.9	1147	2	US-08-735-893-3 Sequence 2, Appl
30	110.5	5.9	1165	2	US-08-144-121-2 Sequence 2, Appl
31	110.5	5.9	1165	2	US-08-735-893-2 Sequence 2, Appl
32	110.5	5.9	2214	1	US-08-727-034-7 Sequence 7, Appl
33	110	5.9	2523	1	US-08-185-432-18 Sequence 18, Appl
34	110	5.9	2523	4	US-08-899-232-3 Sequence 3, Appl
35	108	5.7	299	3	US-09-188-930-192 Sequence 192, App
36	108	5.7	299	3	US-09-188-930-192 Sequence 192, App
37	108	5.7	299	4	US-09-312-283C-192 Sequence 192, App
38	108	5.7	299	4	US-09-312-283C-192 Sequence 192, App
39	108	5.7	1170	1	US-08-313-288B-20 Sequence 20, Appl
40	107.5	5.7	799	1	US-08-054-077C-2 Sequence 2, Appl
41	107.5	5.7	2556	1	US-08-185-432-17 Sequence 17, Appl
42	107.5	5.7	2556	4	US-08-899-232-2 Sequence 2, Appl
43	106.5	5.7	652	6	US-08-185-432-16 Patent No. 5258288
44	106	5.6	2471	1	US-08-185-432-16 Patent No. 5258288
45	106	5.6	2471	1	US-08-083-590A-19 Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-09-161-241-9
Sequence 9, Application US/09161241
Patent No. 6344541
GENERAL INFORMATION:
APPLICANT: Bass, Michael B
APPLICANT: Sullivan, John K
APPLICANT: Rhell, Lars E
APPLICANT: Wang, Daqiang
TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
FILE REFERENCE: A-548
CURRENT APPLICATION NUMBER: US/09/161,241
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 350
TYPE: PRT
ORGANISM: Human
US-09-161-241-9

Query Match	100.0%	Score 1880	DB 4	Length 350
Best Local Similarity	100.0%	Pred. No. 1.6e-151		
Matches 350	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MORLGATLLCLLAAAVPTAPAPAPATATAPYKPGPALSYPOEATLNMFEVELEMD	60	
DB	1	MORLGATLLCLLAAAVPTAPAPATATAPYKPGPALSYPOEATLNMFEVELEMD	60	
QY	61	TOHKRSANVEEAEBAKASSEVNLNLPSSYNENETDTCKGNNTTHHREIHKTN	120	
DB	61	TOHKRSANVEEAEBAKASSEVNLNLPSSYNENETDTCKGNNTTHHREIHKTN	120	
QY	121	NOTGQWFESEVITSGDEGRSHCEIIDDCGSMYCOFASFOYTQPCRGQMLCTR	180	
DB	121	NOTGQWFESEVITSGDEGRSHCEIIDDCGSMYCOFASFOYTQPCRGQMLCTR	180	
QY	181	DSECCDQJCWGHCTKATRGSGNGTICNDQDCQGLCAFORGLIPVCTPLPYEGTL	240	
DB	181	DSECCDQJCWGHCTKATRGSGNGTICNDQDCQGLCAFORGLIPVCTPLPYEGTL	240	
QY	241	CHDPASRLDLITWELPFGALDRCPGASGLICQPHSHSLVYVCKPTFGSGRDQGEILL	300	
DB	241	CHDPASRLDLITWELPFGALDRCPGASGLICQPHSHSLVYVCKPTFGSGRDQGEILL	300	
QY	301	PREVPDEYVGSFMEVROELDLERSLTENALGEPAAAAALLGGEET 350		
DB	301	PREVPDEYVGSFMEVROELDLERSLTENALGEPAAAAALLGGEET 350		

RESULT 2
US-09-161-241-8
Sequence 8, Application US/09161241
Patent No. 6344541
GENERAL INFORMATION:
APPLICANT: Bass, Michael B
APPLICANT: Sullivan, John K
APPLICANT: Theill, Lars E
TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
FILE REFERENCE: A-548
CURRENT APPLICATION NUMBER: US/09/161,241
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 349
TYPE: PRT
ORGANISM: Mouse
US-09-161-241-8

Query Match 84.5%; Score 1589; DB 4; Length 349;
Best Local Similarity 82.5%; Pred. No. 7,4e-127;
Matches 288; Conservative 26; Mismatches 33; Indels 2; Gaps 1;

QY 1 MORLGATLLCLLAAVPTAPAPATATAPVKPGPALSYPOEATLNMFRVEELMD 60
DB 1 MORLGATLLCLLAAVPTAPAPATATAPVKPGPALSYPOEATLNMFRVEELMD 60
QY 61 TQHKLSAVEEMEAERAAASSEVNLANLPSTYHNETNTDTYGNNTTIVHREIKTN 120
DB 61 TQHKLSAVEEMEAERAAASSEVNLANLPSTYHNETNTDTYGNNTTIVHREIKTN 120
QY 121 NOTGOWFSEVITVSDEBGRSHCECTIDEDCGPSMYCOFASFOYTCOPCRQMLCTR 180
DB 121 NOTGOWFSEVITVSDEBGRSHCECTIDEDCGPSMYCOFASFOYTCOPCRQMLCTR 180
QY 121 NOSQGVFSEVITVSDEBGRSHCECTIDEDCGPTRVCOFSSFKTTCQPCRQMLCTR 180
DB 121 NOSQGVFSEVITVSDEBGRSHCECTIDEDCGPTRVCOFSSFKTTCQPCRQMLCTR 180
QY 181 DSECCGDLQVWGHCTMATRGSNGTICDNQRCQPLCCAFQRLFPVCTPLPYEGEL 240
DB 181 DSECCGDLQVWGHCTMATRGSNGTICDNQRCQPLCCAFQRLFPVCTPLPYEGEL 240
QY 241 CHDPAQLLITLITELPDDALDPCASGLLCOPHSHSVYVCKPFFVSRQDEILL 300
DB 241 CHDPAQLLITLITELPDDALDPCASGLLCOPHSHSVYVCKPFFVSRQDEILL 300
QY 301 PREVPDEYVGSFMEVYRQELDLERSITLTEMALGEPAAAAALLGSEE 349
DB 301 PREVPDEYVGSFMEVYRQELDLERSITLTEMALGEPAAAAALLGSEE 349
QY 301 PREVPDEYVGSFMEVYRQELDLERSITLTEMALGEPAAAAALLGSEE 349
DB 301 PREVPDEYVGSFMEVYRQELDLERSITLTEMALGEPAAAAALLGSEE 349

RESULT 3
US-09-161-241-14
Sequence 14, Application US/09161241
Patent No. 6344541
GENERAL INFORMATION:
APPLICANT: Bass, Michael B
APPLICANT: Sullivan, John K
APPLICANT: Theill, Lars E
TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
FILE REFERENCE: A-548
CURRENT APPLICATION NUMBER: US/09/161,241
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 224
TYPE: PRT
ORGANISM: Human
US-09-161-241-14
Query Match 11.4%; Score 214.5; DB 4; Length 224;
Best Local Similarity 26.5%; Pred. No. 1.2e-10;

Matches 57; Conservative 21; Mismatches 72; Indels 65; Gaps 7;
QY 124 GOWFSEVITVSDEBGRSHCECTIDEDCGPSMYCOFASFOYTCOPCRQMLCTR 181
DB 17 GALVLDFFNNISSADLDGARKGSQCLSDTDCNTRKFCLOPRDEKPFATCRGLRRRCQD 76
QY 182 SECCGDLQVWGHCTMATRGSNGTICDNQRCQPLCCAFQRLFPVCTPLPYEGEL 240
DB 77 AMCCPGTLCVADVCTTMDATPILERQLDQDGTGHAEGTGHVQENQPKRKSIRKSQ 136
QY 200 TRGSNGTICDNQRCQPLCCAFQRLFPVCTPLPYEGEL---HDPASRLDLITWE 255
DB 137 RKGGEGESCLATPFGQPLCCA--RHFTKTKCKVLLGQVCSRGKMDAQAPEI---- 190
QY 256 LEPDGLDRCPCASGLLCOF---HSHSLVYVCK 285
DB 191 ---FORCPCGGLLCRSQSLTSNRQHLRLVQ 219

RESULT 4
US-09-161-241-10
Sequence 10, Application US/09161241
Patent No. 6344541
GENERAL INFORMATION:
APPLICANT: Bass, Michael B
APPLICANT: Sullivan, John K
APPLICANT: Theill, Lars E
TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
FILE REFERENCE: A-548
CURRENT APPLICATION NUMBER: US/09/161,241
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 266
TYPE: PRT
ORGANISM: Human
US-09-161-241-10

Query Match 9.3%; Score 174.5; DB 4; Length 266;
Best Local Similarity 25.6%; Pred. No. 3.7e-07;
Matches 50; Conservative 18; Mismatches 60; Indels 67; Gaps 8;
QY 145 HECITDEDCGSMYCOF---ASFQYTCOPCRQMLCTRDECCGDLQVWGHCT 195
DB 83 YPCAEDCEGTDYCYASPTRGDAGVQ--ICLACKRRRRCKRHAMCCPGNYCKXNGICVSS 141
QY 196 -----TXM-ATRGSNGTICDNQRCQPLCCAFQRLFPVCTPLPYEGEL 240
DB 142 DONHFRGIEBETTESFANDHSTLDYSRRTTSSKMYHTTGQSGSYCLRSDDCASGLIC 201
QY 221 AFQRLGFPVCTPLPYEGELC---HDPASRLDLITWELEPDGLDRCPCASGLIC 273
DB 202 A--RHFMGKICKPVLKEGQVCTKRRKSHGLEI-----FORCYCEBGLSCRIQK 249
QY 274 ---QPHSHSVYVCK 285
DB 250 DHHQASNSRLHTQ 264

RESULT 5
US-09-161-241-13
Sequence 13, Application US/09161241
Patent No. 6344541
GENERAL INFORMATION:
APPLICANT: Bass, Michael B
APPLICANT: Sullivan, John K
APPLICANT: Theill, Lars E
TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
FILE REFERENCE: A-548
CURRENT APPLICATION NUMBER: US/09/161,241

C 154	30	1.2	454	24	ABN94930	Gene #1418 used to	1.2	454	24	ABN94930	Gene #1418 used to	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22	AAH15319	Human CDNA sequenc	1.2	1563	22
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QY 661 CATGCCGGGGCCAGAGATGCTCTGCAACCGGGACAGTGAAGTCTGTGAGAACCACTGT 720
Db 661 CATGCCGGGGCCAGAGATGCTCTGCAACCGGGACAGTGAAGTCTGTGAGAACCACTGT 720
QY 721 GTGTCTGGGGGTCACTGACCAAAATGGCCACAGAGGGGAGCAATGGGAACATGTGTGA 780
Db 721 GTGTCTGGGGGTCACTGACCAAAATGGCCACAGAGGGGAGCAATGGGAACATGTGTGA 780
QY 781 ACCAGAGGAACTGCGCAGCCGGGGCTGTGCTGTGCTTCCAGAGAGGCTGTGCTTCC 840
Db 781 ACCAGAGGAACTGCGCAGCCGGGGCTGTGCTGTGCTTCCAGAGAGGCTGTGCTTCC 840
QY 841 TGTGCAACACCCCTGCGCTGGAGGGGAGAGCTTTGCACTGACCCCGGAGCGGCTTCTG 900
Db 841 TGTGCAACACCCCTGCGCTGGAGGGGAGAGCTTTGCACTGACCCCGGAGCGGCTTCTG 900
QY 901 ACCTCATCACTGGAGAGCTGAGAGCTGTGAGAGCTTTGACCGATGCGCTTGTGCCAGTG 960
Db 901 ACCTCATCACTGGAGAGCTGAGAGCTGTGAGAGCTTTGACCGATGCGCTTGTGCCAGTG 960
QY 961 GCTTCTCTGCGACACCCCAAGCCACAGCCTGTGTGTATGTGTGCAAGCCGACCTTGTG 1020
Db 961 GCTTCTCTGCGACACCCCAAGCCACAGCCTGTGTGTATGTGTGCAAGCCGACCTTGTG 1020
QY 1021 GGAGCCGCTGACCAAGATGGGGAGATCTGCTGCTGCCAGAGAGCTCCCGATGATGTAAG 1080
Db 1021 GGAGCCGCTGACCAAGATGGGGAGATCTGCTGCTGCCAGAGAGCTCCCGATGATGTAAG 1080
QY 1081 TTGGCAGCTTCATGAGAGAGGTGCGCCAGAGCTGAGAGACTGTGAGAGAGAGCTTACTG 1140
Db 1081 TTGGCAGCTTCATGAGAGAGGTGCGCCAGAGCTGAGAGACTGTGAGAGAGAGCTTACTG 1140
QY 1141 AAGAGATGGCGCTGGGGAGAGCTGCGCTGCGCCGCTGCACTGCTGGAGGGAGAGAG 1200
Db 1141 AAGAGATGGCGCTGGGGAGAGCTGCGCTGCGCCGCTGCACTGCTGGAGGGAGAGAG 1200
QY 1201 TTTAGATCTGGACCAAGCTGTGGGTAGATGTGCATATGAAATAGCTAATTTATTTCCCA 1260
Db 1201 TTTAGATCTGGACCAAGCTGTGGGTAGATGTGCATATGAAATAGCTAATTTATTTCCCA 1260
QY 1261 GGTGTGAGCTTTAGAGCGTGGGCTGACCAAGGCTTCTTCTCATCTTTTCCAGTAAGTT 1320
Db 1261 GGTGTGAGCTTTAGAGCGTGGGCTGACCAAGGCTTCTTCTCATCTTTTCCAGTAAGTT 1320
QY 1321 TCCCTCTGCTGACACAGATGAGGTGTGTGCAATTTGTCACTGCCCAAGGCTGTCT 1380
Db 1321 TCCCTCTGCTGACACAGATGAGGTGTGTGCAATTTGTCACTGCCCAAGGCTGTCT 1380
QY 1381 CCAGGCTTCAAGTCTGGTGTGGAGAGTCAAGGAGGTTAACTGCAAGGAGAGTT 1440
Db 1381 CCAGGCTTCAAGTCTGGTGTGGAGAGTCAAGGAGGTTAACTGCAAGGAGAGTT 1440
QY 1441 GCCACCCCTGTGCAAGATTAATGCTGTGCTTCTCAACAGTTGGCAGAGACCGGTGTG 1500
Db 1441 GCCACCCCTGTGCAAGATTAATGCTGTGCTTCTCAACAGTTGGCAGAGACCGGTGTG 1500
QY 1501 TCTACATGCTTTGATTAATTTTGGAGGGAGAGATGAGAAACATGTGAGTCTCCCTC 1560
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Db 1681 CAGCTGTGCAAGATGAATTTCTGTTGACCCCTGATTAATGATGTTTATTCATCCAGCA 1740

QY 1741 GTGTGCTCACTCTCTACTCTCTGTGTCAGAGGAGACATTTTCAATCCAAATCAATCCC 1800
Db 1741 GTGTGCTCACTCTCTACTCTCTGTGTCAGAGGAGACATTTTCAATCCAAATCAATCCC 1800
QY 1801 TCTCTCAGCAGAGCTTGGAGAGGGGTCAATGTCTCTCCCTGTCATCAGGATCTCAGAG 1860
Db 1801 TCTCTCAGCAGAGCTTGGAGAGGGGTCAATGTCTCTCCCTGTCATCAGGATCTCAGAG 1860
QY 1861 GCTCAGAGACTGCAAGTCTTGTGCTCCCAAGTCAACACTAGTGAAGACAGAGAGTTTC 1920
Db 1861 GCTCAGAGACTGCAAGTCTTGTGCTCCCAAGTCAACACTAGTGAAGACAGAGAGTTTC 1920
QY 1921 ATCTGTGTGATCACTTAAGCTCAAGTGTCTCTCACTAACCACAGGCTTGTGCTCA 1980
Db 1921 ATCTGTGTGATCACTTAAGCTCAAGTGTCTCTCACTAACCACAGGCTTGTGCTCA 1980
QY 1981 CCAAAAAGTCTCCCAAAAAGAGAGATGGATTTTCTTGAAGGATGACATCTTGA 2040
Db 1981 CCAAAAAGTCTCCCAAAAAGAGAGATGGATTTTCTTGAAGGATGACATCTTGA 2040
QY 2041 ATTAAGTCAACTAATCTCACATCCCTCTAAAGTAACTACTGTTAGGACAGAGT 2100
Db 2041 ATTAAGTCAACTAATCTCACATCCCTCTAAAGTAACTACTGTTAGGACAGAGT 2100
QY 2101 GTTCTCAGAGTGGGGCAGCCGCTCTTATGAGAGCAATGATTTGACACTGTCCCT 2160
Db 2101 GTTCTCAGAGTGGGGCAGCCGCTCTTATGAGAGCAATGATTTGACACTGTCCCT 2160
QY 2161 CTTTGGCAGTTGCACTTATTAATCTTTGAAAGGTATATGCTGAGGCTGACATACAGTTAA 2220
Db 2161 CTTTGGCAGTTGCACTTATTAATCTTTGAAAGGTATATGCTGAGGCTGACATACAGTTAA 2220
QY 2221 CCTGAGAAACAGATCTTAGGTAAATGTAGGCGAGATTAATAATGAATTTGCAAAAT 2280
Db 2221 CCTGAGAAACAGATCTTAGGTAAATGTAGGCGAGATTAATAATGAATTTGCAAAAT 2280
QY 2281 CACTTAGAGAGCACTGAGAGCAATTAATCAACAGGTGAGAGAAATCAACGAGAGGGC 2340
Db 2281 CACTTAGAGAGCACTGAGAGCAATTAATCAACAGGTGAGAGAAATCAACGAGAGGGC 2340
QY 2341 TGTGTGAACAATGTTGTAATATGAGAGCTGCGAACTGAACTCTGACGCACTCCACAA 2400
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QY 2401 TGAATTTTCAAGTGTCACTGAGCTGTGCGACACATGATTAATCAATCAGGTTCTTAAAGTT 2460
Db 2401 TGAATTTTCAAGTGTCACTGAGCTGTGCGACACATGATTAATCAATCAGGTTCTTAAAGTT 2460
QY 2461 TAAAGTTGACATGATGATTAAGCATGCTTCTTGAAGTTTAAATATGATTAACAT 2520
Db 2461 TAAAGTTGACATGATGATTAAGCATGCTTCTTGAAGTTTAAATATGATTAACAT 2520
QY 2521 AAGTTGCAATTTGAAATCAAGATTAATCACTTCACTGCAAAAAAATTTTTTTTTT 2580
Db 2521 AAGTTGCAATTTGAAATCAAGATTAATCACTTCACTGCAAAAAAATTTTTTTTTT 2580
QY 2581 AAAAAA 2586
Db 2581 AAAAAA 2586

RESULT 2
AA92061
ID AA92061 standard; cDNA; 2586 BP.
XX
XX AA92061;
XX AC
XX DT 15-MAY-2001 (first entry)
XX DE Human PRO295 cDNA.
XX KM Human; PRO protein; mapping; ss.
XX

XX	Homo sapiens.
XX	
PN	MO200116318-A2.
XX	
PD	08-MAR-2001.
PF	
PR	24-AUG-2000; 2000OWO-US23328.
XX	
PR	01-SEP-1999; 99WO-US20111.
PR	15-SEP-1999; 99WO-US21090.
PR	07-DEC-1999; 99US-0169495.
PR	09-DEC-1999; 99US-0170262.
PR	11-JUN-2000; 2000US-0175481.
PR	18-FEB-2000; 2000WO-US04341.
PR	18-FEB-2000; 2000WO-US04342.
PR	22-FEB-2000; 2000WO-US04414.
PR	01-MAR-2000; 2000WO-US05601.
PR	03-MAR-2000; 2000US-0187202.
PR	25-APR-2000; 2000US-0199397.
PR	22-MAY-2000; 2000WO-US14042.
PR	05-JUN-2000; 2000US-0209832.
XX	
PA	(GETH) GENENTECH INC.
PI	Eaton D., Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI	Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI,
XX	
XX	WPI; 2001-183260/18.
DR	P-PDB; AAA87529.
PT	
PT	Eighty four nucleic acids encoding PRO polypeptides, useful in
XX	molecular biology, including use as hybridization probes, and in
XX	chromosome and gene mapping. -
PS	Claim 2; Fig 7; 27bp; English.
CC	
CC	The present sequence is the coding sequence for a human PRO polypeptide
CC	(secreted and transmembrane). The PRO protein, and PRO agonists, PRO
CC	antagonists or anti-PRO antibodies are useful for preparation of a
CC	medament useful in the treatment of a condition which is responsive to
CC	the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
CC	protein may also be employed as molecular weight markers for protein
CC	electrophoresis. The PRO coding sequence has applications in molecular
CC	biology, including use as hybridisation probes, and in chromosome and
CC	gene mapping.
XX	
SQ	Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;
XX	
Query Match	100.0%; Score 2586; DB 22; Length 2586;
	Best Local Similarity 100.0%; Pred. No. 0;
Matches 2586;	Conservative 0; Mismatches 0; Indels 0; Gaps 0
YY	
DY	1 CGCGGGCTCCCGCAGCCGCGGCCCGCCACCGCGCGGTCCGCATCTGCACCGCGACG 60
DB	1 CGCGCGCTCCCGCAGCCGCGGCCCGCCACCGCGGTCCGCATCTGCACCGCGACG 60
YY	
DY	61 CCGCGCGCTCCCGCGGAGGAGCAAGATCAGTCCGCGCCGCGAGCGCAACTCGGTCCA 120
DB	61 CCGCGCGCTCCCGCGGAGGAGCAAGATCAGTCCGCGCCGCGAGCGCAACTCGGTCCA 120
YY	
DY	121 GTGCGGGGCGCGGCTTCGCGGCGCAAGCGAGATGCAAGCGCTTGCGGCCAACCCTGCTG 180
DB	121 GTGCGGGGCGCGGCTTCGCGGCGCAAGCGAGATGCAAGCGCTTGCGGCCAACCCTGCTG 180
YY	
DY	181 GCCTGTGTGTGGGCGGCGGATCCCCACAGGCCCCCGCGCTCCGACGCGACCTCGG 240
DB	181 GCCTGTGTGTGGGCGGCGGATCCCCACAGGCCCCCGCGCTCCGACGCGACCTCGG 240
YY	
DY	241 CTCGACTCAAAGCCCGGCGCGCTCACATCAACCGCGAGAGAGAGCCACCTCAAGAAGA 300
DB	241 CTCGACTCAAAGCCCGGCGCGCTCACATCAACCGCGAGAGAGAGCCACCTCAAGAAGA 300
YY	
DY	301 TGTTCCGAGAGTTGAAGAACTGATGAAGACAACGACACAATAATTGCGAGCGCGGTG 360

Db	301	TGTTCCGCGAGGTTTGGAGAACTGATGAGAGACACGACGACCAATTGGCGCGGGTGG	360
Qy	361	AAAGAGATGAGGAGAGAAAGAAAGCTGCTGCTAAAGCATCATGAGAAGTGAACCTGGCAAAT	420
Db	361	AAAGAGATGAGGAGAGAAAGAAAGCTGCTGCTAAAGCATCATGAGAAGTGAACCTGGCAAAT	420
Qy	421	TACCTCCAGACTTATCACAATGAGACCAACACAGACAGGAAGTTGGAAATATATCCATCC	480
Db	421	TACCTCCAGACTTATCACAATGAGACCAACACAGACAGGAAGTTGGAAATATATCCATCC	480
Qy	481	ATCTGACACCGAGAAATTCACAAATTAACCAACACAGATGTGGACAATAGTCTTTTCAG	540
Db	481	ATCTGACACCGAGAAATTCACAAATTAACCAACACAGATGTGGACAATAGTCTTTTCAG	540
Qy	541	AGACAGTTATACATCTGTGTGGAGACGAGAAAGGACAGAAAGACCAAGTGCATCATCG	600
Db	541	AGACAGTTATACATCTGTGTGGAGACGAGAAAGGACAGAAAGACCAAGTGCATCATCG	600
Qy	601	ACAGAGACTGTGGGCCCCAGACATGTACTGCGCAGTTTGGCAGCTTCCAGTACACCTGCACG	660
Db	601	ACAGAGACTGTGGGCCCCAGACATGTACTGCGCAGTTTGGCAGCTTCCAGTACACCTGCACG	660
Qy	661	CATGCCGGGGCCAGAGAGATGCTCTGCAACCCGGGACAGTGAAGTGTGTGAGACCACTGT	720
Db	661	CATGCCGGGGCCAGAGAGATGCTCTGCAACCCGGGACAGTGAAGTGTGTGAGACCACTGT	720
Qy	721	GTGTCTGGGGTCACTGACACAAATGGCCACACGAGGACACATGGGACCATCTGTGACA	780
Db	721	GTGTCTGGGGTCACTGACACAAATGGCCACACGAGGACACATGGGACCATCTGTGACA	780
Qy	781	ACCAAGAGGAATGACCAAGCCGAGGCTGTGTGTGCTCTTCCAGAGAGGCTGTGTTCCCTG	840
Db	781	ACCAAGAGGAATGACCAAGCCGAGGCTGTGTGTGCTCTTCCAGAGAGGCTGTGTTCCCTG	840
Qy	841	TGTGACACACCCCTGCGCGGTGTGAGAGGACAGCTTTTGGCATGACCCCGCAGCCGCTTCTGG	900
Db	841	TGTGACACACCCCTGCGCGGTGTGAGAGGACAGCTTTTGGCATGACCCCGCAGCCGCTTCTGG	900
Qy	901	ACCTCATCACTGAGGAGCTAAGAGCTGTATGAGACTTTGAAACCGATGCTTTGTGECAGTG	960
Db	901	ACCTCATCACTGAGGAGCTAAGAGCTGTATGAGACTTTGAAACCGATGCTTTGTGECAGTG	960
Qy	961	GCCCTCCTCAGCCGCCCAAGCAACAGCAAGCTGTGGTATGTGTGCAACCCGACTTCCGTGG	1020
Db	961	GCCCTCCTCAGCCGCCCAAGCAACAGCAAGCTGTGGTATGTGTGCAACCCGACTTCCGTGG	1020
Qy	1021	GGAGCCCTGTACCAAGATGGGAGATCTCTGTGCCACAGAGAGTCCCGATGAGATATAG	1080
Db	1021	GGAGCCCTGTACCAAGATGGGAGATCTCTGTGCCACAGAGAGTCCCGATGAGATATAG	1080
Qy	1081	TTTGGCAGCTTCATGAGAGAGTGTGGCCAGAGACTGTGAGAGACCTTGGAGAGAGCTGTACTG	1140
Db	1081	TTTGGCAGCTTCATGAGAGAGTGTGGCCAGAGACTGTGAGAGACCTTGGAGAGAGCTGTACTG	1140
Qy	1141	AAGAGATGCGCTGTGGGAGAGCTGTGCGCTGCGCCGCTGCACTGTGAGAGGGAAGAAGA	1200
Db	1141	AAGAGATGCGCTGTGGGAGAGCTGTGCGCTGCGCCGCTGCACTGTGAGAGGGAAGAAGA	1200
Qy	1201	TTTATGATCTGAAACAGAGCTGTGGGTATATGTGCAATGAATAATGCTAATTTATTTCCCA	1260
Db	1201	TTTATGATCTGAAACAGAGCTGTGGGTATATGTGCAATGAATAATGCTAATTTATTTCCCA	1260
Qy	1261	GGTGTGTGCTTTAAGGCTGTGGCTGTGACCAAGGCTTTCTTCAATTTTCTTCCCAATTAAGT	1320
Db	1261	GGTGTGTGCTTTAAGGCTGTGGCTGTGACCAAGGCTTTCTTCAATTTTCTTCCCAATTAAGT	1320
Qy	1321	TCCCTCTGTGCTTACACAGATGAGAGTGTGTGCAATTTGTTCAGCTTCCCCAGGCTGTCT	1380
Db	1321	TCCCTCTGTGCTTACACAGATGAGAGTGTGTGCAATTTGTTCAGCTTCCCCAGGCTGTCT	1380
Qy	1381	CCAGGCTTACAGTCTGTGTGTGGAGATCAGGACGGTTAACTGACGGAACAGTTT	1440

Db 1381 CCAGGCTTACAGTCTGCTGCTGGAGAGTCAGGAGGCTTAACTGACGAGCAGTTT 1440
 QY 1441 GCCACCCCTGTCAGATTAATTTGGCTGCTTGGCTCTACACAGTTGGCAGACAGCGTTTGT 1500
 Db 1441 GCCACCCCTGTCAGATTAATTTGGCTGCTTGGCTCTACACAGTTGGCAGACAGCGTTTGT 1500
 QY 1501 TCTACATGCTTTGATTAATTTGGAGGAGAGAGTGAACAAATGTGATGCTCCCTC 1560
 Db 1501 TCTACATGCTTTGATTAATTTGGAGGAGAGAGTGAACAAATGTGATGCTCCCTC 1560
 QY 1561 TGATTTGTTTGGGAAATGTGAGAAAGATGCTGCTTGGCAAAACATCACTGGCA 1620
 Db 1561 TGATTTGTTTGGGAAATGTGAGAAAGATGCTGCTTGGCAAAACATCACTGGCA 1620
 QY 1621 AAATGCAACAAATGAATTTTCCAGCAGTTCTTTCCATGGGCATAGGTAGCTGTGCTT 1680
 Db 1621 AAATGCAACAAATGAATTTTCCAGCAGTTCTTTCCATGGGCATAGGTAGCTGTGCTT 1680
 QY 1681 CAGCTGTTGACAGATGAATGTTCTGTTCACTGATTAATGATGTTTATTCACAGCA 1740
 Db 1681 CAGCTGTTGACAGATGAATGTTCTGTTCACTGATTAATGATGTTTATTCACAGCA 1740
 QY 1741 GTGTTGCTCAGCTCTTACCTCTGTCGCAAGGAGCATTTCATATCCAGATCAATTCCT 1800
 Db 1741 GTGTTGCTCAGCTCTTACCTCTGTCGCAAGGAGCATTTCATATCCAGATCAATTCCT 1800
 QY 1801 TCTCTCAGCAGAGCTGGGAGGAGGAGTCTGTTCTCTGCTGCATCAGGATCTCAGAG 1860
 Db 1801 TCTCTCAGCAGAGCTGGGAGGAGGAGTCTGTTCTCTGCTGCATCAGGATCTCAGAG 1860
 QY 1861 GCTCAGAGACTGCAAGCTGCTTCCCAAGTCAACAGCTAGTGAAGACAGAGAGTTTC 1920
 Db 1861 GCTCAGAGACTGCAAGCTGCTTCCCAAGTCAACAGCTAGTGAAGACAGAGAGTTTC 1920
 QY 1921 ATCTGTTGATGACTCTAAGCTCAGTGTCTCTCCAGTACCCACACAGGCTTGTGCA 1980
 Db 1921 ATCTGTTGATGACTCTAAGCTCAGTGTCTCTCCAGTACCCACACAGGCTTGTGCA 1980
 QY 1981 CCAAAAGTCTCCCAAAAGAGAGAGATGGATTTTCTTGAAGCATGCATCTGGA 2040
 Db 1981 CCAAAAGTCTCCCAAAAGAGAGAGATGGATTTTCTTGAAGCATGCATCTGGA 2040
 QY 2041 ATTAAGGCAACTAATTTCTACATCCCTCTAAAGTAACTCTGTTAGAAACAGAGT 2100
 Db 2041 ATTAAGGCAACTAATTTCTACATCCCTCTAAAGTAACTCTGTTAGAAACAGAGT 2100
 QY 2101 GTTCTCAGAGTGTGGGAGGAGCGCTCTCTAATGAGAAACATGATTTGACACTGTCC 2160
 Db 2101 GTTCTCAGAGTGTGGGAGGAGCGCTCTCTAATGAGAAACATGATTTGACACTGTCC 2160
 QY 2161 CTTTGGCAGTGTGATTAATTTGAAAGTAAATGATGAGGTGATGATGATGATTA 2220
 Db 2161 CTTTGGCAGTGTGATTAATTTGAAAGTAAATGATGAGGTGATGATGATGATTA 2220
 QY 2221 CTTGCGCAGTGTGATTAATTTGAAAGTAAATGATGAGGTGATGATGATGATTA 2280
 Db 2221 CTTGCGCAGTGTGATTAATTTGAAAGTAAATGATGAGGTGATGATGATGATTA 2280
 QY 2281 CACTTAGAGCACTGAAGACAAATTAATCAACAGTGAAGAAATCAACCGAGCGGC 2340
 Db 2281 CACTTAGAGCACTGAAGACAAATTAATCAACAGTGAAGAAATCAACCGAGCGGC 2340
 QY 2341 TGTGTAAGCACTGTTGATTAATGCACTGCAAGTGAATCTAGCCACTCCACAA 2400
 Db 2341 TGTGTAAGCACTGTTGATTAATGCACTGCAAGTGAATCTAGCCACTCCACAA 2400
 QY 2401 TGAATGTTTCAAGGTGATGATGAGTGTGCAACCATGATTCATCAAGTCTTTAAAGT 2460
 Db 2401 TGAATGTTTCAAGGTGATGATGAGTGTGCAACCATGATTCATCAAGTCTTTAAAGT 2460
 QY 2461 TAAAGTTCATATGATTAATGATGATGATGATGATGATGATGATGATGATGAT 2520
 Db 2461 TAAAGTTCATATGATTAATGATGATGATGATGATGATGATGATGATGATGAT 2520

QY 2521 AAGTTGATTTAGAAATCAACATTAATCACTCACTGCAAAAAA 2580
 Db 2521 AAGTTGATTTAGAAATCAACATTAATCACTCACTGCAAAAAA 2580
 QY 2581 AAAAAA 2586
 Db 2581 AAAAAA 2586
 RESULT 3
 AAF72413
 ID AAF72413 standard; CDNA; 2586 BP.
 XX
 AC AAF72413;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Human PRO295 CDNA.
 XX
 KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
 KW antiparkinsonian neurotropic; neuroprotective; vulnerary; cardiant;
 KW antiangiogenic; vasotropic; antiaesthetic; antineumatic; cancer;
 KW antiautistic; antinfertility; antidiabetic; antiviral; diabetes;
 KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
 KW ischaemia; inflammation; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200104311-A1.
 XX
 PD 18-JAN-2001.
 XX
 PF 22-FEB-2000; 2000MO-US04414.
 XX
 PR 07-JUL-1999; 99US-0143048.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146222.
 PR 08-SEP-1999; 99MO-US20594.
 PR 13-SEP-1999; 99MO-US20944.
 PR 15-SEP-1999; 99MO-US21090.
 PR 15-SEP-1999; 99MO-US21547.
 PR 05-OCT-1999; 99MO-US23089.
 PR 29-NOV-1999; 99MO-US28214.
 PR 30-NOV-1999; 99MO-US28313.
 PR 16-DEC-1999; 99MO-US30095.
 PR 20-DEC-1999; 99MO-US30911.
 PR 20-DEC-1999; 99MO-US30999.
 PR 05-JAN-2000; 99MO-US00219.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Botstein D, Desnoyers J, Eaton DL, Ferrara N,
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
 PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kijavits IJ,
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D,
 PI Williams PM, Wood WT;
 XX
 DR MPI, 2001-081051/09.
 DR F-PSDB; AAB80252.
 XX
 PT Sixty one nucleic acids encoding PRO polypeptides which are useful in
 PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung
 PT squamous cell carcinoma) and neurodegenerative diseases (e.g.
 PT Alzheimer's disease) -
 XX
 PS Claim 2, Fig 83; 393pp; English.
 XX
 CC The present sequence is one of sixty one nucleic acids encoding novel
 CC secreted and transmembrane PRO polypeptides. The PRO polypeptides are
 CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung
 CC squamous cell carcinoma), gastrointestinal disorders (e.g.
 CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,

QY 1981 CCAAAAGTGTCCCAAAAGAGAGAGATGATTTTCTTGAGCATGACATCTGGA 2040
 DB 1981 CCAAAAGTGTCCCAAAAGAGAGAGATGAGATTTTCTTGAGCATGACATCTGGA 2040
 QY 2041 ATTAAAGTCAAACTAATTTCTCAATCCCTCTAAAGTAACTCTGTTGGAACACACAT 2100
 DB 2041 ATTAAAGTCAAACTAATTTCTCAATCCCTCTAAAGTAACTCTGTTGGAACACACAT 2100
 QY 2101 GTTCTCAAGTGTGGGAGCCGCTCTTATGAGAACATGATATTGACATGTCCT 2160
 DB 2101 GTTCTCAAGTGTGGGAGCCGCTCTTATGAGAACATGATATTGACATGTCCT 2160
 QY 2161 CTTTGAGCATGTCATTGTAATCTTGAAGATATATACCTGACCGTGCATACAGTTAA 2220
 DB 2161 CTTTGAGCATGTCATTGTAATCTTGAAGATATATACCTGACCGTGCATACAGTTAA 2220
 QY 2221 CCTGAGAGAACAGTACTAGTATGTTAGGCGAGGATATATAATGAAATTTGCAAAAT 2280
 DB 2221 CCTGAGAGAACAGTACTAGTATGTTAGGCGAGGATATATAATGAAATTTGCAAAAT 2280
 QY 2281 CACTTACAGCACTGAAAGACATTTATCAACACGTGGAAGAAATCAACCGACGCGC 2340
 DB 2281 CACTTACAGCACTGAAAGACATTTATCAACACGTGGAAGAAATCAACCGACGCGC 2340
 QY 2341 TGTGTGAAACATGTTGTAATATATGCGACTGCGAACACTGAACCTCTACGCCATCCACAA 2400
 DB 2341 TGTGTGAAACATGTTGTAATATATGCGACTGCGAACACTGAACCTCTACGCCATCCACAA 2400
 QY 2401 TGATGTTTTCAGTGTGCATGAGCATGTTGCCACATGATTCATCCAGATTTCTTAAAGTT 2460
 DB 2401 TGATGTTTTCAGTGTGCATGAGCATGTTGCCACATGATTCATCCAGATTTCTTAAAGTT 2460
 QY 2461 TAAAGTTCACATGATTTGTAATATGAGCATGCTTCTTGAAGTTTAAATTAATGTAACAAT 2520
 DB 2461 TAAAGTTCACATGATTTGTAATATGAGCATGCTTCTTGAAGTTTAAATTAATGTAACAAT 2520
 QY 2521 AAGTTGCATTAGAAATCAAGCATTAATCACTTCACTGCAAAAAA 2580
 DB 2521 AAGTTGCATTAGAAATCAAGCATTAATCACTTCACTGCAAAAAA 2580
 QY 2581 AAAAAA 2586
 DB 2581 AAAAAA 2586

RESULT 4
 ID ABS74381 standard; cDNA; 2586 BP.
 XX ABS74381;

AC ABS74381;
 DT 10-DEC-2002 (first entry)
 DE Human cDNA encoding secreted/transmembrane protein PRO295.
 XX
 KW Human; ss; gene; secreted protein; transmembrane protein; antirheumatic;
 KW antiarthritic; osteopathic; sports-related joint problem;
 KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN US2002119130-A1.
 PD 29-AUG-2002.
 PF 06-DEC-2001; 2001US-0006867.
 PR 29-OCT-1997; 97US-063435P.
 PR 29-OCT-1997; 97US-064215P.
 PR 22-APR-1998; 98US-082797P.
 PR 29-APR-1998; 98US-083495P.
 PR 15-MAY-1998; 98US-083579P.
 PR 10-JUN-1998; 98US-088811P.

PR 10-JUN-1998; 98US-088824P.
 PR 10-JUN-1998; 98US-088825P.
 PR 11-JUN-1998; 98US-088863P.
 PR 12-JUN-1998; 98US-089105P.
 PR 16-JUN-1998; 98US-089514P.
 PR 16-SEP-1998; 98WO-US19310.
 PR 08-MAR-1999; 98WO-US05028.
 PR 14-MAY-1999; 98WO-US10733.
 PR 02-JUN-1999; 98WO-US12252.
 PR 01-SEP-1999; 98WO-US20111.
 PR 15-SEP-1999; 98WO-US21090.
 PR 15-SEP-1999; 98WO-US21194.
 PR 22-DEC-1999; 98WO-US30720.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32378.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 XX
 XX (GENENTECH INC.
 XX Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 XX Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 DR MPI: 2002-731348/79.
 DR P-PSDB; ABG95854.
 XX
 XX New isolated secreted and transmembrane PRO polypeptide useful for
 PT modulating biological activity of a cell, or for treating
 PT sports-related joint problems, osteoarthritis or rheumatoid arthritis
 XX
 PS Claim 2: Fig 7; 399pp; English.
 CC The invention relates to an isolated secreted and transmembrane PRO
 CC polypeptide having 80 or fewer associated signal peptide, or a sequence of
 CC as ABG95851-ABG95934 or their associated signal peptide, or a sequence of
 CC an extracellular domain of the proteins with their associated signal
 CC peptide or lacking its associated signal peptide. Also included are
 CC the nucleic acids encoding the proteins, vectors, host cells,
 CC fusion proteins and antibodies which specifically bind to the proteins.
 CC The proteins are useful for detecting a polypeptide designated as A, B, C
 CC or D in a sample suspected of containing an A, B, C or D polypeptide,
 CC by contacting the sample with a polypeptide designated as E, F, G, H or
 CC I (or vice versa) and determining the formation of a A/E, B/F, B/G, C/H
 CC or D/I polypeptide conjugate in the sample, where the formation of the
 CC conjugate is indicative of the presence of an A, B, C or D polypeptide
 CC in the sample, where A is a PRO10272 polypeptide, B is a PRO20110
 CC polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide,
 CC E is a PRO5801 polypeptide, F is a PRO1 polypeptide, G is a PRO20040
 CC polypeptide, H is a PRO20233 polypeptide and I is a PRO1990
 CC polypeptide. The sample comprises a cell suspected of expressing the A,
 CC B, C or D polypeptide. The A, B, F, G, H or I polypeptide is labeled with
 CC a detectable label or is attached to a solid support. The proteins are
 CC useful for linking a bioactive molecule to a cell expressing a
 CC polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive
 CC molecule is a toxin, a radiolabel or an antibody. The bioactive molecule
 CC causes death of the cell A, B, C, D, E, F, G, H, or I, or antibodies
 CC against them are useful for modulating a biological activity of a cell
 CC expressing a polypeptide designated as A, B, C or D or E, F, G, H, or
 CC I. The cell is killed. The proteins are useful for identifying
 CC agonists or antagonists, for the preparation of a medicament useful in
 CC the treatment of a condition which is responsive to the proteins, as
 CC molecular weight markers for protein electrophoresis purposes, and as
 CC therapeutic agents for treating sports-related joint problems,


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Db 1921 ACTGTTGTGACTCTTAAGCTAGTCTCTCTCCACTACCCACACAGCCTGGTGCA 1980
Qy 1981 CCAAAAGTCTCTCCCAAGAGAGAGATGGATTTTCTTGAGGAGTGCACATCTGGA 2040
Db 1981 CCAAAAGTCTCTCCCAAGAGAGAGATGGATTTTCTTGAGGAGTGCACATCTGGA 2040
Qy 2041 ATTAAGTCAAACTAATCTCAATCCCTCTAAAGTAATCTGTTAGAACAGCAGT 2100
Db 2041 ATTAAGTCAAACTAATCTCAATCCCTCTAAAGTAATCTGTTAGAACAGCAGT 2100
Qy 2101 GTTCTCAAGTGTGGGCGAGCCCTCTTCTAATGAGAAATGATTAACAGTCTCCCT 2160
Db 2101 GTTCTCAAGTGTGGGCGAGCCCTCTTCTAATGAGAAATGATTAACAGTCTCCCT 2160
Qy 2161 CTTTGACAGTGTGATTAAGTAAAGTAAATGATTAAGTAAATGATTAAGTAAAT 2220
Db 2161 CTTTGACAGTGTGATTAAGTAAAGTAAATGATTAAGTAAATGATTAAGTAAAT 2220
Qy 2221 CTTGACAGAAAGTACTAGTAAATGATTAAGTAAATGATTAAGTAAATGATTA 2280
Db 2221 CTTGACAGAAAGTACTAGTAAATGATTAAGTAAATGATTAAGTAAATGATTA 2280
Qy 2281 CACTTACAGCACTGAGCAATTAATCAACAGTGAAGAAATCAACAGCAAGGCGC 2340
Db 2281 CACTTACAGCACTGAGCAATTAATCAACAGTGAAGAAATCAACAGCAAGGCGC 2340
Qy 2341 TGTGTGAACATGTTGTAATATGCGACTGCGAAGCTCTGCGCATCCCAAA 2400
Db 2341 TGTGTGAACATGTTGTAATATGCGACTGCGAAGCTCTGCGCATCCCAAA 2400
Qy 2401 TGAATGTTTGAAGTGTGATGATGAGTGTGAGTGTGAGTGTGAGTGTGAGT 2460
Db 2401 TGAATGTTTGAAGTGTGATGATGAGTGTGAGTGTGAGTGTGAGTGTGAGT 2460
Qy 2461 TAAAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520
Db 2461 TAAAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520
Qy 2521 AAGTGCATTTAGAAATCAAGCAATTAATCACTCACTGCAAAAAA 2580
Db 2521 AAGTGCATTTAGAAATCAAGCAATTAATCACTCACTGCAAAAAA 2580
Qy 2581 AAAAAA 2586
Db 2581 AAAAAA 2586

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PR 25-JUL-2000; 2000US-220664P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-0643657.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 07-SEP-2000; 2000US-230978P.
PR 15-SEP-2000; 2000US-000000P.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-0709238.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 01-JUN-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
PR 28-JUN-2001; 2001WO-US19692.
PR 28-JUN-2001; 2001WO-US00000.
XX (GETH ) GENENTECH INC.
PA (BAKE/) BAKER K F.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANC/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
XX Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI: 2002-171999/22.
XX P-PSDB; ABB95447.
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX infarction), endothelial or angiogenic disorders in a mammal -
XX Claim 1; Fig 49; 567pp; English.
XX The present invention provides the protein and coding sequences of human
XX PRO proteins. These are useful for treating or diagnosing a
XX cardiovascular, endothelial or angiogenic disorder, including cardiac
XX hypertrophy, trauma, cancer, age-related macular degeneration,
XX atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
XX angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumor
XX angiogenesis (such as breast carcinoma and liver carcinoma) and wound

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CC healing. The present sequence is a coding sequence of the invention.

XX Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;

Query Match 100.0%; Score 2586; DB 24; Length 2586;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CGCCGGGCTCCGCGACCCGCGGCCCGCCACCGCGCGCTCCCGCATCTGCAACCCGAC 60
DB 1 CGCCGGGCTCCGCGACCCGCGGCCCGCCACCGCGCGCTCCCGCATCTGCAACCCGAC 60
QY 61 CCGCGCGCTCCCGCGCGGAGCAGACAGATCCAGTCCGCGCGCGACGCGCACTCGTCA 120
DB 61 CCGCGCGCTCCCGCGCGGAGCAGACAGATCCAGTCCGCGCGCGACGCGCACTCGTCA 120
QY 121 GTGCGGGCGCGGCTGTGGGCGGACAGACGAGATGACAGCGCTTGGGGCCACCTGCTGT 180
DB 121 GTGCGGGCGCGGCTGTGGGCGGACAGACGAGATGACAGCGCTTGGGGCCACCTGCTGT 180
QY 181 GCCTGCTGTGGGCGGCGGCTCCCAACGCGCCCGCGCGCTCCGACGCGGACCTCGG 240
DB 181 GCCTGCTGTGGGCGGCGGCTCCCAACGCGCCCGCGCGCTCCGACGCGGACCTCGG 240
QY 241 CTCGAGTCAGACCCCGCGCGCTTCACTCACTCCGACGAGAGGCGCACTTCAATGAGA 300
DB 241 CTCGAGTCAGACCCCGCGCGCTTCACTCACTCCGACGAGAGGCGCACTTCAATGAGA 300
QY 301 TGTTCGCGAGGTGAGGAATGATGAGAGCAACGACGCAAAATTCGAGAGCGGCTGG 360
DB 301 TGTTCGCGAGGTGAGGAATGATGAGAGCAACGACGCAAAATTCGAGAGCGGCTGG 360
QY 361 AAGAGATGAGGAGAAAGACTGCTGCTTAAGCATCATGAAATGAACTTGGCAAATCT 420
DB 361 AAGAGATGAGGAGAAAGACTGCTGCTTAAGCATCATGAAATGAACTTGGCAAATCT 420
QY 421 TACCTCCGAGTATCAATGAGACCAACGACGACGAGGTTGGAAATATATACATCC 480
DB 421 TACCTCCGAGTATCAATGAGACCAACGACGACGAGGTTGGAAATATATACATCC 480
QY 481 ATGTGACCGAGAAATTCACAGATTAACAAACAACGACTGAGCAAAATGTCTTTTCA 540
DB 481 ATGTGACCGAGAAATTCACAGATTAACAAACAACGACTGAGCAAAATGTCTTTTCA 540
QY 541 AGACAGTTATCAATCTGTGGAGACGAAAGAGGCAAGAGCCAGAGTGCATATCG 600
DB 541 AGACAGTTATCAATCTGTGGAGACGAAAGAGGCAAGAGCCAGAGTGCATATCG 600
QY 601 ACGAGGACTGTGGGCCAGAGATGTACTGCAAGTTTGCAGCTTCCAGTACACTGCGACG 660
DB 601 ACGAGGACTGTGGGCCAGAGATGTACTGCAAGTTTGCAGCTTCCAGTACACTGCGACG 660
QY 661 CATCCCGGGGCGCAGAGATGTCTGCAACCCGGGACAGTGAATGTCTGTGGAGACAAGTGT 720
DB 661 CATCCCGGGGCGCAGAGATGTCTGCAACCCGGGACAGTGAATGTCTGTGGAGACAAGTGT 720
QY 721 GTGTCTGGGGTCACTGACCAAAATGCGCAACAGGGGCAAGATGGAGCAATCTGTGACA 780
DB 721 GTGTCTGGGGTCACTGACCAAAATGCGCAACAGGGGCAAGATGGAGCAATCTGTGACA 780
QY 781 ACGAGAGGACTGTGCGAGCGGGGCTGTGCTGTGCTTCCAGAGAGGCTGTCTGTCCCTG 840
DB 781 ACGAGAGGACTGTGCGAGCGGGGCTGTGCTGTGCTTCCAGAGAGGCTGTCTGTCCCTG 840
QY 841 TGTGACACACCCCTGCGCGGAGGAGGCTTTCAGTGAACCCGCGACGCGGTTTGG 900
DB 841 TGTGACACACCCCTGCGCGGAGGAGGCTTTCAGTGAACCCGCGACGCGGTTTGG 900
QY 901 ACCTCATCACTGTGAGCTTAGAGCTTGAATGAGAGCTTGTGACCGATGCTTGTGCGCAGTG 960
DB 901 ACCTCATCACTGTGAGCTTAGAGCTTGAATGAGAGCTTGTGACCGATGCTTGTGCGCAGTG 960
QY 961 GCCTCCTGTGCGAGGCCACAGCAAGCCTGTGTATGTGTGAAAGCCGACCTTCGTGG 1020
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DB 961 GCCTCCTGTGCGAGGCCACAGCAAGCCTGTGTATGTGTGAAAGCCGACCTTCGTGG 1020
QY 1021 GGAACCGTGAACCAAGATGGGAGAGATCTCTGCTGCCAAGAGAGTCCCGATGATGATGAG 1080
DB 1021 GGAACCGTGAACCAAGATGGGAGAGATCTCTGCTGCCAAGAGAGTCCCGATGATGATGAG 1080
QY 1081 TTGGCAGCTTCATGAGAGAGGTGCGCCAGAGAGCTGAGAGACCTGAGAGAGAGCTGACTG 1140
DB 1081 TTGGCAGCTTCATGAGAGAGGTGCGCCAGAGAGCTGAGAGACCTGAGAGAGAGCTGACTG 1140
QY 1141 AAGAGATGCGCTGGGAGAGCTGCGGCTGCGCGCTGCACTGCTGGAGGGGAGAGA 1200
DB 1141 AAGAGATGCGCTGGGAGAGCTGCGGCTGCGCGCTGCACTGCTGGAGGGGAGAGA 1200
QY 1201 TTTAGATGTGACCAAGCTGTGGTGAATGTGCAATAGAAATATTAATTTTCCCA 1260
DB 1201 TTTAGATGTGACCAAGCTGTGGTGAATGTGCAATAGAAATATTAATTTTCCCA 1260
QY 1261 GGTGTGTCTTTAGCGGTGGCTGACAGGCTTCTTCTACATCTTCTCCAGTAAGT 1320
DB 1261 GGTGTGTCTTTAGCGGTGGCTGACAGGCTTCTTCTACATCTTCTCCAGTAAGT 1320
QY 1321 TCCCTCTGCTTGAACAGCATGAGGTGTGACATTTGTCAGCTCCCGCAGGCTGTCT 1380
DB 1321 TCCCTCTGCTTGAACAGCATGAGGTGTGACATTTGTCAGCTCCCGCAGGCTGTCT 1380
QY 1381 CCAGGCTTCAAGTGTGTGGAGAGTGCAGGCAAGGTTAAATGACAGAGACAGTT 1440
DB 1381 CCAGGCTTCAAGTGTGTGGAGAGTGCAGGCAAGGTTAAATGACAGAGACAGTT 1440
QY 1441 GCGACCCCTGTCAGATATATGAGCTTGTGCTCTACAGTGTGGCAGACAGCGTGTGT 1500
DB 1441 GCGACCCCTGTCAGATATATGAGCTTGTGCTCTACAGTGTGGCAGACAGCGTGTGT 1500
QY 1501 TCTACATGCTTTGATTAATTTGTTGAGGGGAGAGATGAAACAATGTGAGTCTCCCTC 1560
DB 1501 TCTACATGCTTTGATTAATTTGTTGAGGGGAGAGATGAAACAATGTGAGTCTCCCTC 1560
QY 1561 TGATGTGTTTGGGAAATGTGAGAGAGTGCCTGCTTGGCAACATCAACTGGGA 1620
DB 1561 TGATGTGTTTGGGAAATGTGAGAGAGTGCCTGCTTGGCAACATCAACTGGGA 1620
QY 1621 AAATGCAAAATGAATTTTCCAGGAGTCTTTCATGAGGCAATGATGATGCTGTGCTT 1680
DB 1621 AAATGCAAAATGAATTTTCCAGGAGTCTTTCATGAGGCAATGATGATGATGCTGTGCTT 1680
QY 1681 CAGCTGTGCAATGAATGTTCTGTTTCAACCTGCAATACATGTGTTATTCATCAGACA 1740
DB 1681 CAGCTGTGCAATGAATGTTCTGTTTCAACCTGCAATACATGTGTTATTCATCAGACA 1740
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QY 1801 TCTCTCAGACAGCTTGGGAGGGGATGATGTCTCTCTGTTCAATGAGATCTCAGAG 1860
DB 1801 TCTCTCAGACAGCTTGGGAGGGGATGATGTCTCTCTGTTCAATGAGATCTCAGAG 1860
QY 1861 GCTCAGAGACTGAGAGCTTGGCCAGAGTCAACAGGTAATGAGAGACAGAGCAGTTTC 1920
DB 1861 GCTCAGAGACTGAGAGCTTGGCCAGAGTCAACAGGTAATGAGAGACAGAGCAGTTTC 1920
QY 1921 ATCTGATGTGACTTAAAGTCACTGTCTCTCACTACCCCAACAGCTTGTGTGCA 1980
DB 1921 ATCTGATGTGACTTAAAGTCACTGTCTCTCACTACCCCAACAGCTTGTGTGCA 1980
QY 1981 CCAAAAGTCTCCCAAAAGAGAGAGATGGGATTTTCTTGAAGCATGCACTGTGA 2040
DB 1981 CCAAAAGTCTCCCAAAAGAGAGAGATGGGATTTTCTTGAAGCATGCACTGTGA 2040
QY 2041 ATTAAGTCAAATTAATTCATATCCCTTAATAAGTAACTACTGTTAGAAAGCAGCT 2100
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Db      2041 ATTAAGTCAAACTAATCTCATACCTCTTAAAGTAATCTGTTAGSAGACGACT 2100
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Db      2101 GTTCTCAGAGTGTGGGGAGCGGCTCTTATAGAGCAATGATATTGACATGTCCT 2160
QY      2161 CTTTGGCAGTTGCACTTAGTAATCTTGAAGGATATGCTAGGCTACATACAGGTTAA 2220
Db      2161 CTTTGGCAGTTGCACTTAGTAATCTTGAAGGATATGCTAGGCTACATACAGGTTAA 2220
QY      2221 CCGTGAAGAAACAGTACTTAGTAAATGTAGAGGCGAGATATTAATGAATTTGCAAAAT 2280
Db      2221 CCGTGAAGAAACAGTACTTAGTAAATGTAGAGGCGAGATATTAATGAATTTGCAAAAT 2280
QY      2281 CACTTGAAGCACTGTAAGCAATTAATCAACCACTGGAGAAATCAACGAGAGGGGC 2340
Db      2281 CACTTGAAGCACTGTAAGCAATTAATCAACCACTGGAGAAATCAACGAGAGGGGC 2340
QY      2341 TGTGTGAACATGTTGTATATGCGACTGCGAACACTGAACCTTACGCCACTCCACAA 2400
Db      2341 TGTGTGAACATGTTGTATATGCGACTGCGAACACTGAACCTTACGCCACTCCACAA 2400
QY      2401 TGAATGTTTCAAGGTGATGACCTGTGCGACCATGATATTCACAGGTTCTTAAATT 2460
Db      2401 TGAATGTTTCAAGGTGATGACCTGTGCGACCATGATATTCACAGGTTCTTAAATT 2460
QY      2461 TAAAGTTGACATGATGTTATAGACATGCTTCTTGAAGTTTAAATATGATTAACAT 2520
Db      2461 TAAAGTTGACATGATGTTATAGACATGCTTCTTGAAGTTTAAATATGATTAACAT 2520
QY      2521 AAGTTGCATTAGAAATCAAGCATTAATCACTTCAACCTGCAAAAAA 2580
Db      2521 AAGTTGCATTAGAAATCAAGCATTAATCACTTCAACCTGCAAAAAA 2580
QY      2581 AAAAAA 2586
Db      2581 AAAAAA 2586

RESULT 6
ABL88096
ID      ABL88096 standard; cDNA; 2586 BP.
AC      ABL88096;
DT      16-MAY-2002 (first entry)
DE      Human PRO295 cDNA sequence SEQ ID NO:49.
XX      Human; angiogenesis; cardiac; cytostatic; antiangiogenic; hypotensive;
XX      Humoral; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
XX      gene therapy; cardiovascular disorder; endothelial disorder; cancer;
XX      angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
XX      age-related macular degeneration; arterial restenosis; angina;
XX      rheumatoid arthritis; myocardial infarction; thrombophlebitis;
XX      lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
XX      wound healing; chromosome mapping; gene mapping; gene; ss.
XX      Homo sapiens.
XX      OS
XX      PN
XX      WO200200690-A2.
XX      PD
XX      03-JAN-2002.
XX      PF
XX      20-JUN-2001; 2001MO-US19692.
XX      PR
XX      23-JUN-2000; 2000US-213637P.
XX      PR
XX      20-JUL-2000; 2000US-219556P.
XX      PR
XX      25-JUL-2000; 2000US-220624P.
XX      PR
XX      25-JUL-2000; 2000US-220664P.
XX      PR
XX      28-JUL-2000; 2000MO-US20710.
XX      PR
XX      02-AUG-2000; 2000US-222695P.
XX      PR
XX      17-AUG-2000; 2000US-0643657.

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PR      23-AUG-2000; 2000MO-US23522.
PR      24-AUG-2000; 2000MO-US23328.
PR      07-SEP-2000; 2000US-230978P.
PR      18-SEP-2000; 2000US-0664610.
PR      18-SEP-2000; 2000US-0665350.
PR      24-OCT-2000; 2000US-242922P.
PR      08-NOV-2000; 2000US-0709238.
PR      08-NOV-2000; 2000MO-US30952.
PR      10-NOV-2000; 2000MO-US30873.
PR      01-DEC-2000; 2000MO-US32678.
PR      20-DEC-2000; 2000US-07447259.
PR      20-DEC-2000; 2000MO-US34956.
PR      22-JAN-2001; 2001US-0767609.
PR      28-FEB-2001; 2001US-0796498.
PR      28-FEB-2001; 2001MO-US06520.
PR      01-MAR-2001; 2001MO-US06666.
PR      09-MAR-2001; 2001US-0802706.
PR      14-MAR-2001; 2001US-0808689.
PR      22-MAR-2001; 2001US-0816744.
PR      05-APR-2001; 2001US-0828366.
PR      10-MAY-2001; 2001US-0854208.
PR      10-MAY-2001; 2001US-0854280.
PR      25-MAY-2001; 2001US-0866028.
PR      25-MAY-2001; 2001US-0866034.
PR      25-MAY-2001; 2001MO-US17092.
PR      30-MAY-2001; 2001US-0870574.
PR      30-MAY-2001; 2001MO-US17443.
PR      01-JUN-2001; 2001MO-US17800.

PA      (GETH ) GENENTECH INC.
PI      Baker KP, Ferrara N, Gerber H, Gertlson ME, Goddard A,
PI      Godowski PJ, Guirney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
PI      Stephen JF, Watanabe CK, Williams PM, Wood WI, Ye M,
XX      WPI: 2002-090516/12.
XX      P-PSDB; ABB84841.
XX      DR
XX      One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX      useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX      infarction), endothelial or angiogenic disorders in a mammal -
XX      Claim 2; Fig 49; 565pp; English.
XX      ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
XX      ABB85003. The PRO proteins and polynucleotides have cardiac, cytostatic,
XX      antiangiogenic, hypotensive, vulnery and antiarteriosclerotic
XX      activities, and can be used in gene therapy. The PRO polynucleotides,
XX      proteins, agonists and antagonists are useful for treating or diagnosing
XX      a cardiovascular, endothelial or angiogenic disorder in a mammal,
XX      e.g. cardiac hypertrophy, trauma, cancer, age-related macular
XX      degeneration, atherosclerosis, hypertension, arterial restenosis,
XX      rheumatoid arthritis, angina, myocardial infarction, thrombophlebitis,
XX      lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
XX      carcinoma), and wound healing. The PRO polynucleotides have applications
XX      in molecular biology, including use as hybridisation probes, and in
XX      chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
XX      probes used in the exemplification of the present invention.
XX      Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;
XX      SO

Query Match      100.0%; Score 2586; DB 24; Length 2586;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 CGCCGCGCTCCCGGACCGCGCGCCCGCCACCGCGCGCTCCGCACTGTGACCCGCGAC 60
Db      1 CGCCGCGCTCCCGGACCGCGCGCCCGCCACCGCGCGCTCCGCACTGTGACCCGCGAC 60
QY      61 CCGGCGGCTCCCGGCGGAGCGAGCATATCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Db      61 CCGGCGGCTCCCGGCGGAGCGAGCATATCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120

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121 GTGCGGGGCGGCGCTGCGGGGCGAGCGGAGTGCAGCGGCTTGCGGGCCACCCTGCTGT 180
Db 121 GTGCGGGGCGGCGCTGCGGGGCGAGCGGAGTGCAGCGGCTTGCGGGCCACCCTGCTGT 180
QY 181 GCCTGCTGTGGCGGCGGCGGCTCCCACGGCGCCCGCGCTCCGACGCGACCTCTCGG 240
Db 181 GCCTGCTGTGGCGGCGGCGGCTCCCACGGCGCCCGCGCTCCGACGCGACCTCTCGG 240
QY 241 CTCGAGTCAAGCCCGGCGCGCTCTCAGCTTACCCGAGGAGAGCCACCTCAATAGA 300
Db 241 CTCGAGTCAAGCCCGGCGCGCTCTCAGCTTACCCGAGGAGAGCCACCTCAATAGA 300
QY 301 TGTTCGCGAGGTTGAGGAATGAGAGACGACGACCAAAATTGCGACGCGGCTGTG 360
Db 301 TGTTCGCGAGGTTGAGGAATGAGAGACGACGACCAAAATTGCGACGCGGCTGTG 360
QY 361 AAGAGATGAGAGCGAGAAAGCTGTGTAAGATCATGCAAGATGACCTGCGCAACT 420
Db 361 AAGAGATGAGAGCGAGAAAGCTGTGTAAGATCATGCAAGATGACCTGCGCAACT 420
QY 421 TACCTCCAGCTATCACAATGAGACCAACACAGACGAGGTTGAAATATATATCATCC 480
Db 421 TACCTCCAGCTATCACAATGAGACCAACACAGACGAGGTTGAAATATATATCATCC 480
QY 481 ATGTGCAACCGAGAAATTCAGAAAGTAACTAACCAACACAGACTGAGCAAAATGCTTTTCAG 540
Db 481 ATGTGCAACCGAGAAATTCAGAAAGTAACTAACCAACACAGACTGAGCAAAATGCTTTTCAG 540
QY 541 AGACAGTTATACATCTGTGGAGAGCAAGAAAGGAGAGAGACGACGAGTGCATCATCG 600
Db 541 AGACAGTTATACATCTGTGGAGAGCAAGAAAGGAGAGAGACGAGTGCATCATCG 600
QY 601 AGAGAGACTGTGCGGCCAGAGATGTACTGCAATTTGCGAGCTTCCAGTACACTGCGCAGC 660
Db 601 AGAGAGACTGTGCGGCCAGAGATGTACTGCAATTTGCGAGCTTCCAGTACACTGCGCAGC 660
QY 661 CATGCGCGGGGCGAGAGATGCTGTGACCCGCGGACAGTGAAGTGTGAGAACAGCTGT 720
Db 661 CATGCGCGGGGCGAGAGATGCTGTGACCCGCGGACAGTGAAGTGTGAGAACAGCTGT 720
QY 721 GTGTCTGGGGTCACTGCACCAAAATGCGCACCGGGGCGAGATGAGAACATCTGTGACA 780
Db 721 GTGTCTGGGGTCACTGCACCAAAATGCGCACCGGGGCGAGATGAGAACATCTGTGACA 780
QY 781 ACCAGAGGAGCTGCGAGCGCGGGGCTGTGCTTCCAGAGAGGCTGTGCTTCCCTG 840
Db 781 ACCAGAGGAGCTGCGAGCGCGGGGCTGTGCTTCCAGAGAGGCTGTGCTTCCCTG 840
QY 841 TGTGCAACCCCTGCGCGGTGAGGGCGAGCTTTGCAATGACCCCGCAGCGGCTTCTGG 900
Db 841 TGTGCAACCCCTGCGCGGTGAGGGCGAGCTTTGCAATGACCCCGCAGCGGCTTCTGG 900
QY 901 ACCTCATCACTGTGGAGCTTAAGGCTTAAGAGGCTTGAACCGAGCTTGTGCAATG 960
Db 901 ACCTCATCACTGTGGAGCTTAAGGCTTAAGAGGCTTGAACCGAGCTTGTGCAATG 960
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QY 1021 GGAAGCCGTATCCAAAGATGGGAGATCTGTCTGTCCAGAGAGGTCCCGATGATGATGAG 1080
Db 1021 GGAAGCCGTATCCAAAGATGGGAGATCTGTCTGTCCAGAGAGGTCCCGATGATGATGAG 1080
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Db 1081 TTGGGAGCTTCAATGAGAGAGTGTGCGCAAGAGCTGGAAGACCTGGAAGCTGACTG 1140
QY 1141 AAGAGATGCGCTGTGGGAGAGCTGTGCGGCTGTGCGGCTGCTGCTGAGGAGGAGAGA 1200
Db 1141 AAGAGATGCGCTGTGGGAGAGCTGTGCGGCTGTGCGGCTGCTGCTGAGGAGGAGAGA 1200
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1201 TTTAGATCTGAGACCAAGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTATTTCCCA 1260
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QY 1321 TCCCTCTGAGCTTGAACAGATGAGGTGTGTGATTTGTTCAGCTTCCCGCAGCTGTCT 1380
Db 1321 TCCCTCTGAGCTTGAACAGATGAGGTGTGTGATTTGTTCAGCTTCCCGCAGCTGTCT 1380
QY 1381 CAGAGCTTACAGCTGTGTGAGAGAGTCAAGGACAGGTTAACTGAGAGAGAGTT 1440
Db 1381 CAGAGCTTACAGCTGTGTGAGAGAGTCAAGGACAGGTTAACTGAGAGAGAGTT 1440
QY 1441 GCGACCCCTGTCCAGATTAATTTGCTGTGCTTGTACAGTTGCGAGACAGCCGTTGT 1500
Db 1441 GCGACCCCTGTCCAGATTAATTTGCTGTGCTTGTACAGTTGCGAGACAGCCGTTGT 1500
QY 1501 TCTACATGCTTTGATTAATTTGTTGAGGGAGAGATGAGAAACATGTGAGAGTCTCCCTC 1560
Db 1501 TCTACATGCTTTGATTAATTTGTTGAGGGAGAGATGAGAAACATGTGAGAGTCTCCCTC 1560
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Db 1801 TCTCTCAGCAGCTGCGGAGAGGGGTCAATGTTCTCTGTCATCAAGGATCTTCAGAG 1860
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QY 1921 ATCTGTGTGATCTTAAGTCAAGTCTCTCTCACTACCCCAACAGCCTTGTGCGCA 1980
Db 1921 ATCTGTGTGATCTTAAGTCAAGTCTCTCTCACTACCCCAACAGCCTTGTGCGCA 1980
QY 1981 CCAAAAGTCTCCCAAAAGAGAGAAATGGGATTTTCTTGAGGACATGCAATGTGGA 2040
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QY 2041 AATTAAGTCAATTAATTTCTCAATCCCTTAATAAGTAATCTAATCTGTTGAGAACAGAGT 2100
Db 2041 AATTAAGTCAATTAATTTCTCAATCCCTTAATAAGTAATCTAATCTGTTGAGAACAGAGT 2100
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DB 2281 CACTTAGCAGCACTGTAAGACATTAATCAACAGCTGAGAAAAATCAACGACGAGGCG 2340
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DB 2341 TGTGTGAAGCACTGTTGTATATATGCGACTGGAACTGTAACTCTTACGCCATCTCCACAAA 2400
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DB 2401 TGATGTTTCAGTGTCTGATGAGCTGTGGCCACCATGTATTCATCCAGAGTTCTTAAAGT 2460
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DB 2461 TAAAGTGCACATATTTGTATAGCATGCTTCTTTGAGTTTAAATATATATTAACAT 2520
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DB 2521 AAGTTGCATTTAGAAATCAAGCATTAATCACTTCACTGCAACCAAAAAAAAAAAAAA 2580
OY 2581 AAAAAA 2586
DB 2581 AAAAAA 2586

RESULT 7
ACAS5002
ID ACAS5002 standard; cDNA; 2586 BP.
XX ACAS5002;
AC ACAS5002;
XX ACAS5002;
DT 05-JUN-2003 (first entry)
DE Novel human secreted and transmembrane protein PRO295 cDNA.
XX
XX Human; secreted and transmembrane protein; gene therapy; psoriasis;
XX enterocolitis; gastrointestinal ulceration; skin disease;
XX keratinocyte differentiation; epithelial cancer; Alzheimer's disease;
XX squamous cell carcinoma; Parkinson's disease; inflammatory disease;
XX amyotrophic lateral sclerosis; rheumatoid arthritis; asthma;
XX multiple sclerosis; organ failure; atherosclerosis; cardiac injury;
XX infertility; birth defect; premature aging; AIDS; cancer;
XX diabetic complication; wound repair; tissue re-growth; Gene; ss.
OS Homo sapiens.
XX
XX US2003017463-A1.
PN
XX
XX 23-JAN-2003.
PD
XX
XX
XX 11-JUL-2001; 2001US-0903640.
PF
XX
XX 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 01-DEC-1998; 98WO-US25108.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30939.
PR 05-JAN-2000; 2000WO-US00219.
PR 11-FEB-2000; 2000WO-US03565.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR

PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 22-MAY-2000; 2000WO-US14042.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 17-SEP-1997; 97US-059113P.
PR 17-SEP-1997; 97US-059115P.
PR 17-SEP-1997; 97US-059117P.
PR 17-SEP-1997; 97US-059119P.
PR 17-SEP-1997; 97US-059121P.
PR 17-SEP-1997; 97US-059122P.
PR 17-SEP-1997; 97US-059184P.
PR 18-SEP-1997; 97US-059263P.
PR 18-SEP-1997; 97US-059266P.
PR 15-OCT-1997; 97US-062125P.
PR 17-OCT-1997; 97US-062285P.
PR 17-OCT-1997; 97US-062287P.
PR 21-OCT-1997; 97US-063486P.
PR 24-OCT-1997; 97US-062814P.
PR 24-OCT-1997; 97US-062816P.
PR 24-OCT-1997; 97US-063045P.
PR 24-OCT-1997; 97US-063120P.
PR 24-OCT-1997; 97US-063120P.
PR 24-OCT-1997; 97US-063121P.
PR 24-OCT-1997; 97US-063127P.
PR 24-OCT-1997; 97US-063128P.
PR 27-OCT-1997; 97US-063327P.
PR 27-OCT-1997; 97US-063329P.
PR 28-OCT-1997; 97US-063541P.
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PR 28-OCT-1997; 97US-063544P.
PR 28-OCT-1997; 97US-063549P.
PR 28-OCT-1997; 97US-063550P.
PR 28-OCT-1997; 97US-063564P.
PR 29-OCT-1997; 97US-063455P.
PR 29-OCT-1997; 97US-063704P.
PR 29-OCT-1997; 97US-063732P.
PR 29-OCT-1997; 97US-063734P.
PR 29-OCT-1997; 97US-063735P.
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PR 29-OCT-1997; 97US-064255P.
PR 31-OCT-1997; 97US-063870P.
PR 31-OCT-1997; 97US-064103P.
PR 03-NOV-1997; 97US-064248P.
PR 07-NOV-1997; 97US-064809P.
PR 12-NOV-1997; 97US-065186P.
PR 17-NOV-1997; 97US-065846P.
PR 18-NOV-1997; 97US-065853P.
PR 21-NOV-1997; 97US-066120P.
PR 21-NOV-1997; 97US-066346P.
PR 24-NOV-1997; 97US-066453P.
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PR 24-NOV-1997; 97US-066511P.
PR 24-NOV-1997; 97US-066770P.
PR 24-NOV-1997; 97US-066772P.
PR 25-NOV-1997; 97US-066840P.
PR 12-DEC-1997; 97US-069425P.
PR 04-JUN-1998; 98US-088026P.
PR 10-SEP-1998; 98US-088036P.
PR 14-SEP-1998; 98US-100262P.
PR 17-SEP-1998; 98US-100858P.
PR 13-OCT-1998; 98US-104030P.
PR 20-NOV-1998; 98US-109304P.
PR 22-DEC-1998; 98US-113296P.
PR 07-JUL-1999; 99US-143048P.
PR 26-JUL-1999; 99US-145688P.
PR 28-JUL-1999; 99US-146222P.
PR 18-SEP-2000; 2000US-0665350.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi A, Botstein D, Desnovers L, Baton DL, Ferrara N,
PI Flivarov E, Fong S, Gao W, Gerder H, Gerritsen ME, Goddard A;

PI Godowski PJ, Gimaldi JC, Gurney AL, Hillan KJ, Klisvin IJ,
PI Mether JP, Pan Y, Paoni NF, Roy MA, Stewart TA, Tumas D,
PI Williams PM, Wood WI;
XX
DR WPI: 2003-341586/32.
DR P-PSDB; ABUS69662.
DR

PT New PRO polypeptides and nucleic acid molecules, useful in diagnosing
PT or treating inflammatory diseases, organ failure, atherosclerosis,
PT cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or
PT Parkinson's disease -

PS Claim 2; Fig 83; 473pp; English.

The invention describes sixty one nucleic acid encoding PRO polypeptides (secreted and transmembrane). The PRO polypeptides and nucleic acids are useful in diagnosing or treating enterocolitis, gastrointestinal ulceration, skin diseases associated with abnormal keratinocyte differentiation, e.g. psoriasis or epithelial cancers such as squamous cell carcinoma, Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, inflammatory diseases, e.g. rheumatoid arthritis, asthma or multiple sclerosis, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, diabetic complications, or mutations in general. The polypeptides are also useful for wound repair and associated therapies concerned with re-growth of tissue. The PRO polypeptides and nucleic acid molecules are also useful in gene therapy, and as molecular weight markers for protein electrophoresis purposes. The anti-PRO antibodies may be used in diagnostic assays for PRO, or for the affinity purification of PRO from recombinant cell culture or natural sources. This sequence encodes a novel human PRO polypeptide.

Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;

Query Match	100.0%;	Score 2586;	DB 25;	Length 2586;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2586;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	CGCGCGGCTCCCGCACCCGCGGCGCGCCACCGCGCGCTCCGCAATCTCAACCGCAC	60
Db	1	CGCGCGGCTCCCGCACCCGCGGCGCGCCACCGCGCGCTCCGCAATCTCAACCGCAC	60
QY	61	CGCGCGGCTCCCGCGGCGGAGCGAGTCAGTCGGGCTCCGACGCGCACTCGGTCCA	120
Db	61	CGCGCGGCTCCCGCGGCGGAGCGAGTCAGTCGGGCTCCGACGCGCAACTCGGTCCA	120
QY	121	GTGGGGCGCGCGCTCCGCGCGCGCAGAGCGAGATCCAGCGCTTGGGGCCACCTGCTGT	180
Db	121	GTGGGGCGCGCGCTCCGCGCGCGCAGAGCGAGATCCAGCGCTTGGGGCCACCTGCTGT	180
QY	181	GCCTGCTGTGGCGGCGGCGATCCCGACGGCCCCCGCGCTCCGACGCGGCACTCGG	240
Db	181	GCCTGCTGTGGCGGCGGCGATCCCGACGGCCCCCGCGCTCCGACGCGGCACTCGG	240
QY	241	CTCCAGTCAAGCCCCCGGCTCCGCGCTCTCAGCTACCCGCGAGAGAGGCGCACCTGAATGAG	300
Db	241	CTCCAGTCAAGCCCCCGGCTCCGCGCTCTCAGCTACCCGCGAGAGAGGCGCACCTGAATGAG	300
QY	301	TGTTCCGCGAGTGTGAGAACTGATGAGAGCAGCAGACCAAAATTGCGAGCGCGTGG	360
Db	301	TGTTCCGCGAGTGTGAGAACTGATGAGAGCAGCAGACCAAAATTGCGAGCGCGTGG	360
QY	361	AAGAGATGAGGAGAGAGAGAGTGTGCTGCTAAAGCTATCATGAAAGTAACTTGCGAAACT	420
Db	361	AAGAGATGAGGAGAGAGAGAGTGTGCTGCTAAAGCTATCATGAAAGTAACTTGCGAAACT	420
QY	421	TACCTCCCACTATCACAATGAGACCAACAGACAGAGAGTTGAAATTAATACATCC	480
Db	421	TACCTCCCACTATCACAATGAGACCAACAGACAGAGAGTTGAAATTAATACATCC	480
QY	481	ATGTGACCGAGAAATTCACMAATTAACCAACACACACTGGCAAAATGCTTTTCAG	540
Db	481	ATGTGACCGAGAAATTCACMAATTAACCAACACACACTGGCAAAATGCTTTTCAG	540

QY	541	AGACAGTTATCA	CAATCTGTGGAGAGGAAGAAAGACCAAGACCAAGATGCATATCG	600
Db	541	AGACAGTTATCA	CAATCTGTGGAGAGGAAGAAAGACCAAGACCAAGATGCATATCG	600
QY	601	ACGAGGACTGTGG	3CCAGCATGTACTGCCAGTTTGCAGCTTTCAGTACACTGTCAGC	660
Db	601	ACGAGGACTGTGG	3CCAGCATGTACTGTCAGCATTTTGCAGCTTTCAGTACACTGTCAGC	660
QY	661	CATACCAGGGGAC	AGAGATGCTCTGCACCCGGGAGACAGTAGTGTCTGTGGAGACAGACTGT	720
Db	661	CATGCCGGGGAC	AGAGATGTCTCTGCACCCGGGAGACAGTAGTGTCTGTGGAGACAGACTGT	720
QY	721	GTTGTTGGGGTCA	CTGCACCAAAATGGCCACAGGGGACCAATGGGACCATCTGTGACA	780
Db	721	GTTGTTGGGGTCA	CTGCACCAAAATGGCCACAGGGGACCAAAATGGGACCATCTGTGACA	780
QY	781	ACCAGAGGAACTG	CCAGCCGGGGCTGTGCTGTGACCTTCCAGAAAGGCTCTGTTCCTTG	840
Db	781	ACCAGAGGAACTG	CCAGCCGGGGGCTGTGCTGTCTTCCAGAAAGGCTCTGTTCCTTG	840
QY	841	TGTGCAACA	CCCCCTGCGGTGGAAGGGCGAGCTTTTGCCATACCCCCGCTACCGGGCTTTTG	900
Db	841	TGTGCAACA	CCCCCTGCGGTGGAAGGGCGAGCTTTTGCCATACCCCCGCTACCGGGCTTTTG	900
QY	901	ACCTCATCACTG	GGAGACTAGAGGCTGATGAGACCTTGACCCGATGCCCTTGTGCGCAGTG	960
Db	901	ACCTCATCACTG	GGAGACTAGAGGCTGATGAGAGCTTGTAGCCGATGCCCTTGTGCGCAGTG	960
QY	961	GCTTCCTCTG	CAGCCCCCAACGCCACAGCTTGTTGTATGTGTGCAAGCCGACCTTCGTTG	1020
Db	961	GCTTCCTCTG	CAGCCCCCAACGCCACAGCTTGTTGTATGTGTGCAAGCCGACCTTCGTTG	1020
QY	1021	GGAGCCGTGAC	CAAGATGGGGAAGTCTGTGTCGCCAGAGAGGTCCCCGATGAGTATGAAG	1080
Db	1021	GGAGCCGTGAC	CAAGATGGGGAAGTCTGTGTGCCAGAGAGGTCCCCGATGAGTATGAAG	1080
QY	1081	TTGGCAGCTTCA	TGGAAGAGTGTGCGCCAGAGACTTGAAGACCTTGGAAGAGAGCTGTGCTG	1140
Db	1081	TTGGCAGCTTCA	TGGAAGAGTGTGCGCCAGAGAGCTGTGAAGACCTTGGAAGAGAGCTGTGCTG	1140
QY	1141	AAGAGATGAG	CGCTGGGGAAGCTTGCGGCTCGCCGCTGCACTGTCTGGAGAGGGGAAAGAG	1200
Db	1141	AAGAGATGAG	CGCTGGGGAAGCTTGCGGCTCGCCGCTGCACTGTCTGGAGAGGGGAAAGAG	1200
QY	1201	TTTTCAGTCTG	GAACAGGCTGTGGGTATATGTGCATATGAAATAGCTATTTATTTCCCA	1260
Db	1201	TTTTCAGTCTG	GAACAGGCTGTGGGTATATGTGCATATGAAATAGCTATTTATTTCCCA	1260
QY	1261	GATGTGTGCTT	TAAAGGCTGGGCTGACCAAGGCTTCTTCTCATCTTCTTCCCAATGAAGTT	1320
Db	1261	GATGTGTGCTT	TAAAGGCTGGGCTGACCAAGGCTTCTTCTCATCTTCTTCCCAATGAAGTT	1320
QY	1321	TCCCTCTG	GCTTGAACAGATGAGTGTGTGGCATTTTGTCAAGTCCCCCAAGGCTGTCT	1380
Db	1321	TCCCTCTG	GCTTGAACAGATGAGTGTGTGGCATTTTGTCAAGTCCCCCAAGGCTGTCT	1380
QY	1381	CCAGGCTTCA	CAGATCTGGTCTTGGGAGAGTCAGGACGAGGTTAACTGCAGGACAGATT	1440
Db	1381	CCAGGCTTCA	CAGATCTGGTCTTGGGAGAGTCAGGACGAGGTTAACTGCAGGACAGATT	1440
QY	1441	GCCACCCCTG	CCAGATTAATGTGGCTTGGCCCTTACAGTTGGGACAGACGCGTTTGT	1500
Db	1441	GCCACCCCTG	CCAGATTAATGTGGCTTGGCCCTTACAGTTGGGACAGACGCGTTTGT	1500
QY	1501	TCTACATG	GGCTTTGATAATTTGTTGAGGGGAGAGATGAAAACAATGTGAGTCTCCCTC	1560
Db	1501	TCTACATG	GGCTTTGATAATTTGTTGAGGGGAGAGATGAAAACAATGTGAGTCTCCCTC	1560
QY	1561	TGATTGTGTTT	GGGGAATGTGGAAGAGAGCCCTGTTTGCAAACATCAACTGTGGCAA	1620
Db	1561	TGATTGTGTTT	GGGGAATGTGGAAGAGAGCCCTGTTTGCAAACATCAACTGTGGCAA	1620

QY 1621 AAATGCAAAATGATTTTCCAGCAGTCTTTCCATGCGGCAATAGGTAGTGTGCTT 1680
 DB 1621 AAATGCAAAATGATTTTCCAGCAGTCTTTCCATGCGGCAATAGGTAGTGTGCTT 1680
 QY 1681 CAGCTGTGAGATGAAATGTTCTGTTCACCTGECATATGATGTTTATTCATCCAGCA 1740
 DB 1681 CAGCTGTGAGATGAAATGTTCTGTTCACCTGECATATGATGTTTATTCATCCAGCA 1740
 QY 1741 GTGTGCTCAGCTCTTACCTCTGTGCGGAGGAGCATTTTCATATCCAAATGATTTCC 1800
 DB 1741 GTGTGCTCAGCTCTTACCTCTGTGCGGAGGAGCATTTTCATATCCAAATGATTTCC 1800
 QY 1801 TCTCTCAGCAGCTGCGGAGGAGGAGTCAATGTTCTCTGTCATCAGGATCTCAGAG 1860
 DB 1801 TCTCTCAGCAGCTGCGGAGGAGGAGTCAATGTTCTCTGTCATCAGGATCTCAGAG 1860
 QY 1861 GCTCAGAGACTGCAAGTCTGCTGCGGAGTCAACAGCTAGTGAAGCCAGAGCAGTTTC 1920
 DB 1861 GCTCAGAGACTGCAAGTCTGCTGCGGAGTCAACAGCTAGTGAAGCCAGAGCAGTTTC 1920
 QY 1921 ATCTGTTGTGACTCTTAAGCTCAGTGTCTCTCCACTACCCACACAGCCTTGTCGCA 1980
 DB 1921 ATCTGTTGTGACTCTTAAGCTCAGTGTCTCTCCACTACCCACACAGCCTTGTCGCA 1980
 QY 1981 CCAAAAGTCTCCCAAAAGGAGGAGATGGGATTTTCTTGAGGATGCACTCTGGA 2040
 DB 1981 CCAAAAGTCTCCCAAAAGGAGGAGATGGGATTTTCTTGAGGATGCACTCTGGA 2040
 QY 2041 AATTAAGGCAACTAATTTCTCAGATCCCTCTAAAGTAACTACTGTTAGGAAACAGAGT 2100
 DB 2041 AATTAAGGCAACTAATTTCTCAGATCCCTCTAAAGTAACTACTGTTAGGAAACAGAGT 2100
 QY 2101 GTTCTCAGAGTGTGGGAGCGGCTCTTCTAATGAAGACATGATTTGACACTGTCCCT 2160
 DB 2101 GTTCTCAGAGTGTGGGAGCGGCTCTTCTAATGAAGACATGATTTGACACTGTCCCT 2160
 QY 2161 CTTTGGCAGTTGCACTTGTATCTTGAAGGTAATGACTGAGGAGTACAGGTTAA 2220
 DB 2161 CTTTGGCAGTTGCACTTGTATCTTGAAGGTAATGACTGAGGAGTACAGGTTAA 2220
 QY 2221 CCTGAGAAACAGTACTTAACTTGTAGGCGAGGATTAATAATGAAATTTTGCAAAAT 2280
 DB 2221 CCTGAGAAACAGTACTTAACTTGTAGGCGAGGATTAATAATGAAATTTTGCAAAAT 2280
 QY 2281 CACTTAGAGAGCACTGAAGCAATATATCAACAGTGGAGAAATCAAAACGAGCAGGGC 2340
 DB 2281 CACTTAGAGAGCACTGAAGCAATATATCAACAGTGGAGAAATCAAAACGAGCAGGGC 2340
 QY 2341 TGTGTGAACAATGTTGTATATGAGACTGCGAACTGAACTCTAGCGCATCTCCACAA 2400
 DB 2341 TGTGTGAACAATGTTGTATATGAGACTGCGAACTGAACTCTAGCGCATCTCCACAA 2400
 QY 2401 TGATGTTTTCAGGAGTGTATGAGCTGTGCGCACTGATATATCAACAGTCTTAAAGT 2460
 DB 2401 TGATGTTTTCAGGAGTGTATGAGCTGTGCGCACTGATATATCAACAGTCTTAAAGT 2460
 QY 2461 TAAAGTTGCAATGATTTGTATATGAGATGCTTTCTTTGATTTTAAATATATGATTAACAT 2520
 DB 2461 TAAAGTTGCAATGATTTGTATATGAGATGCTTTCTTTGATTTTAAATATATGATTAACAT 2520
 QY 2521 AAGTTGCACTTTAGAAATCAAGCATTAATCACTTCACTGCAAAAAAATTTTTAAAAA 2580
 DB 2521 AAGTTGCACTTTAGAAATCAAGCATTAATCACTTCACTGCAAAAAAATTTTTAAAAA 2580
 QY 2581 AAAAAA 2586
 DB 2581 AAAAAA 2586

RESULT 8
 ACAS8487
 ID ACAS8487 standard; cDNA; 2586 BP.
 XX

AC ACAS8487;
 XX
 DT 10-JUN-2003 (first entry)
 DE
 XX cDNA encoding human PRO polypeptide #41.
 DE
 XX Human; secreted and transmembrane protein; PRO polypeptide; cancer;
 KW Alzheimer's disease; ischemia; cytostatic; nootropic; vasotropic;
 KW neuroprotective; gene; ss.
 OS Homo sapiens.
 XX
 PN US2002192659-A1.
 PD 19-DEC-2002.
 XX
 PF 10-JUL-2001; 2001US-0902853.
 XX
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19177.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 01-DEC-1998; 98WO-US25108.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 01-DEC-1999; 99WO-US28301.
 PR 02-DEC-1999; 99WO-US28564.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 17-SEP-1997; 97US-059113P.
 PR 17-SEP-1997; 97US-059115P.
 PR 17-SEP-1997; 97US-059117P.
 PR 18-SEP-1997; 97US-059266P.
 PR 15-OCT-1997; 97US-062125P.
 PR 17-OCT-1997; 97US-062285P.
 PR 17-OCT-1997; 97US-062287P.
 PR 21-OCT-1997; 97US-063486P.
 PR 24-OCT-1997; 97US-062814P.
 PR 24-OCT-1997; 97US-062816P.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Ashkenazi A, Borstein D, Desnoyers L, Eaton DL, Ferrara N;
 PI Filveroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillian KJ, Kijavits ID;
 PI Mather JP, Pan U, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PM, Wood WI;
 XX
 DR WPI; 2003-361832/34.
 DR P-PDB; ABU71485.
 XX
 PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or
 PT PRO168, useful in molecular biology, chromosome and gene mapping, in
 PT generating antisense RNA and DNA, and in gene therapy
 XX
 PS Claim 2; Fig 83; 474pp; English.
 XX
 CC The present invention relates to the isolation of novel human secreted
 CC and transmembrane proteins (PRO polypeptides), and the polynucleotide
 CC sequences encoding them. The polynucleotide sequences are useful in
 CC molecular biology, as hybridisation probes, in chromosome and gene
 CC mapping, in generating antisense RNA and DNA, and in gene therapy. The
 CC polynucleotide sequences may also be used in preparing PRO polypeptides

CC by recombinant techniques, and in generating either transgenic animals
 CC or knock-out animals which, in turn, are useful in the development and
 CC screening of therapeutically useful reagents. The PRO polypeptides or
 CC their antibodies are useful in preparing a medicament for treating a
 CC condition responsive to the polypeptide or antibody, such as cancer,
 CC Alzheimer's disease or ischaemia, and in various diagnostic assays.
 CC The present sequence encodes a human PRO polypeptide of the invention.

XX Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;

Query Match 100.0%; Score 2586; DB 25; Length 2586;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CGCCGCGCTCCCGACCCCGCGCCCGCCACCGCGCCCTCCCGCATCTGCACCCGAGC 60
DB 1 CGCGCGCTCCCGACCCCGCGCCCGCCCGCCCGCTCCCGCATCTGCACCCGAGC 60
QY 61 CGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
DB 61 CGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 121 GTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
DB 121 GTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 181 GCTTGTCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
DB 181 GCTTGTCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
QY 241 CTCGCGGTAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
DB 241 CTCGCGGTAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 301 TGTTCGCGAGGTTGAGAACTGAGAGAGACAGCGACCAAAATTGGCGCGCGGTG 360
DB 301 TGTTCGCGAGGTTGAGAACTGAGAGAGACAGCGACCAAAATTGGCGCGCGGTG 360
QY 361 AAGAGATGAGAGCGAGAAAGTGTGTAAAGCATCTAGAAAGTAACTGGCAACT 420
DB 361 AAGAGATGAGAGCGAGAAAGTGTGTAAAGCATCTAGAAAGTAACTGGCAACT 420
QY 421 TACCTCCGAGCTATCAGATGAGACCAACAGACAGCAAGGTTGAAATATATCATCC 480
DB 421 TACCTCCGAGCTATCAGATGAGACCAACAGACAGCAAGGTTGAAATATATCATCC 480
QY 481 ATGTGCACTCGAGAAATTCAGAAATTCAGAAATTCAGAAATTCAGAAATTCAG 540
DB 481 ATGTGCACTCGAGAAATTCAGAAATTCAGAAATTCAGAAATTCAGAAATTCAG 540
QY 541 AGACAGTTATCATCTGTGGGAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 541 AGACAGTTATCATCTGTGGGAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 601 ACGAGAGCTGTGGGCGCGAGCATGTACTGCGAGTTGCGAGCTTCAGATGACCTGCAGC 660
DB 601 ACGAGAGCTGTGGGCGCGAGCATGTACTGCGAGTTGCGAGCTTCAGATGACCTGCAGC 660
QY 661 CATGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 661 CATGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 GTGTCTGAGGTCATGCAACCAAAATGCGCACAGGGGAGAGCAATGGACATCTGTGACA 780
DB 721 GTGTCTGAGGTCATGCAACCAAAATGCGCACAGGGGAGAGCAATGGACATCTGTGACA 780
QY 781 ACCAGAGGAGCTGCGAGCGGGGCTGTGCTGCTTCAGAGAGGCGCTGTGCTGCTG 840
DB 781 ACCAGAGGAGCTGCGAGCGGGGCTGTGCTGCTTCAGAGAGGCGCTGTGCTGCTG 840
QY 841 TGTGCAACCCCTGCGCTGAGAGGGGAGGCTTTGCGATGACCCGCGAGCGGCTTGG 900
DB 841 TGTGCAACCCCTGCGCTGAGAGGGGAGGCTTTGCGATGACCCGCGAGCGGCTTGG 900

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QY 901 ACCGTATCAGCTGGAGAGCTAGAGCGCTGATGAGCGCTGGACCGATGCGCTTGGCAGTG 960
DB 901 ACCGTATCAGCTGGAGAGCTAGAGCGCTGATGAGCGCTTGGACCGATGCGCTTGGCAGTG 960
QY 961 GCTCTCTGCGAGCGCCACAGCCACAGCGCTGTGTATGTGTGCAAGCGGACCTTGTGTG 1020
DB 961 GCTCTCTGCGAGCGCCACAGCCACAGCGCTGTGTATGTGTGCAAGCGGACCTTGTGTG 1020
QY 1021 GAGAGCGGTACCAAGATGGGGAGATCCGTGCGCGAGAGGTCGCCCATGTGATTAAG 1080
DB 1021 GAGAGCGGTACCAAGATGGGGAGATCCGTGCGCGAGAGGTCGCCCATGTGATTAAG 1080
QY 1081 TTGGCAGCTTCAATGAGAGAGAGTGTGCGCAGAGAGCTGAGAGAGCTGAGAGAGCTGACTG 1140
DB 1081 TTGGCAGCTTCAATGAGAGAGAGTGTGCGCAGAGAGCTGAGAGAGCTGAGAGAGCTGACTG 1140
QY 1141 AAGAGATGAGCGCTGGGGAGAGCTGTGGGCTGCGCGCGCTGCACTGCTGTGGAGGGAGAGA 1200
DB 1141 AAGAGATGAGCGCTGGGGAGAGCTGTGGGCTGCGCGCGCTGCACTGCTGTGGAGGGAGAGA 1200
QY 1201 TTATGATCTGAGACAGGCTGTGGGATAGATGTGCAATAGAAATAGCTAATTTATTTCCCA 1260
DB 1201 TTATGATCTGAGACAGGCTGTGGGATAGATGTGCAATAGAAATAGCTAATTTATTTCCCA 1260
QY 1261 GGTGTGTCTTTAAGCGGTGGCTGACAGGCTTCTTCTCAATCTTTCTTCCAGTAACTT 1320
DB 1261 GGTGTGTCTTTAAGCGGTGGCTGACAGGCTTCTTCTCAATCTTTCTTCCAGTAACTT 1320
QY 1321 TCCCTCTGAGCTTGAAGAGATGAGGTGTGCAATTTGTTCAGCTCCCGCAGGCTGTCT 1380
DB 1321 TCCCTCTGAGCTTGAAGAGATGAGGTGTGCAATTTGTTCAGCTCCCGCAGGCTGTCT 1380
QY 1381 CAGGCTTGAAGAGTGTGTGTGGAGAGTCAAGGAGGTTAACTGACAGAGAGAGT 1440
DB 1381 CAGGCTTGAAGAGTGTGTGTGGAGAGTCAAGGAGGTTAACTGACAGAGAGAGT 1440
QY 1441 GCCACCCCTGTCAGATTAATTTGAGCTGCTTGTGCTTACAGTGTGAGAGACAGCGGTTGT 1500
DB 1441 GCCACCCCTGTCAGATTAATTTGAGCTGCTTGTGCTTACAGTGTGAGAGACAGCGGTTGT 1500
QY 1501 TCTACATGAGCTTGTATTAATTTGAGGGAGAGATGAGAACTGAGAGTCTTCTCTC 1560
DB 1501 TCTACATGAGCTTGTATTAATTTGAGGGAGAGATGAGAACTGAGAGTCTTCTCTC 1560
QY 1561 TGAATGCTTTGGGAAATGTGAGAGAGTGCCTGCTTGCATTAATCAATCAACCTGAGCA 1620
DB 1561 TGAATGCTTTGGGAAATGTGAGAGAGTGCCTGCTTGCATTAATCAATCAACCTGAGCA 1620
QY 1621 AATGCAACAAATGAATTTTCCAGAGAGTCTTTCATGGGATAGTAAAGCTGTGCTT 1680
DB 1621 AATGCAACAAATGAATTTTCCAGAGAGTCTTTCATGGGATAGTAAAGCTGTGCTT 1680
QY 1681 CAGCTGTGCAATGAATGTTCTGTTCACCTGTGATTAATGATGTTATTCATCAGAGA 1740
DB 1681 CAGCTGTGCAATGAATGTTCTGTTCACCTGTGATTAATGATGTTATTCATCAGAGA 1740
QY 1681 CAGCTGTGCAATGAATGTTCTGTTCACCTGTGATTAATGATGTTATTCATCAGAGA 1740
DB 1681 CAGCTGTGCAATGAATGTTCTGTTCACCTGTGATTAATGATGTTATTCATCAGAGA 1740
QY 1741 GTGTGCTCAGCTCTTCTGCTGTGCGAGAGAGATTTTCAATTCAGAAATCAATTTCC 1800
DB 1741 GTGTGCTCAGCTCTTCTGCTGTGCGAGAGAGATTTTCAATTCAGAAATCAATTTCC 1800
QY 1801 TCTGTGAGCAAGCTGTGGGAGGGGCTCAATTTCTCTGTGTCATCAGGATCTTCAGAG 1860
DB 1801 TCTGTGAGCAAGCTGTGGGAGGGGCTCAATTTCTCTGTGTCATCAGGATCTTCAGAG 1860
QY 1861 GCTCAGAGAGCTGAGCTCTTGCAGAGTCAAGAGTGAAGAGAGAGAGAGAGAGATTTC 1920
DB 1861 GCTCAGAGAGCTGAGCTCTTGCAGAGTCAAGAGTGAAGAGAGAGAGAGAGAGATTTC 1920
QY 1921 ATCTGTTGATCTTAAGCTCAGTCTCTCTCACTACACCAACAGCTTGTGTGCA 1980
DB 1921 ATCTGTTGATCTTAAGCTCAGTCTCTCTCACTACACCAACAGCTTGTGTGCA 1980

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QY 61 CCGGCGGCTCCCGGCGGAGCGAGCATCCAGTCCGGCCCGAGCGCAACTCGTCCA 120
Db 61 CCGGCGGCTCCCGGCGGAGCGAGCATCCAGTCCGGCCCGAGCGCAACTCGTCCA 120
QY 121 GTCGGGCGGCGGCTGCGGGCGGCAAGCGAGATGCAAGCGGCTTGGGGCCACCTGCTGT 180
Db 121 GTCGGGCGGCGGCTGCGGGCGGCAAGCGAGATGCAAGCGGCTTGGGGCCACCTGCTGT 180
QY 181 GCTGCTGCTGCGGCGGCGGCTGCCAGCGGCGGCGGCGGCTGCCAGCGGCGGCTGCGG 240
Db 181 GCTGCTGCTGCGGCGGCGGCTGCCAGCGGCGGCGGCGGCTGCCAGCGGCGGCTGCGG 240
QY 241 CTCGAGTCAAGCCCGGCGGCTGCTGAGTCAAGCGGCGGCGGCGGCGGCTGCGG 300
Db 241 CTCGAGTCAAGCCCGGCGGCTGCTGAGTCAAGCGGCGGCGGCGGCGGCTGCGG 300
QY 301 TGTTCCGAGGTTGAGGAACTGATGAGGAGCAGCAGCAAAATGGCGGCGGCTGCGG 360
Db 301 TGTTCCGAGGTTGAGGAACTGATGAGGAGCAGCAGCAAAATGGCGGCGGCTGCGG 360
QY 361 AAGAGATGAGGCGAGAGAGAGCTGCTGTAAGCATCATGAAAGTGAACCTGGCAACT 420
Db 361 AAGAGATGAGGCGAGAGAGAGCTGCTGTAAGCATCATGAAAGTGAACCTGGCAACT 420
QY 421 TACCTCCAGCTATCACAATGAGACCAACAGACAGGAGTTGGAATTAATTCATCC 480
Db 421 TACCTCCAGCTATCACAATGAGACCAACAGACAGGAGTTGGAATTAATTCATCC 480
QY 481 ATGTGACCGGAAATTCACAAGATTAACCAACAGACTGAGCAATGGTCTTTTCA 540
Db 481 ATGTGACCGGAAATTCACAAGATTAACCAACAGACTGAGCAATGGTCTTTTCA 540
QY 541 AGAGATGATATCACTGCTGGGAGACCAAGAGGAGAGAGGAGGAGGAGGAGGAGGAG 600
Db 541 AGAGATGATATCACTGCTGGGAGACCAAGAGGAGAGAGGAGGAGGAGGAGGAGGAG 600
QY 601 ACGAGGACTGTGGGCGGAGCATGTACTGCGAGTTGCGAGTTGCGATACCTGCGGAG 660
Db 601 ACGAGGACTGTGGGCGGAGCATGTACTGCGAGTTGCGAGTTGCGATACCTGCGGAG 660
QY 661 CATGCGGCGGCGGAGAGATGCTGTCGACCGGAGCAGTGAAGTGTGGAGACCAAGTGT 720
Db 661 CATGCGGCGGCGGAGAGATGCTGTCGACCGGAGCAGTGAAGTGTGGAGACCAAGTGT 720
QY 721 GTGTCTGGGCTCACTGACCAAAATGCGCACAGGGGAGAGATGAGACCAATCTGTGACA 780
Db 721 GTGTCTGGGCTCACTGACCAAAATGCGCACAGGGGAGAGATGAGACCAATCTGTGACA 780
QY 781 ACCGAGGAGCTGCGAGCGGCGGCTGTGTGCTTCCAGAGAGGCTGTGCTGCTG 840
Db 781 ACCGAGGAGCTGCGAGCGGCGGCTGTGTGCTTCCAGAGAGGCTGTGCTGCTG 840
QY 841 TGTGCAACCCCTGCGGCGGAGGAGGCTTGCATGACCCCGGCGGCGGCTGCTG 900
Db 841 TGTGCAACCCCTGCGGCGGAGGAGGCTTGCATGACCCCGGCGGCGGCTGCTG 900
QY 901 ACTCATCACTGTGAGCTGAGGCTGATGAGGCTTGAACCAATGCGCTTGGGCGG 960
Db 901 ACTCATCACTGTGAGCTGAGGCTGATGAGGCTTGAACCAATGCGCTTGGGCGG 960
QY 961 GCTGCTGCTGCGGCGGAGGAGGAGGCTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
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QY 1021 GAGAGGCTGAGCAAGATGAGGAGGAGGCTGCTGCGGCGGAGAGGAGGAGGAGGAGGAG 1080
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QY 1081 TTGGGAGCTTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
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 Db 2521 AAGTTGCAATTTAGAAATCAGCATTAATCACTTCACTGCAAAAAA 2580
 Qy 2581 AAAAAA 2586
 Db 2581 AAAAAA 2586

RESULT 10
 ID ACA60194 standard; CDNA; 2586 BP.

XX ACA60194;
 AC ACA60194;
 XX 12-JUN-2003 (first entry)
 XX Human CDNA for secreted/transmembrane protein PRO295.
 DE Human; ss; gene; secreted protein; transmembrane protein; PRO;
 KW gene therapy; chromosome identification; chromosome marker.
 XX Homo sapiens.
 OS US2003003530-A1.
 XX 02-JAN-2003.
 XX 11-JUL-2001; 2001US-0904031.
 XX 10-SEP-1998; 98WO-US18924.
 PR 14-SEP-1998; 98WO-US19177.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 01-DEC-1998; 98WO-US25108.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 02-DEC-1999; 99WO-US28564.
 PR 16-DEC-1999; 99WO-US28565.
 PR 20-DEC-1999; 99WO-US30991.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 02-MAR-2000; 2000WO-US05004.
 PR 20-MAR-2000; 2000WO-US05841.
 PR 30-MAR-2000; 2000WO-US07377.
 PR 30-MAR-2000; 2000WO-US08439.

PR 22-MAY-2000; 2000WO-US14042.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 17-SEP-1997; 97US-059113P.
 PR 17-SEP-1997; 97US-059115P.
 PR 17-SEP-1997; 97US-059117P.
 PR 17-SEP-1997; 97US-059119P.
 PR 17-SEP-1997; 97US-059121P.
 PR 17-SEP-1997; 97US-059122P.
 PR 17-SEP-1997; 97US-059184P.
 PR 18-SEP-1997; 97US-059263P.
 PR 15-OCT-1997; 97US-062125P.
 PR 17-OCT-1997; 97US-062285P.
 PR 17-OCT-1997; 97US-062287P.
 PR 21-OCT-1997; 97US-063486P.
 PR 24-OCT-1997; 97US-062814P.
 PR 24-OCT-1997; 97US-062816P.
 PR 24-OCT-1997; 97US-063045P.
 PR 24-OCT-1997; 97US-063120P.
 PR 24-OCT-1997; 97US-063121P.
 PR 24-OCT-1997; 97US-063127P.
 PR 24-OCT-1997; 97US-063128P.
 PR 27-OCT-1997; 97US-063327P.
 PR 27-OCT-1997; 97US-063329P.
 PR 28-OCT-1997; 97US-063541P.
 PR 28-OCT-1997; 97US-063542P.
 PR 28-OCT-1997; 97US-063544P.
 PR 28-OCT-1997; 97US-063549P.
 PR 28-OCT-1997; 97US-063550P.
 PR 28-OCT-1997; 97US-063564P.
 PR 29-OCT-1997; 97US-063435P.
 PR 29-OCT-1997; 97US-063704P.
 PR 29-OCT-1997; 97US-063732P.
 PR 29-OCT-1997; 97US-063734P.
 PR 29-OCT-1997; 97US-063735P.
 PR 29-OCT-1997; 97US-063738P.
 PR 29-OCT-1997; 97US-064215P.
 PR 31-OCT-1997; 97US-063870P.
 PR 31-OCT-1997; 97US-064103P.
 PR 03-NOV-1997; 97US-064248P.
 PR 07-NOV-1997; 97US-064809P.
 PR 12-NOV-1997; 97US-065186P.
 PR 17-NOV-1997; 97US-065846P.
 PR 18-NOV-1997; 97US-065693P.
 PR 21-NOV-1997; 97US-066120P.
 PR 21-NOV-1997; 97US-066364P.
 PR 24-NOV-1997; 97US-066453P.
 PR 24-NOV-1997; 97US-066466P.
 PR 24-NOV-1997; 97US-066511P.
 PR 24-NOV-1997; 97US-066770P.
 PR 24-NOV-1997; 97US-066772P.
 PR 18-SEP-2000; 2000US-0665350.
 XX (GENTH) GENENTECH INC.
 XX Ashkenazi A, Botstein D, Deenoyers L, Eaton DL, Ferrara N;
 PI Pitarroff E, Fong S, Gao W, Garber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavits ID;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TB, Tumas D;
 PI Williams PM, Wood WI;
 XX WPI: 2003-329602/31.
 XX P-PSDB; AB071931.
 XX New transmembrane polypeptides and nucleic acids encoding the
 PT polypeptides, useful in gene therapy, in chromosome identification, as
 PT chromosome markers, in generating probes and in tissue typing
 XX Claim 2, Fig 83; 484pp; English.
 XX The invention relates to an isolated nucleic acid with at least 80%

Db 241 CTCGATGAAGCCGCCGCCGCTCTAGCTACCCGAGAGAGAGGCCACCTCTAATGAGA 300
Qy 301 TGTTCGCGAGGTTGAGGAACCTGATGAGGACAGCAGACACAAATTGGCAGCCGGGTG 360
Db 301 TGTTCGCGAGGTTGAGGAACCTGATGAGGACAGCAGACACAAATTGGCAGCCGGGTG 360
Qy 361 AAGAGATGAGGACAAAGAGGCTGCTGTAAGACATCATGAAAGTGAACCTGGCAACT 420
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Qy 781 ACCAGAGGAGCTGCCAGCCGGGGCTGTGCTGTGCTTCAAGAGGGCTGTGTTCCCTG 840
Db 781 ACCAGAGGAGCTGCCAGCCGGGGCTGTGCTGTGCTTCAAGAGGGCTGTGTTCCCTG 840
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Qy      2581 AAAAAA 2586
Db      2581 AAAAAA 2586

RESULT 13
ACA05532
ID ACA05532 standard; cDNA; 2586 BP.
XX
AC ACA05532;
XX
DT 29-MAY-2003 (first entry)
DE
DE cDNA encoding human secreted protein PRO295.
XX
XX Human; gene therapy; mucosal lesion; ulcer; enterocolitis; skin disease;
XX psoriasis; cancer; lung cancer; colon cancer; nerve cell disease;
XX Alzheimer's disease; Parkinson's disease; Usher syndrome; angiogenesis;
XX atrophla areata; inflammatory disease; asthma; rheumatoid arthritis;
XX leishemia; ss; gene.
XX
OS Homo sapiens.
XX
XX US2003023054-A1.
PN
PD 30-JUN-2003.
XX
PF 16-JUL-2001; 2001US-0906742.
XX
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 01-DEC-1998; 98WO-US25108.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 28-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28213.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30919.
PR 05-JAN-2000; 2000WO-US00219.
PR 11-FEB-2000; 2000WO-US03565.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US05004.

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PR	02-MAR-2000;	2000MO-US05841.
PR	20-MAR-2000;	2000MO-US07377.
PR	30-MAR-2000;	2000MO-US08049.
PR	22-MAY-2000;	2000MO-US14042.
PR	02-JUN-2000;	2000MO-US15264.
PR	28-JUL-2000;	2000MO-US20710.
PR	24-AUG-2000;	2000MO-US23328.
PR	17-SEP-1997;	97US-059115P.
PR	17-SEP-1997;	97US-059115P.
PR	17-SEP-1997;	97US-059117P.
PR	17-SEP-1997;	97US-059119P.
PR	17-SEP-1997;	97US-059121P.
PR	17-SEP-1997;	97US-059123P.
PR	17-SEP-1997;	97US-059184P.
PR	18-SEP-1997;	97US-059263P.
PR	18-SEP-1997;	97US-059266P.
PR	15-OCT-1997;	97US-062125P.
PR	17-OCT-1997;	97US-062285P.
PR	17-OCT-1997;	97US-062287P.
PR	21-OCT-1997;	97US-063486P.
PR	24-OCT-1997;	97US-063814P.
PR	24-OCT-1997;	97US-063815P.
PR	24-OCT-1997;	97US-063048P.
PR	24-OCT-1997;	97US-063120P.
PR	24-OCT-1997;	97US-063121P.
PR	24-OCT-1997;	97US-063127P.
PR	24-OCT-1997;	97US-063128P.
PR	27-OCT-1997;	97US-063327P.
PR	27-OCT-1997;	97US-063329P.
PR	26-OCT-1997;	97US-063541P.
PR	26-OCT-1997;	97US-063542P.
PR	28-OCT-1997;	97US-063544P.
PR	28-OCT-1997;	97US-063549P.
PR	28-OCT-1997;	97US-063550P.
PR	28-OCT-1997;	97US-063564P.
PR	29-OCT-1997;	97US-063435P.
PR	29-OCT-1997;	97US-063704P.
PR	29-OCT-1997;	97US-063732P.
PR	29-OCT-1997;	97US-063734P.
PR	29-OCT-1997;	97US-063738P.
PR	29-OCT-1997;	97US-063738P.
PR	29-OCT-1997;	97US-064215P.
PR	31-OCT-1997;	97US-063870P.
PR	31-OCT-1997;	97US-064103P.
PR	03-NOV-1997;	97US-064248P.
PR	07-NOV-1997;	97US-064809P.
PR	12-NOV-1997;	97US-065186P.
PR	17-NOV-1997;	97US-065846P.
PR	18-NOV-1997;	97US-065693P.
PR	21-NOV-1997;	97US-066120P.
PR	21-NOV-1997;	97US-066463P.
PR	24-NOV-1997;	97US-066453P.
PR	24-NOV-1997;	97US-066466P.
PR	24-NOV-1997;	97US-066511P.
PR	24-NOV-1997;	97US-066770P.
PR	24-NOV-1997;	97US-066772P.
PR	25-NOV-1997;	97US-066840P.
PR	12-DEC-1997;	97US-069425P.
PR	04-JUN-1998;	98US-098026P.
PR	10-SEP-1998;	98US-099803P.
PR	14-SEP-1998;	98US-100262P.
PR	17-SEP-1998;	98US-100858P.
PR	13-OCT-1998;	98US-104080P.
PR	20-NOV-1998;	98US-109304P.
PR	22-DEC-1998;	98US-113266P.
PR	07-JUL-1999;	99US-143048P.
PR	26-JUL-1999;	99US-145698P.
PR	28-JUL-1999;	99US-146222P.
PR	18-SEP-2000;	2000US-0665350.
XX		
XX	(GETH) GENENTECH INC.	
XX		
XX	Ashtkenazi A, Botschein D, Desnoyers L, Eaton DL, Ferrara N,	

PI Flyvbjerg E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin JF;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D,
 PI Williams PM, Wood WI;
 XX
 XX WPI; 2003-331485/31.
 DR P-PSDB; AB067385.
 DR
 XX
 XX Sixty one isolated nucleic acids encoding a PBO polypeptide, e.g.
 PT PRO255 or PRO1868, useful in chromosome and gene mapping, in generating
 PT antisense RNA and DNA, and in treating cancer and Alzheimer's disease -
 XX
 XX Example 38; Fig 83; 481pp; English.
 PS

CC The invention relates to sixty one nucleic acids encoding PRO
CC polypeptides (secreted and transmembrane). The polynucleotide is useful
CC in molecular biology, including uses as hybridisation probes, in
CC chromosome and gene mapping, in generating antisense RNA and DNA, and in
CC gene therapy. The polynucleotide may also be used in preparing PRO
CC polypeptides by recombinant techniques, and in generating either
CC transgenic animals or knock-out animals which, in turn, are useful in the
CC development and screening of therapeutically useful reagents. The PRO
CC polypeptide or the antibody is used in preparing a medicament for
CC treating a condition responsive to the polypeptide or antibody, such as
CC mucosal lesions e.g. ulcers and enterocolitis, skin disease e.g.
CC psoriasis, cancer e.g. lung cancer and colon cancer, nerve cell disease
CC e.g. Alzheimer's disease and Parkinson's disease, Usher syndrome,
CC atrophia areata, angiogenesis, inflammatory disease e.g. asthma and
CC rheumatoid arthritis, ischaemia, and in various diagnostic assays. The
CC present sequence represents an cDNA which encodes a PRO polypeptide.
CC
CC
CC Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;
CC
CC

Query Match	100.0%	Score 2586	DB 25	Length 2586
Best Local Similarity	100.0%	Pred. No.0		
Matches 2586	0	Mismatches	0	Gaps 0

QY	1	CGCGCGGCTCCCGGACACCGCGCGCCCGGCCACCGGCGCGCTCCCGGATCTGACCCGACG	60
Db	1	CGCGCGGCTCCCGGACACCGCGCGCCCGGCCACCGGCGCGCTCCCGGATCTGACCCGCGAC	60
QY	61	CGCGCGGCTCCCGGCGGAGGAGACAGATCACTGCGGCGCGGAGCGCACTCGGTCCA	120
Db	61	CGCGCGGCTCCCGGCGGAGGAGACAGATCACTGCGGCGCGGAGCGCACTCGGTCCA	120
QY	121	GTCGGGGCGCGCGCTTCGCGGCGCGAGAGCGAGATGCGAGCGGCTTTGGGGGCCACCTGCTG	180
Db	121	GTCGGGGCGCGCGCTTCGCGGCGCGAGAGGAGAGATGCGAGCGGCTTTGGGGGCCACCTGCTG	180
QY	181	GCTGTGCTGTGGCGGCGCGGAGTCCCGACGAGCCCCGCGCGCTTCGAGCGGCGACTTCG	240
Db	181	GCTGTGCTGTGGCGGCGCGGAGTCCCGACGAGCCCCGCGCGCTTCGAGCGGCGACTTCG	240
QY	241	CTCCAGTCAAGCCCGGCGCGGCTCTCACTTACCCGAGAGAGAGGCCACTCAATGAGA	300
Db	241	CTCCAGTCAAGCCCGGCGCGGCTCTCACTTACCCGAGAGAGAGGCCACTCTAATGAGA	300
QY	301	TGTTCCGCGAGGTTTGGAGAACTGATGAGAGACAGCGACCAAAATTGCGGCGGCTGG	360
Db	301	TGTTCCGCGAGGTTTGGAGAACTGATGAGAGAGACAGCGACCAAAATTGCGGCGGCTGG	360
QY	361	AAAGAGATGAGAGGAGAGAGAGTGTGTAAAGATCATCGAAGTGAACCTGGCAACT	420
Db	361	AAAGAGATGAGAGGAGAGAGAGTGTGTAAAGATCATCGAAGTGAACCTGGCAACT	420
QY	421	TACCTCCAGCTTACCAATGAGACCAACAGACACGAGGTTGGAAATATATACATCC	480
Db	421	TACCTCCAGCTTACCAATGAGACCAACAGACACGAGGTTGGAAATATATACATCC	480
QY	481	ATGTGACCGGAGAAATTCACAGATTAACCAACACGAGCTGGACAATGGTCTTTTCAG	540
Db	481	ATGTGACCGGAGAAATTCACAGATTAACCAACACGAGCTGGACAATGGTCTTTTCAG	540

QY 541 AGAAGTTATCATCTGTGGAGACGAAAGGACCAAGATGATCATCTG 600
Db 541 AGAAGTTATCATCTGTGGAGACGAAAGGACCAAGATGATCATCTG 600
QY 601 ACGAGACTGTGGGCGCCAGCATGTACTGCGAGTTTGACAGTTTCACTACACCGCCAGC 660
Db 601 ACGAGACTGTGGGCGCCAGCATGTACTGCGAGTTTGACAGTTTCACTACACCGCCAGC 660
QY 661 CATGCCGGGCGCAAGAGATGCTGTGACCCGGGACAGTGAAGTGTGTGAGACCACTGT 720
Db 661 CATGCCGGGCGCAAGAGATGCTGTGACCCGGGACAGTGAAGTGTGTGAGACCACTGT 720
QY 721 GTGTGGGAGTCACTGACCAAAATGGCCACACAGGGGACAAATGGGACCATCTGTACA 780
Db 721 GTGTGGGAGTCACTGACCAAAATGGCCACACAGGGGACAAATGGGACCATCTGTACA 780
QY 781 ACCAGAGGACTGCGACGCGGGGCTGTGTGTGCTTCCAGAGAGGCTGTGTCTCTG 840
Db 781 ACCAGAGGACTGCGACGCGGGGCTGTGTGTGCTTCCAGAGAGGCTGTGTCTCTG 840
QY 841 TGTGACACCCCTGCGCGTGGAGGGGCGAGTTTGCAATGACCCGCGACGCGCTTCTG 900
Db 841 TGTGACACCCCTGCGCGTGGAGGGGCGAGTTTGCAATGACCCGCGACGCGCTTCTG 900
QY 901 ACCTCATACCTGGGAGCTAGAGCTGTATGAGAGCCTTGACCGATGCCCTTGTGCCAGT 960
Db 901 ACCTCATACCTGGGAGCTAGAGCTGTATGAGAGCCTTGACCGATGCCCTTGTGCCAGT 960
QY 961 GCTTCCTTGTGCGACCCGACACGACCCGAGCTGTGTATGTGTGAAAGCCGACCTTGTG 1020
Db 961 GCTTCCTTGTGCGACCCGACACGACCCGAGCTGTGTATGTGTGAAAGCCGACCTTGTG 1020
QY 1021 GGAAGCCTGACCAAGATGGGAGATCTGTGCTGCCAGAGAGTCCCGATGATGATAG 1080
Db 1021 GGAAGCCTGACCAAGATGGGAGATCTGTGCTGCCAGAGAGTCCCGATGATGATAG 1080
QY 1081 TTGGCAGCTTATGAGAGAGGTGCGCCAGAGCTGTGAGAGACTTGAAGAGCCTGACTG 1140
Db 1081 TTGGCAGCTTATGAGAGAGGTGCGCCAGAGCTGTGAGAGACTTGAAGAGCCTGACTG 1140
QY 1141 AAGAGATGGCGCTGGGGAGGCTGTGGGCTGCGCGCTGCGACTGCTGGAGGGGAGAGA 1200
Db 1141 AAGAGATGGCGCTGGGGAGGCTGTGGGCTGCGCGCTGCGACTGCTGGAGGGGAGAGA 1200
QY 1201 TTTAGATGTGACACAGGCTGTGGGTATGATGTGCAATAGAAATAGCTAATTTATCCCA 1260
Db 1201 TTTAGATGTGACACAGGCTGTGGGTATGATGTGCAATAGAAATAGCTAATTTATCCCA 1260
QY 1261 GGTGTGTCTTAAAGCGTGGGCTGACAGGCTTCTCTCATCTCTTCCAGTAAGT 1320
Db 1261 GGTGTGTCTTAAAGCGTGGGCTGACAGGCTTCTCTCATCTCTTCCAGTAAGT 1320
QY 1321 TCCCTCTGGCTTGAACAGCATGAGGTGTGTGCAATTTGTCAGTCTCCCGAGGCTGTCT 1380
Db 1321 TCCCTCTGGCTTGAACAGCATGAGGTGTGTGCAATTTGTCAGTCTCCCGAGGCTGTCT 1380
QY 1381 CCAGGCTTCAAGCTGTGGTGTGGGAGAGTCAAGGAGGTTAAACTGTGACAGACAGTT 1440
Db 1381 CCAGGCTTCAAGCTGTGGTGTGGGAGAGTCAAGGAGGTTAAACTGTGACAGACAGTT 1440
QY 1441 GCAACCCCTGTCCAGATTAATGCTGTGCTTTCCTTACAGTTGGCAGACGCGTTGT 1500
Db 1441 GCAACCCCTGTCCAGATTAATGCTGTGCTTTCCTTACAGTTGGCAGACGCGTTGT 1500
QY 1501 TCTAATGCTTGTATTAATTTGTGAGGGGAGAGATGGAACAAATGTGAGTCTCCCTC 1560
Db 1501 TCTAATGCTTGTATTAATTTGTGAGGGGAGAGATGGAACAAATGTGAGTCTCCCTC 1560
QY 1561 TGATTTGTTTGGGAAATGTGAGAGAGTCCCTGCTTTGCAAAACATCAACCTGGGAA 1620
Db 1561 TGATTTGTTTGGGAAATGTGAGAGAGTCCCTGCTTTGCAAAACATCAACCTGGGAA 1620
QY 1621 AATGCAACAAATGAATTTTCCAGCAGTCTTTTCCATGGGCAATGATGATGCTGCTT 1680

Db 1621 AATGCAACAAATGAATTTTCCAGCAGTCTTTTCCATGGGCAATGATGATGCTGCTT 1680
QY 1681 CAGCTGTTCAGATGAATTTCTGTGTCAACCTGTGATTAATGATGTTTATTCACAGA 1740
Db 1681 CAGCTGTTCAGATGAATTTCTGTGTCAACCTGTGATTAATGATGTTTATTCACAGA 1740
QY 1741 GTTGTCTGAGTCTCTCACTCTGTGTGCGAGGAGATTTTCAATCCAAATCAATTTCC 1800
Db 1741 GTTGTCTGAGTCTCTCACTCTGTGTGCGAGGAGATTTTCAATCCAAATCAATTTCC 1800
QY 1801 TCTCTCAGCAGCCTGTGGGAGGGGATGATTTCTCTCTGTCTCATCAGGATCTCAGAG 1860
Db 1801 TCTCTCAGCAGCCTGTGGGAGGGGATGATTTCTCTCTGTCTCATCAGGATCTCAGAG 1860
QY 1861 GCTCAGAGCTGCAAGCTGTCTGCTCCCAAGTCAACAAGTATGAGAACCAAGAGCTTTC 1920
Db 1861 GCTCAGAGCTGCAAGCTGTCTGCTCCCAAGTCAACAAGTATGAGAACCAAGAGCTTTC 1920
QY 1921 ATCTGTTGTGACTCTAAGCTCAGTGTCTCTCACTACCCGACACGCTTGTGCGCA 1980
Db 1921 ATCTGTTGTGACTCTAAGCTCAGTGTCTCTCACTACCCGACACGCTTGTGCGCA 1980
QY 1981 CCAAAAGTCTCCCAAAAGAGAGAAATGGGATTTTCTTGAAGCATGACATCTGGA 2040
Db 1981 CCAAAAGTCTCCCAAAAGAGAGAAATGGGATTTTCTTGAAGCATGACATCTGGA 2040
QY 2041 AATTAAGGTCAAACTAATGTCATCTCCCTTAAAGTAACTACTGTTAGGAACAGCAGT 2100
Db 2041 AATTAAGGTCAAACTAATGTCATCTCCCTTAAAGTAACTACTGTTAGGAACAGCAGT 2100
QY 2101 GTTCTCAGATGTGGGAGCGGCTCTTCTTAATGAAGCAATGATTTGCACTGTCTCT 2160
Db 2101 GTTCTCAGATGTGGGAGCGGCTCTTCTTAATGAAGCAATGATTTGCACTGTCTCT 2160
QY 2161 CTTTGGCAGTTGCAATTAATGTAATTTGAAGATATGACTGAGCGTGAATACAGTTTA 2220
Db 2161 CTTTGGCAGTTGCAATTAATGTAATTTGAAGATATGACTGAGCGTGAATACAGTTTA 2220
QY 2221 CCTGCAAAACAGTACTTAATGTAATTTGAGGCGAGAGATTAATTAATTAATTTGCAAAAT 2280
Db 2221 CCTGCAAAACAGTACTTAATGTAATTTGAGGCGAGAGATTAATTAATTAATTTGCAAAAT 2280
QY 2281 CACTTACAGCAATGAAACATTAATCAACAAGTGGAGAAATCAAAACGAGCAGGCG 2340
Db 2281 CACTTACAGCAATGAAACATTAATCAACAAGTGGAGAAATCAAAACGAGCAGGCG 2340
QY 2341 TGTGTAAACATGTTGTATATGCGACTGCGAACAAGTGAATCAAGCTCAAGCAAAA 2400
Db 2341 TGTGTAAACATGTTGTATATGCGACTGCGAACAAGTGAATCAAGCTCAAGCAAAA 2400
QY 2401 TGAATTTTCAAGTGTCAAGACTGTGTGACACATGATTAATCAAGAGTCTTAAGT 2460
Db 2401 TGAATTTTCAAGTGTCAAGACTGTGTGACACATGATTAATCAAGAGTCTTAAGT 2460
QY 2461 TAAAGTTGACATGATGTATTAAGCATGCTTCTTGAATTTTAATTAATTAATTAAT 2520
Db 2461 TAAAGTTGACATGATGTATTAAGCATGCTTCTTGAATTTTAATTAATTAATTAAT 2520
QY 2521 AAGTTGCAATTTAGAAATCAAGCATTAATCACTTCAACTGCAAAAAAATTAATTAAT 2580
Db 2521 AAGTTGCAATTTAGAAATCAAGCATTAATCACTTCAACTGCAAAAAAATTAATTAAT 2580
QY 2581 AAAAAA 2586
Db 2581 AAAAAA 2586
RESULT 14
ABX96211
ID ABX96211 standard, cDNA; 2586 BP.
XX
AC ABX96211;

Db 61 CCGGCGGCTCCCGCGGGAGCGAGATCCAGTCCGGCCCGGAGCGCAACTCGGCCA 120
Qy 121 GTGCGGCGCGGCGGTGCGGGGCGAGCGAGATGCGACCGGCTTGGGGCCACCTGTGT 180
Db 121 GTGCGGCGCGGCGGTGCGGGGCGAGCGAGATGCGACCGGCTTGGGGCCACCTGTGT 180
Qy 181 GCGTGTGCTGCGCGCGCGGTCCCGACGCGCCCGCGCCGCTCCGACGCGACCTCGG 240
Db 181 GCGTGTGCTGCGCGCGCGGTCCCGACGCGCCCGCGCCGCTCCGACGCGACCTCGG 240
Qy 241 CTCCAGTCAAGCCCGCGCGCTCTCACTACCCGCGAGAGAGCCACCTTCAATGAGA 300
Db 241 CTCCAGTCAAGCCCGCGCGCTCTCACTACCCGCGAGAGAGCCACCTTCAATGAGA 300
Qy 301 TGTTCGCGAGGTTGAGGAACTGATGAGAGACGCGACCAAAATTGCGAGCGCGTGG 360
Db 301 TGTTCGCGAGGTTGAGGAACTGATGAGAGACGCGACCAAAATTGCGAGCGCGTGG 360
Qy 361 AAGAGATGAGGCGAAGAAAGCTGTCTAAAGCATCATGAAGTGAACCTGGCAACT 420
Db 361 AAGAGATGAGGCGAAGAAAGCTGTCTAAAGCATCATGAAGTGAACCTGGCAACT 420
Qy 421 TACCTCCAGCTATCAAAATGAGACCAACAGACAGAGGTTGAAATTAATACATCC 480
Db 421 TACCTCCAGCTATCAAAATGAGACCAACAGACAGAGGTTGAAATTAATACATCC 480
Qy 481 ATGTGACCGGAAATTCACAGATTAACCAACACAGACTGACCAAAATGCTTTTCAG 540
Db 481 ATGTGACCGGAAATTCACAGATTAACCAACACAGACTGACCAAAATGCTTTTCAG 540
Qy 541 AAGACATTAATCAATCTGTGAGAGACGAAGAGGCAAGAGGCAAGATTCATCTCG 600
Db 541 AAGACATTAATCAATCTGTGAGAGACGAAGAGGCAAGAGGCAAGATTCATCTCG 600
Qy 601 ACGAGACTGTGGGCGCCAGCATGTACTGCGAGTTGCGAGCTTCCAGTACACCTGCGAGC 660
Db 601 ACGAGACTGTGGGCGCCAGCATGTACTGCGAGTTGCGAGCTTCCAGTACACCTGCGAGC 660
Qy 661 CATGCGGCGGCGAAGAGATGCTTGCACCCGCGACAGTGAAGTCTGTGAGAGACCACTGT 720
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Qy 721 GTGTCTGGGGTCACTGCAACCAAAATGCGCACGAGGGCGAGCAATGGGACCATCTGTACA 780
Db 721 GTGTCTGGGGTCACTGCAACCAAAATGCGCACGAGGGCGAGCAATGGGACCATCTGTACA 780
Qy 781 ACCAGAGGACTGCCAGCGCGGCTGTGTGCTGTGCTTCCAGAGAGGCTGTGTTCCCTG 840
Db 781 ACCAGAGGACTGCCAGCGCGGCTGTGTGCTGTGCTTCCAGAGAGGCTGTGTTCCCTG 840
Qy 841 TGTGCAACCCCTGCGCGGTGAGAGGCGAGCTTTGCAATGACCCGCGACGCGGTTTCGG 900
Db 841 TGTGCAACCCCTGCGCGGTGAGAGGCGAGCTTTGCAATGACCCGCGACGCGGTTTCGG 900
Qy 901 ACTTCATCACTGTGGAGCTAGAGCTGTATGAGAGCTTGTGACCGATGCTTGTGCGAGT 960
Db 901 ACTTCATCACTGTGGAGCTAGAGCTGTATGAGAGCTTGTGACCGATGCTTGTGCGAGT 960
Qy 961 GCGTCTGTGCGAGCGCCACAGCCACAGCTGTGTATGTGTGAGAGCGACCTTGTGCG 1020
Db 961 GCGTCTGTGCGAGCGCCACAGCCACAGCTGTGTATGTGTGAGAGCGACCTTGTGCG 1020
Qy 1021 GGAGCGGTGACCAAGATGGGAGATCTGTGCTCCGAGAGAGTCCCGATGATGATGAG 1080
Db 1021 GGAGCGGTGACCAAGATGGGAGATCTGTGCTCCGAGAGAGTCCCGATGATGATGAG 1080
Qy 1081 TTGCGAGCTTCAATGAGAGAGTGTGCGCGAGAGCTGTGAGAGACTTGTGAGAGAGCTGTG 1140
Db 1081 TTGCGAGCTTCAATGAGAGAGTGTGCGCGAGAGCTGTGAGAGACTTGTGAGAGAGCTGTG 1140
Qy 1141 AAGAGATGCGGCTGGGGAGCTGTGCGGCTGCGCGCTGCTGTGAGAGGAGAGAGA 1200
Db 1141 AAGAGATGCGGCTGGGGAGCTGTGCGGCTGCGCGCTGCTGTGAGAGGAGAGAGA 1200

Db 1141 AAGAGATGCGGCTGGGGAGCTGTGCGGCTGCGCGCTGCTGTGAGAGGAGAGAGA 1200
Qy 1201 TTTAGATCGAGACGAGGCTGTGGAGATGTGCAATAGAAATAGCTAATTTATTTCCCA 1260
Db 1201 TTTAGATCGAGACGAGGCTGTGGAGATGTGCAATAGAAATAGCTAATTTATTTCCCA 1260
Qy 1261 GGTGTGTCTTTAGGCGGTGGCGTACAGAGCTTCTTCTACATCTTCTTCCAGTAAGTT 1320
Db 1261 GGTGTGTCTTTAGGCGGTGGCGTACAGAGCTTCTTCTACATCTTCTTCCAGTAAGTT 1320
Qy 1321 TCCCTCTGGCTTGACACATGAGGTGTGTGCAATTTGTGAGCTCCCGCGGCTTCT 1380
Db 1321 TCCCTCTGGCTTGACACATGAGGTGTGTGCAATTTGTGAGCTCCCGCGGCTTCT 1380
Qy 1381 CCAGGCTTCAAGTGTGTGCTTGGAGAGTCAAGCAGGTTAACTGAGAGGCAATT 1440
Db 1381 CCAGGCTTCAAGTGTGTGCTTGGAGAGTCAAGCAGGTTAACTGAGAGGCAATT 1440
Qy 1441 GCCACCCCTGTCCAGATTAATTTGCTGCTTGTGCTTACAGTTGGAGACAGCGTGT 1500
Db 1441 GCCACCCCTGTCCAGATTAATTTGCTGCTTGTGCTTACAGTTGGAGACAGCGTGT 1500
Qy 1501 TCTACATGCTTTGATTAATTTGTTGAGGGGAGAGATGAGAACAATGTGAGTCTCCCTC 1560
Db 1501 TCTACATGCTTTGATTAATTTGTTGAGGGGAGAGATGAGAACAATGTGAGTCTCCCTC 1560
Qy 1561 TGAATGTTTTGGGAAATGTGAGAGAGTCCCTGCTTGGCAAACTCACTTGGCA 1620
Db 1561 TGAATGTTTTGGGAAATGTGAGAGAGTCCCTGCTTGGCAAACTCACTTGGCA 1620
Qy 1621 AATGCAAAATGAAATTTTCCAGCAGTCTTCCATGAGGCAATGATGAGTGTGCTT 1680
Db 1621 AATGCAAAATGAAATTTTCCAGCAGTCTTCCATGAGGCAATGATGAGTGTGCTT 1680
Qy 1681 CAGCTGTGAGATGAATGTTCTGTCAACCTGCAATTAATGATGATTTATTCACAGA 1740
Db 1681 CAGCTGTGAGATGAATGTTCTGTCAACCTGCAATTAATGATGATTTATTCACAGA 1740
Qy 1741 GTGTGCTGAGCTCTTACCTGTGTGCGAGGAGATTTCTATTCAGATCAATTTCCC 1800
Db 1741 GTGTGCTGAGCTCTTACCTGTGTGCGAGGAGATTTCTATTCAGATCAATTTCCC 1800
Qy 1801 TCTCTCAGCAGCCTGTGGGAGGAGGTCAATGTTCTCTGTCTGTCATCAGGATCTCAG 1860
Db 1801 TCTCTCAGCAGCCTGTGGGAGGAGGTCAATGTTCTCTGTCTGTCATCAGGATCTCAG 1860
Qy 1861 GCTCAGAGCTGAGAGCTGCTTCCCAAGTCAACAAGCTAGAGAGACAGAGAGTTTC 1920
Db 1861 GCTCAGAGCTGAGAGCTGCTTCCCAAGTCAACAAGCTAGAGAGACAGAGAGTTTC 1920
Qy 1921 ACTGTGTGTGACTTAAGCTCAGTGTCTCTCACTACCCACACAGCCTTGTGTCCA 1980
Db 1921 ACTGTGTGTGACTTAAGCTCAGTGTCTCTCACTACCCACACAGCCTTGTGTCCA 1980
Qy 1981 CCAAAAGTCTCCCAAAAGAGAGAAATGAGATTTTCTTGAAGCATGCAATCTGGA 2040
Db 1981 CCAAAAGTCTCCCAAAAGAGAGAAATGAGATTTTCTTGAAGCATGCAATCTGGA 2040
Qy 2041 AATTAAGTCAAACTAATTTCTCAATCCCTCTAAAGTAACTACTGTGAGAAAGAGT 2100
Db 2041 AATTAAGTCAAACTAATTTCTCAATCCCTCTAAAGTAACTACTGTGAGAAAGAGT 2100
Qy 2101 GTTCTCAGAGTGTGGGAGCGGCTCTTAAATGAAGCAATGATTTGACACTGTCCCT 2160
Db 2101 GTTCTCAGAGTGTGGGAGCGGCTCTTAAATGAAGCAATGATTTGACACTGTCCCT 2160
Qy 2161 CTTTGGCAGTTGATTAATTAATTTGAAGGATTAATGAGCTGAGCTGAGATTA 2220
Db 2161 CTTTGGCAGTTGATTAATTAATTTGAAGGATTAATGAGCTGAGCTGAGATTA 2220
Qy 2221 CTTGCAAAACAGTACTTAATTAATTTGAGGCGAGAGATTAATTAATTTGCAAAAT 2280
Db 2221 CTTGCAAAACAGTACTTAATTAATTTGAGGCGAGAGATTAATTAATTTGCAAAAT 2280

Db 1 CGCCGCGCTCCGGAACCCGCGGCCGCCACCGCGCGCTCCGCACTGTGACACCCGAGC 60
Qy 61 CGCGCGCTCCCGCGCGGAGAGAGATGCAATCGCGCCCGGAGGCAATCGGTCCA 120
Db 61 CGCGCGCTCCCGCGCGGAGAGAGATGCAATCGCGCCCGGAGGCAATCGGTCCA 120
Qy 121 GTCGCGCGCGCGCTGCGCGGAGAGAGATGCAATCGCGCTTGCGGAGCAATCGGTCT 180
Db 121 GTCGCGCGCGCGCTGCGCGGAGAGAGATGCAATCGCGCTTGCGGAGCAATCGGTCT 180
Qy 181 GCTGCTGCTGCGCGCGGCTGCCAGAGGCCCCCGCGCTCCGAGCGGCACTTCG 240
Db 181 GCTGCTGCTGCGCGCGGCTGCCAGAGGCCCCCGCGCTCCGAGCGGCACTTCG 240
Qy 241 CTCGAGTCAAGCCCGCGCGCTCTCAGCTACCCGCGAGAGAGAGCACTCTCATAGA 300
Db 241 CTCGAGTCAAGCCCGCGCGCTCTCAGCTACCCGCGAGAGAGAGCACTCTCATAGA 300
Qy 301 TGTTCGCGAGGTTGAGGAACTGATGAGGACAGCGCAACAAATGCGCAGCGGTGG 360
Db 301 TGTTCGCGAGGTTGAGGAACTGATGAGGACAGCGCAACAAATGCGCAGCGGTGG 360
Qy 361 AAGAGATGAGGCGAGAGAGAGCTGTGCTAAAGCATCATGAAAGTGAACCTGGCAACT 420
Db 361 AAGAGATGAGGCGAGAGAGAGCTGTGCTAAAGCATCATGAAAGTGAACCTGGCAACT 420
Qy 421 TACCTCCGAGCTTACATGATGAGACCAACAGACACGAGAGTTGAAATTAATACATCC 480
Db 421 TACCTCCGAGCTTACATGATGAGACCAACAGACACGAGAGTTGAAATTAATACATCC 480
Qy 481 ATGTGCAACGAGAAATTCAGAAATTAACCAACAGACAGCTGCAATGCTTTTCAG 540
Db 481 ATGTGCAACGAGAAATTCAGAAATTAACCAACAGACAGCTGCAATGCTTTTCAG 540
Qy 541 AGACAGTATACATCTGTGGAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Db 541 AGACAGTATACATCTGTGGAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Qy 601 ACGAGAGCTGTGGGCGCCAGCATGTACTGCGAGTTTGGCACTTCCAGTACACCTGCG 660
Db 601 ACGAGAGCTGTGGGCGCCAGCATGTACTGCGAGTTTGGCACTTCCAGTACACCTGCG 660
Qy 661 CATGCGCGGCGCGAGAGATGCTGACCCGCGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 661 CATGCGCGGCGCGAGAGATGCTGACCCGCGAGAGAGAGAGAGAGAGAGAGAGAG 720
Qy 721 GTGCTGTGGGCTCATGCAACCAAAATGCGCACAGGCGGAGCAATGAGCACTGTGACA 780
Db 721 GTGCTGTGGGCTCATGCAACCAAAATGCGCACAGGCGGAGCAATGAGCACTGTGACA 780
Qy 781 ACCAGAGGAGCTGCGAGCGCGGCTGTGCTGCTTCCAGAGAGAGAGAGAGAGAGAG 840
Db 781 ACCAGAGGAGCTGCGAGCGCGGCTGTGCTGCTTCCAGAGAGAGAGAGAGAGAGAG 840
Qy 841 TGTGCAACCCCTGCGCGGAGGCGAGCTTTCATGACCCGCGAGCGGCTTTCG 900
Db 841 TGTGCAACCCCTGCGCGGAGGCGAGCTTTCATGACCCGCGAGCGGCTTTCG 900
Qy 901 ACCCTATACCTGCGAGAGCTGAGGCTGAGAGCTTTCATGAGAGAGAGAGAGAGAG 960
Db 901 ACCCTATACCTGCGAGAGCTGAGGCTGAGAGCTTTCATGAGAGAGAGAGAGAGAG 960
Qy 961 GCTTCCTTGCAGGCGCCAGCGAGCTGTGTATGTGTGCAAGCGCACTTTCG 1020
Db 961 GCTTCCTTGCAGGCGCCAGCGAGCTGTGTATGTGTGCAAGCGCACTTTCG 1020
Qy 1021 GAGAGCGCTGACCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Db 1021 GAGAGCGCTGACCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Qy 1081 TTGAGAGCTTTCATGAG 1140
Db 1081 TTGAGAGCTTTCATGAG 1140

Qy 1141 AAGAGATGAGCGCTGTGGGAGAGAGCTGCGCGCTGCGCGCTGCACTGTGAGAGAGAGAGAG 1200
Db 1141 AAGAGATGAGCGCTGTGGGAGAGAGCTGCGCGCTGCGCGCTGCACTGTGAGAGAGAGAGAG 1200
Qy 1201 TTTAGATCTGGAACCAAGCTGTGGGAGAGAGATGCAATGAGAAATAGCTAATTTTCCCA 1260
Db 1201 TTTAGATCTGGAACCAAGCTGTGGGAGAGAGATGCAATGAGAAATAGCTAATTTTCCCA 1260
Qy 1261 GGTGTGTGCTTTAAGGAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
Db 1261 GGTGTGTGCTTTAAGGAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
Qy 1321 TCCCTCTGAGCTTGAACAGCATGAGTGTGCTGCTTACAGTGTGCTGCTGCTGCTGCT 1380
Db 1321 TCCCTCTGAGCTTGAACAGCATGAGTGTGCTGCTTACAGTGTGCTGCTGCTGCTGCT 1380
Qy 1381 CCAGGCTTCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
Db 1381 CCAGGCTTCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
Qy 1441 GCCACCCCTGTCAGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
Db 1441 GCCACCCCTGTCAGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
Qy 1501 TCTACATGCTTGTATTAATTTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Db 1501 TCTACATGCTTGTATTAATTTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Qy 1561 TGAATGCTTGTGGGAG 1620
Db 1561 TGAATGCTTGTGGGAG 1620
Qy 1621 AAATGCAAAATGAATTTTCAAGAGTCTTTCATGAGGAGAGAGAGAGAGAGAGAG 1680
Db 1621 AAATGCAAAATGAATTTTCAAGAGTCTTTCATGAGGAGAGAGAGAGAGAGAGAG 1680
Qy 1681 CAGCTGTGAGATGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
Db 1681 CAGCTGTGAGATGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
Qy 1741 GTGTGCTGAGCTCTTACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
Db 1741 GTGTGCTGAGCTCTTACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
Qy 1801 TCTCTGAGAGAGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
Db 1801 TCTCTGAGAGAGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
Qy 1861 GCTCAGAGAGCTGCGAG 1920
Db 1861 GCTCAGAGAGCTGCGAG 1920
Qy 1921 ATCTGCTGTGAGCTTAAGCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
Db 1921 ATCTGCTGTGAGCTTAAGCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
Qy 1981 CCAAAAGTGTCCCAAAAG 2040
Db 1981 CCAAAAGTGTCCCAAAAG 2040
Qy 2041 ATTAAGGTCAATTAATTTCTCATCTCTTAAAGTAATTAATTAATTAATTAATTAAT 2100
Db 2041 ATTAAGGTCAATTAATTTCTCATCTCTTAAAGTAATTAATTAATTAATTAATTAAT 2100
Qy 2101 GTTCTCAGAGTGTGGGAG 2160
Db 2101 GTTCTCAGAGTGTGGGAG 2160
Qy 2161 CTTTGGCAGTTGATTAATTAATTTGAAAGGATTAATTAATTAATTAATTAATTAAT 2220
Db 2161 CTTTGGCAGTTGATTAATTTGAAAGGATTAATTAATTAATTAATTAATTAATTAAT 2220

Db 974 ACCGATCAGCTGGAGCTAGAGCTGATGGAGCTTGAGACCAATGCCCTTGCCAGT 1033
 Qy 961 GCTCTCTTGGCAGCCCCACACAGCTGCTGTAATGTGTGAAGCCGACCTTGCTG 1020
 Db 1034 GCTCTCTTGGCAGCCCCACACAGCTGCTGTAATGTGTGAAGCCGACCTTGCTG 1093
 Qy 1021 GGAGCCCGGACCAAGATGGGAGATCCGCTGCCAGAGAGGTCCCGATGAGATGAG 1080
 Db 1094 GGAAGCCGACCAAGATGGGAGATCCGCTGCCAGAGAGGTCCCGATGAGATGAG 1153
 Qy 1081 TTGGAGCTTCATGAGAGAGGTGCGCCAGAGCTGAGAGACCTGAGAGAGACCTG 1140
 Db 1154 TTGGAGCTTCATGAGAGAGGTGCGCCAGAGCTGAGAGACCTGAGAGAGACCTG 1213
 Qy 1141 AAGAGATGGCCCTGGGAGAGCTGCGCTGCCGCGCTGCACTGCTGGAGGGAGAGA 1200
 Db 1214 AAGAGATGGCCCTGGGAGAGCTGCGCTGCCGCGCTGCACTGCTGGAGGGAGAGA 1273
 Qy 1201 TTAGATCTGAGACAGGCTGTGGTAGATGTGCAATAGAAATAGCTAATTTATCCCA 1260
 Db 1274 TTAGATCTGAGACAGGCTGTGGTAGATGTGCAATAGAAATAGCTAATTTATCCCA 1333
 Qy 1261 GGTGTGTCTTTAGGCGGTGGGCTGACCCAGGCTTCTCTCAATCTTCTCCAGTAGT 1320
 Db 1334 GGTGTGTCTTTAGGCGGTGGGCTGACCCAGGCTTCTCTCAATCTTCTCCAGTAGT 1393
 Qy 1321 TCCCTCTGGCTTGAAGCATGAGGTGTGTGCAATTTGTCAGCTCCCGAGGCTGCT 1380
 Db 1394 TCCCTCTGGCTTGAAGCATGAGGTGTGTGCAATTTGTCAGCTCCCGAGGCTGCT 1453
 Qy 1381 CAGGCTTCAAGTCTGTGCTTGGAGAGTCAAGCAGGGTTAACTGCAAGAGAGCTT 1440
 Db 1454 CAGGCTTCAAGTCTGTGCTTGGAGAGTCAAGCAGGGTTAACTGCAAGAGAGCTT 1513
 Qy 1441 GCAACCCCTGCCAGATTATGAGCGCTTGGCTTCCCTACAGTTGGAGAGAGCGCTTGT 1500
 Db 1514 GCAACCCCTGCCAGATTATGAGCGCTTGGCTTCCCTACAGTTGGAGAGAGCGCTTGT 1573
 Qy 1501 TCTACATGCTTTGTAATTTGTTAGAGGAGAGAGATGAAACATGTGAGTCTCCTC 1560
 Db 1574 TCTACATGCTTTGTAATTTGTTAGAGGAGAGAGATGAAACATGTGAGTCTCCTC 1633
 Qy 1561 TGATTGCTTTGGGGAATGTGGAGAGAGTCCCTGTTGCAAAATCACTGAGCAA 1620
 Db 1634 TGATTGCTTTGGGGAATGTGGAGAGAGTCCCTGTTGCAAAATCACTGAGCAA 1693
 Qy 1621 AATGCAACAATGAAATTTCCAGCAGTCTTTCCATGGAGCATAGTAAGCTGTGCTT 1680
 Db 1694 AATGCAACAATGAAATTTCCAGCAGTCTTTCCATGGAGCATAGTAAGCTGTGCTT 1753
 Qy 1681 CAGCTGTGGAGATGAATGTTCTGTTCACCTGATTAACATGTGTTATTAATCCAGCA 1740
 Db 1754 CAGCTGTGGAGATGAATGTTCTGTTCACCTGATTAACATGTGTTATTAATCCAGCA 1813
 Qy 1741 GTGTGCTCAGTCTTACCTCTGTGTCAGAGGAGCATTTTCATCCAAAGTCAATCCC 1800
 Db 1814 GTGTGCTCAGTCTTACCTCTGTGTCAGAGGAGCATTTTCATCCAAAGTCAATCCC 1873
 Qy 1801 TCTCTCAGACAGCTGGGAGAGGGGTCAATGTTCTCTGCTCCATCAGGATCTCAGAG 1860
 Db 1874 TCTCTCAGACAGCTGGGAGAGGGGTCAATGTTCTCTGCTCCATCAGGATCTCAGAG 1933
 Qy 1861 GCTCAGAGCTGCAAGCTGCTTGCACCAAGTCAACAGCTAATGAAACCAAGAGAGTTTC 1920
 Db 1934 GCTCAGAGCTGCAAGCTGCTTGCACCAAGTCAACAGCTAATGAAACCAAGAGAGTTTC 1993
 Qy 1921 ATCTGCTTGAAGCTTAAGCTCAGTCTCTCTCCACTACCCCAACAGAGCTTGCTGCA 1980
 Db 1994 ATCTGCTTGAAGCTTAAGCTCAGTCTCTCTCCACTACCCCAACAGAGCTTGCTGCA 2053
 Qy 1981 CCAAAAGTCTCCCAAAAGAGAGAGATGGAGATTTTTC--TTGAGGATGACATCTG 2038

Db 2054 CCAAAAGTCTCCCAAAAGAGAGAGATGGATTTTCTTTGAGGATGACATCTG 2113
 Qy 2039 GAATTAAGTCAAACTAATTTCTCATATCCCTTAATAAGTAACTCTGTAGAGACAGA 2098
 Db 2114 GAATTAAGTCAAACTAATTTCTCATATCCCTTAATAAGTAACTCTGTAGAGACAGA 2173
 Qy 2099 GTGTTCTCAGTGTGGGAGCAGCCCTCTCTAATGAAGACATGATATGACACTGCC 2158
 Db 2174 GTGTTCTCAGTGTGGGAGCAGCCCTCTCTAATGAAGACATGATATGACACTGCC 2233
 Qy 2159 CTCTTTGGAGTTGCAATTAATGTAATTTGAAAGTATAGCTGACCGTATGATACAGTT 2218
 Db 2234 CTCTTTGGAGTTGCAATTAATGTAATTTGAAAGTATAGCTGACCGTATGATACAGTT 2293
 Qy 2219 AACCTCAGAAACAGTACTTAAGTATGTTGAGGCGAGAGATTAATAATTTGCAAA 2278
 Db 2294 AACCTCAGAAACAGTACTTAAGTATGTTGAGGCGAGAGATTAATAATTTGCAAA 2353
 Qy 2279 ATCACTTACAGCACTGAAAGCAATTTATCAACACGTTGAGAGAAATCAACCGAGAG 2338
 Db 2354 ATCACTTACAGCACTGAAAGCAATTTATCAACACGTTGAGAGAAATCAACCGAGAG 2413
 Qy 2339 GCTGTGTGAAACATGAGTGTATATGCGACGTCGAACTGAACCTCTAGCCACTCCCA 2398
 Db 2414 GCTGTGTGAAACATGAGTGTATATGCGACGTCGAACTGAACCTCTAGCCACTCCCA 2473
 Qy 2399 AATGATGTTTTAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2458
 Db 2474 AATGATGTTTTAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2533
 Qy 2459 TTTAAAGTGCACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2518
 Db 2534 TTTAAAGTGCACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2593
 Qy 2519 ATGAGTGCATTTAGAAATCAAGCAATTAATCACTTCAACTGC 2560
 Db 2594 ATGAGTGCATTTAGAAATCAAGCAATTAATCACTTCAACTGC 2635

RESULT 17
 AB281805
 ID AB281805 standard; DNA; 2450 BP.
 XX
 AC AB281805;
 XX
 DT 11-JUN-2003 (first entry)
 XX
 DE Human dickkopf2 nucleic acid sequence.
 XX
 KW Human; dickkopf2; stem cell; stem-loop RNA; anti-anemic;
 KW cerebroprotective; neuroprotective; neotropic; anti-parkinsonian;
 KW cardiant; hepatotropic; antidiabetic; vulnerary; gene therapy;
 KW gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN MO203012082-A2.
 XX
 PD 13-FEB-2003.
 XX
 PF 25-JUL-2002; 2002MO-GB03409.
 XX
 PR 26-JUL-2001; 2001GB-0018223.
 XX
 PA (AXOR-) AXORDIA LTD.
 PI Andrews P, Walsh J, Gokhale P;
 DR WPI; 2003-278398/27.
 XX
 PT Modulating the differentiation state of a stem cell, useful for
 PT treating e.g. pernicious anemia, stroke, cirrhosis, diabetes or a
 PT neurodegenerative disease, comprises contacting a stem cell with a stem

PT loop RNA -
XX
PS Claim 7; Fig 15; 85bp; English.
XX
CC The present sequence is the nucleic acid sequence of human
CC dikephof2. The invention relates to a method of modulating the
CC differentiation state of a stem cell, such as an embryonic stem
CC cell, embryonic germ cell, embryonal carcinoma cell, hematopoietic
CC stem cell, muscle stem cell, nerve stem cell, skin dermal sheath
CC stem cell, liver stem cell or teratocarcinoma cell. The method
CC involves contacting the stem cell with a stem-loop RNA molecule or
CC a nucleic acid molecule or vector encoding the stem-loop RNA, where
CC the nucleic acid is preferably derived from one of the nucleic acid
CC sequences in AB281794-844, including the present sequence, and may
CC encode a cell surface receptor expressed by a stem cell, or a ligand.
CC The RNA molecule, the nucleic acid molecule or the vector is useful
CC for promoting the differentiation of stem cells and for providing
CC differentiated cells/tissues for the treatment of diseases in which
CC cell/tissues are destroyed by the disease. These diseases include
CC pernicious anaemia, stroke, neurodegenerative diseases such as
CC Parkinson's disease and Alzheimer's disease, coronary heart disease,
CC cirrhosis, diabetes, or nerve damage as a consequence of trauma
CC (e.g. replacement of spinal cord tissue) (claimed).

XX
SQ Sequence 2450 BP; 595 A; 622 C; 664 G; 569 T; 0 other;

Query Match 87.28; Score 2255; DB 25; Length 2450;
Best Local Similarity 99.98; Pred. No. 0;

Matches 2435; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 126 GGGCGCGGCTGCGGGCGAGCGAGATGCGCGCTTGCGGCGACCTGCTGCTG 185
Db 8 GGGCGCGGCTGCGGGCGAGCGAGATGCGCGCTTGCGGCGACCTGCTGCTG 67
QY 186 CTGCTGCGCGCGCGCTGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 245
Db 68 CTGCTGCGCGCGCGCTGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 127
QY 246 GTCAAGCCCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 305
Db 128 GTCAAGCCCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 187
QY 306 CGCGAGGTTGAGAACTGATGAGAGACCGAGACAAATTGCGACGCGGTGGAAG 365
Db 188 CGCGAGGTTGAGAACTGATGAGAGACCGAGACAAATTGCGACGCGGTGGAAG 247
QY 366 ATGAGGCGAGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 425
Db 248 ATGAGGCGAGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 307
QY 426 CCCAGCTATCAATGAGACCAACAGACAGACGAAAGTTGAAATATATACATCATG 485
Db 308 CCCAGCTATCAATGAGACCAACAGACAGACGAAAGTTGAAATATATACATCATG 367
QY 486 CACCGAATAATTCACAGATTAACACACACAGCTGGAATGCTTTTCAAGACA 545
Db 368 CACCGAATAATTCACAGATTAACACACACAGCTGGAATGCTTTTCAAGACA 427
QY 546 GTATACATCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 605
Db 428 GTATACATCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 487
QY 606 GACTGTGGGCGCGAGATGTAATGCAAGTTGCGAGCTTCCAGTAACCTCCAGCCATG 665
Db 488 GACTGTGGGCGCGAGATGTAATGCAAGTTGCGAGCTTCCAGTAACCTCCAGCCATG 547
QY 666 CGGGGCGAG 725
Db 548 CGGGGCGAG 607
QY 726 TGGGATCACTGACCAAAATGCGACCAAGGCGAGAGAGAGAGAGAGAGAGAGAG 785
Db 608 TGGGATCACTGACCAAAATGCGACCAAGGCGAGAGAGAGAGAGAGAGAGAGAG 667

QY 786 AGGAGCTGCACCGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 845
Db 668 AGGAGCTGCACCGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 727
QY 846 ACAACCTTGGCCCGTGGAGAGCGAGAGTTTGGCAATGACCCCGCAGCCGCTTGTGAGCTTC 905
Db 728 ACAACCTTGGCCCGTGGAGAGCGAGAGTTTGGCAATGACCCCGCAGCCGCTTGTGAGCTTC 787
QY 906 ATCACTTGGAG 965
Db 788 ATCACTTGGAG 847
QY 966 CTCTCCAGCCCGCAG 1025
Db 848 CTCTCCAGCCCGCAG 907
QY 1026 CGTGAACCAAGATGGGAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1085
Db 908 CGTGAACCAAGATGGGAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 967
QY 1086 AGCTTCATGAG 1145
Db 968 AGCTTCATGAG 1027
QY 1146 ATGCGCTGCGGGGAGAGCTGCGCGCTGCGCGCGCTGCACTGCTGCGAGAGAGAGATTAG 1205
Db 1028 ATGCGCTGCGGGGAGAGCTGCGCGCTGCGCGCGCTGCACTGCTGCGAGAGAGAGATTAG 1087
QY 1206 ATCTGAGACAGAGCTGCGGATGATGATGATGATGATGATGATGATGATGATGATG 1265
Db 1088 ATCTGAGACAGAGCTGCGGATGATGATGATGATGATGATGATGATGATGATGATG 1147
QY 1266 GTGCTTTAGGCGTGGGCTGACCAAGCTTCTTCTCATCTTCTTCTCCAGTAAGTTCCCC 1325
Db 1148 GTGCTTTAGGCGTGGGCTGACCAAGCTTCTTCTCATCTTCTTCTCCAGTAAGTTCCCC 1207
QY 1326 TCTGCTTGAACAGATGAGAGTGTGTGATGATGATGATGATGATGATGATGATGATG 1385
Db 1208 TCTGCTTGAACAGATGAGAGTGTGTGATGATGATGATGATGATGATGATGATGATG 1267
QY 1386 CTTCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1445
Db 1268 CTTCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1327
QY 1446 CCTGCTCAGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1505
Db 1328 CCTGCTCAGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1387
QY 1506 ATGCTTTGATTAATGTTTGAAGGAGAGAGATGAAACAATGTGAGAGTCTCCCTGATTT 1565
Db 1388 ATGCTTTGATTAATGTTTGAAGGAGAGAGATGAAACAATGTGAGAGTCTCCCTGATTT 1447
QY 1566 GGTTTTGGGAGAAATGTGAG 1625
Db 1448 GGTTTTGGGAGAAATGTGAG 1507
QY 1626 CAACAAATGAATTTTCCACGAGATTTTCCATGAGGCAATGATGATGATGATGATGATGATG 1685
Db 1508 CAACAAATGAATTTTCCACGAGATTTTCCATGAGGCAATGATGATGATGATGATGATGATG 1567
QY 1686 GTTGAAGATGAATTTTCTGTTCAACCCGATTAATGATGATGATGATGATGATGATGATG 1745
Db 1568 GTTGAAGATGAATTTTCTGTTCAACCCGATTAATGATGATGATGATGATGATGATGATGATG 1627
QY 1746 GCTGAGCTTCACTCTGCTGCGAGGAGAGATTTTCAATATCAAGATCAATATTCCTCTCT 1805
Db 1628 GCTGAGCTTCACTCTGCTGCGAGGAGAGATTTTCAATATCAAGATCAATATTCCTCTCT 1687
QY 1806 CAGCACACCTGCGGAGAGAGAGATGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1865
Db 1688 CAGCACACCTGCGGAGAGAGAGATGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1747

Db 548 CGGGGCGCAGAGATGCTGTGCAACCCGGGACAGTGAAGTGTGTGAGAACCAAGCTGTGTGTC 607
 Qy 726 TGGGCTACTGTCACCAAAATGCGCCACCAAGGGGCAAGCATGTGGACATCTGTGAACAACG 785
 Db 608 TGGGCTACTGTCACCAAAATGCGCCACCAAGGGGCAAGCATGTGGACATCTGTGTGCAACG 667
 Qy 786 AGGAGTGCAGAGCGGGGCTGTGTGTGCTTCCAGAGAGGCTGTGTGTGCTGTGTGTG 845
 Db 668 AGGAGTGCAGAGCGGGGCTGTGTGTGCTTCCAGAGAGGCTGTGTGTGCTGTGTGTG 727
 Qy 846 ACACCCCTGCTGCTGTGAGGGGAGCTTGGCATGATGCCCGCAGCGGCTTCTGAGCTTC 905
 Db 728 ACACCCCTGCTGCTGTGAGGGGAGCTTGGCATGATGCCCGCAGCGGCTTCTGAGCTTC 787
 Qy 906 ATCACTTGGGAGCTGAGAGCTGTGAGAGCTTGGACCGATGAGCTTGTGCTGTGAGCTTC 965
 Db 788 ATCACTTGGGAGCTGAGAGCTGTGAGAGCTTGGACCGATGAGCTTGTGCTGTGAGCTTC 847
 Qy 966 CTCTGCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCC 1025
 Db 848 CTCTGCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCC 907
 Qy 1026 CGTACCAAGATGGGGAGATCTGTGTGCTGCAAGAGAGTCCGATGATGATGATGATGATG 1085
 Db 908 CGTACCAAGATGGGGAGATCTGTGTGCTGCAAGAGAGTCCGATGATGATGATGATGATG 967
 Qy 1086 AGCTTCAATGAGAGAGTGTGCGCCAGAGAGCTGTGAGAGAGCTGTGAGAGAGCTGTGAG 1145
 Db 968 AGCTTCAATGAGAGAGTGTGCGCCAGAGAGCTGTGAGAGAGCTGTGAGAGAGCTGTGAG 1027
 Qy 1146 ATGGCGCTGGGGGAGGCTGTGCGGCTGCGCGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1205
 Db 1028 ATGGCGCTGGGGGAGGCTGTGCGGCTGCGCGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1087
 Qy 1206 ATCTGACCAAGCTGTGGGTAGATGTGCAATAGCAATAGCAATAGCAATAGCAATAGCA 1265
 Db 1088 ATCTGACCAAGCTGTGGGTAGATGTGCAATAGCAATAGCAATAGCAATAGCAATAGCA 1147
 Qy 1266 GTGCTTTAGGGGTGGGTGACCAAGCTTCTTCTCAATCTTCTTCTTCTTCTTCTTCTTCT 1325
 Db 1148 GTGCTTTAGGGGTGGGTGACCAAGCTTCTTCTCAATCTTCTTCTTCTTCTTCTTCTTCT 1207
 Qy 1326 TCTGAGCTTGAAGATGAGTGTGTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 1385
 Db 1208 TCTGAGCTTGAAGATGAGTGTGTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 1267
 Qy 1386 CTTCACAGCTGTGTGTGTGAGAGTCAAGCAAGGCTTAACTGTGAGAGAGAGCTTGTGCA 1445
 Db 1268 CTTCACAGCTGTGTGTGTGAGAGTCAAGCAAGGCTTAACTGTGAGAGAGAGCTTGTGCA 1327
 Qy 1446 CCTGTTCAGATTTATGTGCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 1505
 Db 1328 CCTGTTCAGATTTATGTGCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 1387
 Qy 1506 ATGCTTTGATTAATTTTGAAGGGAGAGATGAAAAATGTGAGCTTCTCTCTGATTT 1565
 Db 1388 ATGCTTTGATTAATTTTGAAGGGAGAGATGAAAAATGTGAGCTTCTCTCTGATTT 1447
 Qy 1566 GGTTTTGGGGGAAATGTGAGAAAGTGTGCTTGTGCAAAATCAACTGTGAGCAAAAATG 1625
 Db 1448 GGTTTTGGGGGAAATGTGAGAAAGTGTGCTTGTGCAAAATCAACTGTGAGCAAAAATG 1507
 Qy 1626 CAACAATGAATTTTCAAGCAGATTCTTTCATGGGCAATGATGATGATGATGATGATGAT 1685
 Db 1508 CAACAATGAATTTTCAAGCAGATTCTTTCATGGGCAATGATGATGATGATGATGATGAT 1567
 Qy 1686 GTTGAGATGAATTTCTGTTCACCTGTGATCAATGTGTTTATGATGATGATGATGATGAT 1745
 Db 1568 GTTGAGATGAATTTCTGTTCACCTGTGATCAATGTGTTTATGATGATGATGATGATGAT 1627
 Qy 1746 GCTCAGCTCTTACCTGTGTGCGAGGAGCAATTTCAATGCAAGATCAATTTCCCTCTCT 1805
 Db 1628 GCTCAGCTCTTACCTGTGTGCGAGGAGCAATTTCAATGCAAGATCAATTTCCCTCTCT 1687

Qy 1806 CAGACAGCTTGGGAGAGGGGTCAATGTTCTCTCTGTCATCAAGGATCTCAGAGGCTCA 1865
 Db 1688 CAGACAGCTTGGGAGAGGGGTCAATGTTCTCTCTGTCATCAAGGATCTCAGAGGCTCA 1747
 Qy 1866 GAGACTGCAAGCTGTTGCCCAAGTCAACAGCTAGTGAAGACCAAGACAGCACTTCACTG 1925
 Db 1748 GAGACTGCAAGCTGTTGCCCAAGTCAACAGCTAGTGAAGACCAAGACAGCACTTCACTG 1807
 Qy 1926 GTTGAGCTTAAGTCAAGTGTCTCTTCACTTACCCCAACAGCTTGTGAGCAACAAA 1985
 Db 1808 GTTGAGCTTAAGTCAAGTGTCTCTTCACTTACCCCAACAGCTTGTGAGCAACAAA 1867
 Qy 1986 AGTGTCTCCCAAAAGGAAGGAATGGGATTTTTC--TTGAGGAGATGACATCTGAATT 2043
 Db 1868 AGTGTCTCCCAAAAGGAAGGAATGGGATTTTTC--TTGAGGAGATGACATCTGAATT 1927
 Qy 2044 AAGTCAAACTTAATTTCTCAATCTCTTCAAAAGTAACTACTGTTAAGAACAGAGTGT 2103
 Db 1928 AAGTCAAACTTAATTTCTCAATCTCTTCAAAAGTAACTACTGTTAAGAACAGAGTGT 1987
 Qy 2104 CTCAAGTGTGGGAGAGCGGCTCTTCTATGAGACATGATATTTGACACTGTCCCTCT 2163
 Db 1988 CTCAAGTGTGGGAGAGCGGCTCTTCTATGAGACATGATATTTGACACTGTCCCTCT 2047
 Qy 2164 TGGCACTTGCAATTAATCTTTGAAAGGTATATGACTGAGGTGATCAAGGTTAACT 2223
 Db 2048 TGGCACTTGCAATTAATCTTTGAAAGGTATATGACTGAGGTGATCAAGGTTAACT 2107
 Qy 2224 GCAGAAACAGTACTAGGTAATTTGAGGAGAGATTAATGAAATTTGCCAAATCAC 2283
 Db 2108 GCAGAAACAGTACTAGGTAATTTGAGGAGAGATTAATGAAATTTGCCAAATCAC 2167
 Qy 2284 TTAGCAGCACTGAAGCAATTAATCAACAGTGTGAGAAATCAAAACAGAGGCTGT 2343
 Db 2168 TTAGCAGCACTGAAGCAATTAATCAACAGTGTGAGAAATCAAAACAGAGGCTGT 2227
 Qy 2344 GTGAAACATGTGTGAATATGAGCACTGCGAACACTGAACTCAAGCTCAACAAATGA 2403
 Db 2228 GTGAAACATGTGTGAATATGAGCACTGCGAACACTGAACTCAAGCTCAACAAATGA 2287
 Qy 2404 TGTTCAGAGTGTGATGACTGTGTCACCAATGATTCATCCAGATTTAAAGTTTAA 2463
 Db 2288 TGTTCAGAGTGTGATGACTGTGTCACCAATGATTCATCCAGATTTAAAGTTTAA 2347
 Qy 2464 AGTTGCAATGATTTGATTAAGATGCTTCTTGTGATTTAAATGATTAATTAAGATG 2523
 Db 2348 AGTTGCAATGATTTGATTAAGATGCTTCTTGTGATTTAAATGATTAATTAAGATG 2407
 Qy 2524 TTGCATTTAGAAATCAAGCATTAATCACTTCAACTGC 2560
 Db 2408 TTGCATTTAGAAATCAAGCATTAATCACTTCAACTGC 2444

RESULT 19
 ABX75308
 ID ABX75308 standard; cDNA; 2450 BP.
 XX
 AC ABX75308;
 XX
 DT 25-MAR-2003 (first entry)
 XX
 DE Human cDNA for dickkopf3.
 XX
 XX Gene; Notch; Wnt; embryonic stem cell; embryogenesis; ss;
 KM differentiation; ligand; Parkinson's disease; Huntington's disease;
 KM motor neuron disease; heart disease; diabetes; liver disease; human;
 KM cirrhosis; renal disease; AIDS; acquired immunodeficiency syndrome.
 OS Homo sapiens.
 XX
 XX PN WO200277204-A2.
 XX

PD 03-OCT-2002.
 XX 25-MAR-2002, 2002MO-GB01195.
 PF 23-MAR-2001, 2001GB-0007296.
 PR 23-MAR-2001, 2001GB-0007299.
 PR 17-APR-2001, 2001GB-0009346.
 XX
 XX (AXOR-) AXORDIA LTD.
 PA
 XX
 PI Andrews P, Walsh J, Gokhale P;
 PS WPI, 2003-092852/08.
 DR
 XX
 XX Modulating the differentiation of embryonic stem cells by providing
 PT ligands which bind receptors in the Notch and Wnt pathways, useful for
 PT treating diseases such as Parkinson's, Huntington's, heart disease,
 PT diabetes and AIDS
 XX
 XX Disclosure, Fig 26; 121pp, English.
 CC
 CC The invention relates to modulating the differentiation of an embryonic
 CC stem cell, comprising: (a) providing a culture of embryonic stem cells;
 CC (b) providing at least one ligand or its active binding fragment,
 CC capable of binding its cognate receptor polypeptide expressed by the
 CC embryonic stem cell; (c) forming a culture comprising embryonic stem
 CC cells and the ligand; and (d) growing the cell culture. Also included
 CC are: (1) Modulating the differentiation of embryonic stem cells,
 CC comprising: (a) providing a cell transfected with a nucleic acid molecule
 CC selected from: (i) any of 9 fully defined Wnt nucleic acid sequences;
 CC (ii) a nucleic acid molecule that hybridises to the nucleic acid in
 CC (i); and which encodes a ligand capable of modulating embryonic stem
 CC cell differentiation, or capable of binding a Wnt receptor; or
 CC (iii) nucleic acid molecules which are degenerate as a result of the
 CC genetic code to the sequences of (i) or (ii); (b) forming a culture
 CC comprising the cell identified in (a) with an embryonic stem cell; and
 CC (c) growing the culture for the maintenance and/or differentiation of
 CC the embryonic stem cell; (2) Inhibiting the differentiation of embryonic
 CC stem cells, comprising: (a) providing at least one polypeptide or its
 CC active fragment, that are inhibitors of the Wnt signalling pathway;
 CC (b) forming a culture comprising the cell identified in (a) with an
 CC embryonic stem cell; and (c) growing the culture for the maintenance of
 CC the embryonic stem cells in an undifferentiated state; or (3) Inhibiting the
 CC differentiation of embryonic stem cells, comprising: (a) providing a cell
 CC transfected with a nucleic acid molecule selected from: (i) a molecule
 CC encoding a Wnt inhibitory polypeptide; (ii) a molecule which hybridises
 CC to the molecule of (i) and encodes a polypeptide capable of inhibiting
 CC Wnt signalling; and (iii) nucleic acid molecules which are degenerate as
 CC a result of the genetic code to the sequences of (i) or (ii); (b) forming
 CC a culture comprising the cell identified in (a) with an embryonic stem
 CC cell; and (c) growing the culture for the maintenance of embryonic stem
 CC cells in an undifferentiated state; and (4) A cell, therapeutic cell or
 CC cell culture obtainable by any of the methods cited above.
 CC The therapeutic cell of the present invention is useful in the
 CC treatment of an animal, preferably a human, comprising administering a
 CC cell composition comprising embryonic stem cells which have been
 CC induced to differentiate into at least one cell-type. The cell is also
 CC useful for the manufacture of a composition for use in treatment of
 CC diseases such as Parkinson's disease, Huntington's disease, motor
 CC neuron disease, heart disease, diabetes, liver disease (e.g.
 CC cirrhosis), renal disease and AIDS (acquired immunodeficiency syndrome).
 CC The present sequence encodes a Wnt or Notch pathway protein
 CC (i.e. a ligand for the method of the invention).
 XX
 XX Sequence 2450 BP; 595 A; 622 C; 664 G; 569 T; 0 other;
 QQ
 QQ Query Match 87.2%; Score 2255; DB 25; Length 2450;
 QQ Best Local Similarity 99.9%; Pct. No. 0;
 QQ Matches 2435; Conservative 0; Mismatches 0; Indels 2; Gaps 1

QY	186	CTGTGTGGCGGGGAGGGGTGCTCCCAAGGCCCCCGGCGCCGCTCCGACCGGGGACCTGTGGCTCCCA	245
Db	68	CTGTGTGGCGGGGAGGGGTGCTCCCAAGGCCCCCGGCGCCGCTCCGACCGGGGACCTGTGGCTCCCA	127
QY	246	GTCAGGCCCCGGCTCGCTCAAGCTACCCGACAGAGGGGCCACCTCCAAATGAGATGTTCC	305
Db	128	GTCAGGCCCCGGCTCGCTCAAGCTACCCGACAGAGGGGCCACCTCCAAATGAGATGTTCC	187
QY	306	CGGAGGGTTGAGGAACTCGATGAGAGGACAGCGACGACCAAAATTTGGCGACCGGGTGAAGAG	365
Db	188	CGGAGGGTTGAGGAACTCGATGAGAGGACAGCGACGACCAAAATTTGGCGACCGGGTGAAGAG	247
QY	366	ATGAGGGCAGAAAGAGCTGTGCTTAAGCATCATAGAAAGTGAACCTGGCAACTTACCT	425
Db	248	ATGAGGGCAGAAAGAGCTGTGCTTAAGCATCATAGAAAGTGAACCTGGCAACTTACCT	307
QY	426	CCGAGCATATCAATATGAGCAACAACAGACAGCAAGGTTGGAAATATATACATCATATGTG	485
Db	308	CCGAGCATATCAATATGAGCAACAACAGACAGCAAGGTTGGAAATATATACATCATATGTG	367
QY	486	CACCGAGAAATTCACAAAGATPACCAACACACGACTGGACAAATGTCCTTTTCAGAGACA	545
Db	368	CACCGAGAAATTCACAAAGATPACCAACACACGACTGGACAAATGTCCTTTTCAGAGACA	427
QY	546	GTTATTCATCTGTGGGAGAGCGAAGAAAGGACAGACGACGATGATCATATGAGAG	605
Db	428	GTTATTCATCTGTGGGAGAGCGAAGAAAGGACAGACGATGATCATATGAGAG	487
QY	606	GACTGTGGGCCCCAGCATGTATCTGCAGATTGGCCAGCTTCAGATACACTGCGACCATGC	665
Db	488	GACTGTGGGCCCCAGCATGTATCTGCAGATTGGCCAGCTTCAGATACACTGCGACCATGC	547
QY	666	CGGGGCGAGAGATGTCTGTGCACCCCGGGACAGTGTAGTGTGGAGACCAAGCTGTGTCTC	725
Db	548	CGGGGCGAGAGATGTCTGTGCACCCCGGGACAGTGTGTGGAGACCAAGCTGTGTCTC	607
QY	726	TGGGGTCATCTGCACCAAAATGGCCACAGGGGCGACATGGGACATCTGTGACAAACGAG	785
Db	608	TGGGGTCATCTGCACCAAAATGGCCACAGGGGCGACATGGGACATCTGTGACAAACGAG	667
QY	786	AGGAGCTGCCAGCGCGGGGCTGTGTGTGCCCTTCAGAGAGGCGCTGTCTCCCTGTGTGC	845
Db	668	AGGAGCTGCCAGCGCGGGGCTGTGTGTGCCCTTCAGAGAGGCGCTGTCTCCCTGTGTGC	727
QY	846	ACACCTCTGCCCGTGGAGGGGAGCTTTGCCATGACCCCGCAGCGCGCTTCTGSACTTC	905
Db	728	ACACCTCTGCCCGTGGAGGGGAGCTTTGCCATGACCCCGCAGCGCGCTTCTGSACTTC	787
QY	906	ATCACCTGGGAGCTAGAGCTGATGAGAGCTTTGAGCCGATGCGCTTGTGTGCAGTGGCCTC	965
Db	788	ATCACCTGGGAGCTAGAGCTGATGAGAGCTTTGAGCCGATGCGCTTGTGTGCAGTGGCCTC	847
QY	966	CTCTGCCAGCCCCACAGCCACAGCTGTGTATGTGTGCAAGCCGACCTTGTGGGGAGGC	1025
Db	848	CTCTGCCAGCCCCACAGCCACAGCTGTGTATGTGTGCAAGCCGACCTTGTGGGGAGGC	907
QY	1026	CGTACCAAGAATGGAGAGATCTGTCTGCCAGAGAGGCCCCGATAGGTATGAGATTGGC	1085
Db	908	CGTACCAAGAATGGAGAGATCTGTCTGCCAGAGAGTCCCCGATAGGTATGAGATTGGC	967
QY	1086	AGCTTCATGAGAGAGGTGCGCCAGAGCTGGAGACTCTGAGAGAGAGCCTGACTGGAAGAG	1145
Db	968	AGCTTCATGAGAGAGGTGCGCCAGAGACTGGAGACTCTGAGAGAGAGCCTGACTGGAAGAG	1027
QY	1146	ATGCGCGCTGGGGAGAGCTGCGCGCTGCGCGCTCACACTGCTGGAGAGGGGAAAGATTTAG	1205
Db	1028	ATGCGCGCTGGGGAGAGCTGCGCGCTGCGCGCTCACACTGCTGGAGAGGGGAAAGATTTAG	1087
QY	1206	ATCTGAGACCAAGCTGTGGGTGATATGTGCAATAGAAATATTTATTTTCCCAAGGCT	1265
Db	1088	ATCTGAGACCAAGCTGTGGGTGATATGTGCAATAGAAATATTTATTTTCCCAAGGCT	1147


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QY 1266 GTGCTTTAGGGGCTGAGGCTTCTTCTACATCTTCTTCCAGTAAGTTTCCC 1325
DB 1148 GTGCTTTAGGGGCTGAGGCTTCTTCTACATCTTCTTCCAGTAAGTTTCCC 1307
QY 1326 TCTGGCTTTGACAGATGAGTGTGTGTGATTTGTTACAGTCTCCCGAGGCTGTTCCAGG 1385
DB 1208 TCTGGCTTTGACAGATGAGTGTGTGTGATTTGTTACAGTCTCCCGAGGCTGTTCCAGG 1267
QY 1386 CTTCACATCTGTGTGTGTTGGAGAGTCAAGGAGGTTAACTGACAGAGAGATTTGGCAC 1445
DB 1268 CTTCACATCTGTGTGTGTTGGAGAGTCAAGGAGGTTAACTGACAGAGAGATTTGGCAC 1327
QY 1446 CCTGTCCAGATTAATTTGGCTCTTGTGCTTACAGTGTGGAGACAGCCGTTGTTTAC 1505
DB 1328 CCTGTCCAGATTAATTTGGCTCTTGTGCTTACAGTGTGGAGACAGCCGTTGTTTAC 1387
QY 1506 ATGCTTTGATTAATTTGTTGAGGGAGAGATGGAACAAATGTGAGTCTCCCTGATT 1565
DB 1388 ATGCTTTGATTAATTTGTTGAGGGAGAGATGGAACAAATGTGAGTCTCCCTGATT 1447
QY 1566 GGTTTTGGGAGAAATGTGAGAGAGTGCCTGCTTGCACAAACATCACTGGCAAAAATG 1625
DB 1448 GGTTTTGGGAGAAATGTGAGAGAGTGCCTGCTTGCACAAACATCACTGGCAAAAATG 1507
QY 1626 CAACAAATGAATTTTCCACGCAATCTTTCATGCGCATAGTAAAGCTGTGCTTACGT 1685
DB 1508 CAACAAATGAATTTTCCACGCAATCTTTCATGCGCATAGTAAAGCTGTGCTTACGT 1567
QY 1686 GTTCAGATGAAATGTTCTGTTCACCTGCAATTCATGTTTATTTATCCAGAGTGT 1745
DB 1568 GTTCAGATGAAATGTTCTGTTCACCTGCAATTCATGTTTATTCATCCAGAGTGT 1627
QY 1746 GCTCAGCTCTTACCTCTGTGCGCAGGAGAGATTTTCATATCCAAAGATCAATTCCTCTCT 1805
DB 1628 GCTCAGCTCTTACCTCTGTGCGCAGGAGAGATTTTCATATCCAAAGATCAATTCCTCTCT 1687
QY 1806 CAGACAGCTGTGGAGAGGGGTCTATGTTCTCTCTGTCATCAGGATCTCAAGGCTCA 1865
DB 1688 CAGACAGCTGTGGAGAGGGGTCTATGTTCTCTCTGTCATCAGGATCTCAAGGCTCA 1747
QY 1866 GAGACTGAGAGCTGTGGCCCAAGTCAACAGAGTAAAGAGACAGAGGCTTCAATCTG 1925
DB 1748 GAGACTGAGAGCTGTGGCCCAAGTCAACAGAGTAAAGAGACAGAGGCTTCAATCTG 1807
QY 1926 GTTGTGACTTACAGTCACTGTCTCTCACTACCCACACAGCCTGTGTGACACAAA 1985
DB 1808 GTTGTGACTTACAGTCACTGTCTCTCACTACCCACACAGCCTGTGTGACACAAA 1867
QY 1986 AGTGTCTCCCAAGAGAGAGAGATGGGATTTTC -TTAGGCAATGCAATCTGGAATT 2043
DB 1868 AGTGTCTCCCAAGAGAGAGAGATGGGATTTTC -TTAGGCAATGCAATCTGGAATT 1927
QY 2044 AAGTCAAACTAATCTTCAACATCCCTTAATAAGTAATCTCTTGAAGACAGAGTGT 2103
DB 1928 AAGTCAAACTAATCTTCAACATCCCTTAATAAGTAATCTCTTGAAGACAGAGTGT 1987
QY 2104 CTGCACTGTGTGGGACAGCCGCTCTTCAATGAAGACATATATGCACTGTCCCTCT 2163
DB 1988 CTGCACTGTGTGGGACAGCCGCTCTTCAATGAAGACATATATGCACTGTCCCTCT 2047
QY 2164 TGGCAGTTGCACTTGTAACTTTGAAAGTATATGACTGAGAGTCAAGTAAAGT 2223
DB 2048 TGGCAGTTGCACTTGTAACTTTGAAAGTATATGACTGAGAGTCAAGTAAAGT 2107
QY 2224 GCAGAAACGACTTAACTGTATGTAGGCGAGAGATTAAATGAATTTGCAAAATCAC 2283
DB 2108 GCAGAAACGACTTAACTGTATGTAGGCGAGAGATTAAATGAATTTGCAAAATCAC 2167
QY 2284 TTAGCAGCACTGAAGCAATTTATCAACGAGTGAAGAAATCAAAACCGAGCGAGCTGT 2343
DB 2168 TTAGCAGCACTGAAGCAATTTATCAACGAGTGAAGAAATCAAAACCGAGCGAGCTGT 2227
QY 2344 GTGAACAATGAGTTGTAATATGCACTGGAACACTGAATCTTACGCCATCCCAAAATGA 2403

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DB 2228 GTGAACAATGAGTTGTAATATGAGTGCAGAACACTGAACCTACCCCTCACAAATGA 2287
QY 2404 TGTTTTCAAGGTGTGACAGTGTGCTCCACATGTATTCACAGAGTCTTAAAGTTAA 2463
DB 2288 TGTTTTCAAGGTGTGACAGTGTGCTCCACATGTATTCACAGAGTCTTAAAGTTAA 2347
QY 2464 AGTTGCACTGATTTGATTAAGCATGCTTTCTTTGAGTTTAAATTAATGATTAACATAAG 2523
DB 2348 AGTTGCACTGATTTGATTAAGCATGCTTTCTTTGAGTTTAAATTAATGATTAACATAAG 2407
QY 2524 TTGCATTTAGAAATCAACATTAATCACTTCACTGC 2560
DB 2408 TTGCATTTAGAAATCAACATTAATCACTTCACTGC 2444

RESULT 20
AAH45491
ID AAH45491 standard; DNA; 2632 BP.
XX
AC AAH45491;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human reduced expression in immortalised cells DNA sequence SEQ ID 4.
XX
KW REIC; reduced expression in immortalised cells; cancer; tumour;
XX proliferation inhibitor; viral infection; human; ds.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 198..1250
FT /tag=a
FT /product="REIC"
FT /note="Reduced expression in immortalised cells protein"
XX
PN WO200138528-A1.
XX
PD 31-MAY-2001.
XX
PF 30-AUG-2000; 2000MO-JP05879.
XX
PR 19-NOV-1999; 99JP-0330604.
XX
PA (HISM ) HISAMITSU PHARM CO LTD.
XX
PI Namba M, Tsuji T;
XX
XX WPI; 2001-367688/38.
XX
DR P-PSDB; AA62468.
XX
XX
XX Cell proliferation inhibiting protein REIC and polynucleotide encoding
XX it for diagnosis and therapy of cancer and as an antiviral agent -
XX
PS Claim 2; Page 59-60; 66pp; Japanese.
XX
CC This invention relates to a protein designated REIC (reduced expression
CC in immortalised cells) which inhibits proliferation. REIC shows reduced
CC or suppressed expression in immortalised cells such as cancer cells. The
CC invention includes DNA and protein sequences for REIC. The protein is
CC useful for the treatment and diagnosis of a wide range of benign and
CC malignant tumours and of viral infections (including HIV, influenza,
CC hepatitis and Epstein-Barr virus). The present sequence represents DNA
CC encoding REIC.
XX
SQ Sequence 2632 BP; 646 A; 647 C; 740 G; 599 T; 0 other;
XX

Query Match 87.2%; Score 2255; DB 22; Length 2632;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2435; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
QY 126 GCGCGGCGCTGCGGCGCAGAGCGAGATGCGAGCGCTTGGGGCCACACCTGTGTGCTG 185

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Db 171 GGGCGCGCTGCGGCGGAGAGCGAGATGACGGCTTGGGGCCACCTGCTGTGCTG 230
Qy 186 CTGCTGGGGGGGGGGTCCCCACGGCCCCCGCGCGCTCCGAGGGGACCTGGCTCCA 245
Db 231 CTGCTGGGGGGGGGGTCCCCACGGCCCCCGCGCGCTCCGAGGGGACCTGGCTCCA 290
Qy 246 GTCAAGCCCGCGCGCTCTCAGCTACCCGAGAGGAGGCCACCTCAATGAGATGTC 305
Db 291 GTCAAGCCCGCGCGCTCTCAGCTACCCGAGAGGAGGCCACCTCAATGAGATGTC 350
Qy 306 CGCGAGGTTGAGAACTGATGAGAGCACGAGACCAATTTGCCAGCGGGTGAAGAG 365
Db 351 CGCGAGGTTGAGAACTGATGAGAGCACGAGACCAATTTGCCAGCGGGTGAAGAG 410
Qy 366 ATGAGAGGAGAAAGCTGTCTAAAGCATCATGAGTGAAGTGGCAATCTTCACT 425
Db 411 ATGAGAGGAGAAAGCTGTCTAAAGCATCATGAGTGAAGTGGCAATCTTCACT 470
Qy 426 CCCAGCTATCAATGAGACCAACACAGACGAGGTTGAAATTAATCCATCATGTG 485
Db 471 CCCAGCTATCAATGAGACCAACACAGACGAGGTTGAAATTAATCCATCATGTG 530
Qy 486 CACGAGAAATTCACAGATTAACCAACACAGACTGGAACAATGCTTTTCAGAGCA 545
Db 531 CACGAGAAATTCACAGATTAACCAACACAGACTGGAACAATGCTTTTCAGAGCA 590
Qy 546 GTTATCATCTGTGGAGAGCAAGAAAGGAGAGGAGCCAGAGTCATCATGAGAG 605
Db 591 GTTATCATCTGTGGAGAGCAAGAAAGGAGAGGAGCCAGAGTCATCATGAGAG 650
Qy 606 GACTGTGGGGCCAGCATGTACTGTGCACTTTGCCAGTTCACCTGCAAGCCATGTC 665
Db 651 GACTGTGGGGCCAGCATGTACTGTGCACTTTGCCAGTTCACCTGCAAGCCATGTC 710
Qy 666 CGGGGCGAGAGGATGCTCTGCAACCGGGAGCATGAGTGTGGAGACCAAGCTGTGTC 725
Db 711 CGGGGCGAGAGGATGCTCTGCAACCGGGAGCATGAGTGTGGAGACCAAGCTGTGTC 770
Qy 726 TGGGGTCACTGACCAAAAATGGCCACAGGGGGAGCAATGGGACCATCTGTGACACAG 785
Db 771 TGGGGTCACTGACCAAAAATGGCCACAGGGGGAGCAATGGGACCATCTGTGACACAG 830
Qy 786 AGGACTGCGACCGGGGCTGTGCTGTGCTTCCAGAGAGGCTGTGCTTCCGTGTGTC 845
Db 831 AGGACTGCGACCGGGGCTGTGCTGTGCTTCCAGAGAGGCTGTGCTTCCGTGTGTC 890
Qy 846 ACACCCCTGCTGTGAGAGGAGCTTTGCCATGACCCCGCAGCCGGCTTTGTGACCTC 905
Db 891 ACACCCCTGCTGTGAGAGGAGCTTTGCCATGACCCCGCAGCCGGCTTTGTGACCTC 950
Qy 906 ATCACTGGGAGCTAGAGCTGATGAGGCTTGGACGATGAGGCTTGGCAAGTGGCTC 965
Db 951 ATCACTGGGAGCTAGAGCTGATGAGGCTTGGACGATGAGGCTTGGCAAGTGGCTC 1010
Qy 966 CTGTGCGAGCCCAAGCAGCAAGCTGTGTATGTGTGCAAGCCGACCTTGTGGGGAGC 1025
Db 1011 CTGTGCGAGCCCAAGCAGCAAGCTGTGTATGTGTGCAAGCCGACCTTGTGGGGAGC 1070
Qy 1026 CGTGAACCAAGTGGGGAGATCTGTGCTGCCAGAGAGTCCCGCATGATGAGTGGC 1085
Db 1071 CGTGAACCAAGTGGGGAGATCTGTGCTGCCAGAGAGTCCCGCATGATGAGTGGC 1130
Qy 1086 AGCTTCAATGAGAGGTTGCGCAGAGAGCTGAGAGACCTGAGAGAGCTGAGTGAAG 1145
Db 1131 AGCTTCAATGAGAGGTTGCGCAGAGAGCTGAGAGACCTGAGAGAGCTGAGTGAAG 1190
Qy 1146 ATGGCGCTGGGGAGAGCTGTGGCGCTGCTGCACTGTGGAGGGGAGAGATTTAG 1205
Db 1191 ATGGCGCTGGGGAGAGCTGTGGCGCTGCTGCACTGTGGAGGGGAGAGATTTAG 1250
Qy 1206 ATTCGAGCAAGGCTGTGGGTGATGTGCAATAGAAATAGCTAATTTATTTCCAGGTTG 1265
Db 1251 ATTCGAGCAAGGCTGTGGGTGATGTGCAATAGAAATAGCTAATTTATTTCCAGGTTG 1310
Qy 1266 GTGCTTTAGCGGTGGGCTGACACAGGCTTCTCTACATCTTCCAGTAGTTTCCC 1325
Db 1311 GTGCTTTAGCGGTGGGCTGACACAGGCTTCTCTACATCTTCCAGTAGTTTCCC 1370
Qy 1326 TCTGGCTTGACAGCATGAGGTGTGTGATTTGTTCACTCCCGAGGCTGTTCCAGG 1385
Db 1371 TCTGGCTTGACAGCATGAGGTGTGTGATTTGTTCACTCCCGAGGCTGTTCCAGG 1430
Qy 1386 CTTCACAGTCTGTGCTTGGGAGATCAGGCGAGGTTAACTGCGAGAGCACTTGGCCAC 1445
Db 1431 CTTCACAGTCTGTGCTTGGGAGATCAGGCGAGGTTAACTGCGAGAGCACTTGGCCAC 1490
Qy 1446 CCTGTCCAGATTATTTGGCTGTTGCCCTTACAGTGTGGCAGACGCGTTTGTCTAC 1505
Db 1491 CCTGTCCAGATTATTTGGCTGTTGCCCTTACAGTGTGGCAGACGCGTTTGTCTAC 1550
Qy 1506 ATGGCTTTGATATTTGTTGAGGGAGAGATGAAACAATGTGAGTCTCCCTGAT 1565
Db 1551 ATGGCTTTGATATTTGTTGAGGGAGAGATGAAACAATGTGAGTCTCCCTGAT 1610
Qy 1566 GGTTTTGGGAAATGTGAGAGAGAGTGGCCCTGTTGCAACATCAACCTGGCAAAATG 1625
Db 1611 GGTTTTGGGAAATGTGAGAGAGAGTGGCCCTGTTGCAACATCAACCTGGCAAAATG 1670
Qy 1626 CAACAAATGATTTTCCAGCAGTCTTTCCATGGGCAATGGGAACTGTGCTTCACT 1685
Db 1671 CAACAAATGATTTTCCAGCAGTCTTTCCATGGGCAATGGGAACTGTGCTTCACT 1730
Qy 1686 GTTGAGAGAAATGTTCTGTTCAACCTGCAATTAATGTTTATTTCCAGAGTGT 1745
Db 1731 GTTGAGAGAAATGTTCTGTTCAACCTGCAATTAATGTTTATTTCCAGAGTGT 1790
Qy 1746 GCTAGCTCTTACTCTGTGCGAGGGAGCATTTTCATATCCAGATCAATTCCTCTCT 1805
Db 1791 GCTAGCTCTTACTCTGTGCGAGGGAGCATTTTCATATCCAGATCAATTCCTCTCT 1850
Qy 1806 CAGCACAAGCTTGGGAGAGGGGCTATTTGTTCTCTGTCATAGAGGATCTCAGAGCTCA 1865
Db 1851 CAGCACAAGCTTGGGAGAGGGGCTATTTGTTCTCTGTCATAGAGGATCTCAGAGCTCA 1910
Qy 1866 GAGACTGCAAGCTGTGTTGCCAAGTCAACAAGTGTGAAGACAGAGAGTTTCATCTG 1925
Db 1911 GAGACTGCAAGCTGTGTTGCCAAGTCAACAAGTGTGAAGACAGAGAGTTTCATCTG 1970
Qy 1926 GTTGTGACTTAAAGCTCAGTGTCTCTCTCACTAACCCACACAGCTTGTGTCACAA 1985
Db 1971 GTTGTGACTTAAAGCTCAGTGTCTCTCTCACTAACCCACACAGCTTGTGTCACAA 2030
Qy 1986 AGTGTCCCCCAAAAGAGAGAGATGGGATTTTCTTTTGAAGCATGACATCTGGAAAT 2043
Db 2031 AGTGTCCCCCAAAAGAGAGAGATGGGATTTTCTTTTGAAGCATGACATCTGGAAAT 2090
Qy 2044 AAGTTCAAAATTTCTCACTCCTCTTAAAGTAACTACTGTGTAGGACAGAGTGT 2103
Db 2091 AAGTTCAAAATTTCTCACTCCTCTTAAAGTAACTACTGTGTAGGACAGAGTGT 2150
Qy 2104 CTCAAGTGTGGGAGAGCGCTCTTCTAATGAGACATGATTTAGACAGTGTCCCTCT 2163
Db 2151 CTCAAGTGTGGGAGAGCGCTCTTCTAATGAGACATGATTTAGACAGTGTCCCTCT 2210
Qy 2164 TGGCAGTTGCAATTAATCTTGAAGGATTAAGTAGAGCGTAGCATCAAGTTAACT 2223
Db 2211 TGGCAGTTGCAATTAATCTTGAAGGATTAAGTAGAGCGTAGCATCAAGTTAACT 2270
Qy 2224 GCGAGAAACGATCTTAAGTAATTTAGGGCGAGATTTAATGAAATTTGCAAAATCAC 2283
Db 2271 GCGAGAAACGATCTTAAGTAATTTAGGGCGAGATTTAATGAAATTTGCAAAATCAC 2330
Qy 2284 TTAGCAGCAACTGAAGACATTTATCAACAGTGTGAGAAATCAACCGAGAGGGCTGT 2343
Db 2331 TTAGCAGCAACTGAAGACATTTATCAACAGTGTGAGAAATCAACCGAGAGGGCTGT 2390

QY	2344	GTGAACAATGGTTGTAATATGCGAATCGGAACACATGAACCTTACGCGACTCCAAATGA	2403
Db	2391	GTGAACAATGGTTGTAATATGCGAATCGGAACACATGAACCTTACGCGACTCCAAATGA	2450
QY	2404	TGTTTTCAGGTGTCATGAGCACTGTTGCCACCACTGATTCATCCAGAGTCTTAAAGTTTAA	2463
Db	2451	TGTTTTCAGGTGTCATGAGCACTGTTGCCACCACTGATTCATCCAGAGTCTTAAAGTTTAA	2510
QY	2464	AGTTCACATGATGTATATAGCATGCTTCTTGGTTTAAATATAGTATATTAACATAG	2523
Db	2511	AGTTCACATGATGTATATAGCATGCTTCTTGGTTTAAATATATGATATTAACATAG	2570
QY	2524	TTGCATTTAGAAATCAAGCATTAATCACTTCAACTGC	2560
Db	2571	TTGCATTTAGAAATCAAGCATTAATCACTTCAACTGC	2607

RESULT 21

ABL92089	ABL92089	standard; cDNA; 2608 BP.
XX	XX	ABL92089;
XX	XX	30-MAY-2002 (first entry)
DE	XX	Human Tumour Endothelial Marker polynucleotide SEQ ID NO 201.
XX	XX	Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
KW	XX	normal endothelial marker; pan-endothelial marker; immunostimulant;
KW	XX	antiangiogenic; tumour; neovascularization; vascularised tumour;
KW	XX	polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
XX	XX	psoriasis; gene; ss.
OS	XX	Homo sapiens.
PN	XX	WO200210217-A2.
PD	XX	07-FEB-2002.
PF	XX	01-AUG-2001; 2001WO-US24031.
PR	XX	02-AUG-2000; 2000US-222599P.
PR	XX	11-AUG-2000; 2000US-224360P.
PR	XX	11-APR-2001; 2001US-282850P.
PA	XX	(UYJO) UNIV JOHNS HOPKINS.
FL	XX	St Croix B, Kinzler KW, Vogelstein B;
DR	XX	WPI; 2002-291856/33.
DR	XX	P-PSDB; ABB90735.
XX	XX	
PT	XX	An isolated molecule comprising an antibody variable region which
PT	XX	specifically binds to an extracellular domain of a tumor endothelial
PT	XX	marker (TEM) protein, useful for inhibiting tumor growth -
XX	XX	
PS	XX	Claim 58; Page 155-156; 331pp; English.
XX	XX	
CC	XX	The invention relates to an isolated molecule comprising an antibody
CC	XX	variable region which specifically binds to an extracellular domain of a
CC	XX	tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
CC	XX	ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
CC	XX	proteins have cytostatic, immunostimulant and antiangiogenic activity.
CC	XX	They are useful for inhibiting tumour growth, neovascularisation in
CC	XX	subjects bearing a vascularised tumour, polycystic kidney disease,
CC	XX	diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse
CC	XX	and rat TEM genes and the encoded proteins (AB192075-AB192141 and
CC	XX	AB1907221-AB190789) are disclosed, as are marker oligonucleotide
CC	XX	sequences, tumour endothelial markers (TEM) AB191986-AB192041 and
CC	XX	AB192143-AB192191, normal endothelial markers (NEM) AB192042-AB192074;
CC	XX	and pan-endothelial markers (PEM) AB191903-AB191995.
XX	XX	

[illegible]

QY 1173 GCCGCTGACTGCTGGAGGGGAAAGATTAGATCTGGAACGAGCTGTGGGTAGATGTG 1232
 Db 1218 GCCGCTGACTGCTGGAGGGGAAAGATTAGATCTGGAACGAGCTGTGGGTAGATGTG 1277
 QY 1233 CAATGAAATAGCTTAATTTATTTCCCAAGTGTGTCTTAAAGCGTGGCTGACAGGCT 1292
 Db 1278 CAATGAAATAGCTTAATTTATTTCCCAAGTGTGTCTTAAAGCGTGGCTGACAGGCT 1337
 QY 1293 TCTTCTCATCTTTTCCCAAGTGTGTCTTAAAGCGTGGCTGACAGGCTGTG 1352
 Db 1338 TCTTCTCATCTTTTCCCAAGTGTGTCTTAAAGCGTGGCTGACAGGCTGTG 1397
 QY 1353 CATTTGTTCACTCCCAAGGCTGTCTCAAGCTTCAAGTGTGTGTGGAGAGTC 1412
 Db 1398 CATTTGTTCACTCCCAAGGCTGTCTCAAGCTTCAAGTGTGTGTGGAGAGTC 1457
 QY 1413 AGGAGGGTTAACTGAGAGAGAGTTGGCAACCCCTGTCCAGATTAAATGGCTGTG 1472
 Db 1458 AGGAGGGTTAACTGAGAGAGAGTTGGCAACCCCTGTCCAGATTAAATGGCTGTG 1517
 QY 1473 CTCTACAGTTGGAGAGAGAGCCGTTGTCTACATGGCTTTGATTAATGTTTGAAGGAG 1532
 Db 1518 CTCTACAGTTGGAGAGAGAGCCGTTGTCTACATGGCTTTGATTAATGTTTGAAGGAG 1577
 QY 1533 GAGATGGAAGAAATGTGAGTCTCCCTCTGATTTGGTGGGAAATGTGAGAGAGTG 1592
 Db 1578 GAGATGGAAGAAATGTGAGTCTCCCTCTGATTTGGTGGGAAATGTGAGAGAGTG 1637
 QY 1593 CCCTGCTTTGCAAACTCAACCTGCGCAAAATGCAAAATGATTTTCCAGCGAGTCT 1652
 Db 1638 CCCTGCTTTGCAAACTCAACCTGCGCAAAATGCAAAATGATTTTCCAGCGAGTCT 1697
 QY 1653 TTCCATGGGCAATGTAAGCTGTGCTTCAAGCTTTGCAATGTAATGTTCTGTCAACC 1712
 Db 1698 TTCCATGGGCAATGTAAGCTGTGCTTCAAGCTTTGCAATGTAATGTTCTGTCAACC 1757
 QY 1713 TGCATTCATGTTTATTTATTCACGAGAGTGTGCTCAAGCTTCTGTGCAAGGCT 1772
 Db 1758 TGCATTCATGTTTATTTATTCACGAGAGTGTGCTCAAGCTTCTGTGCAAGGCT 1817
 QY 1773 AGCATTTTCATATCCAAAGATTAATTCCTCTCTCAGACAGCTGTGGGAGGGGTCAATG 1832
 Db 1818 AGCATTTTCATATCCAAAGATTAATTCCTCTCTCAGACAGCTGTGGGAGGGGTCAATG 1877
 QY 1833 TTCTCCTGCTCATCAGGAGATCTCAGAGGCTCAGAGCTCAGAGCTGCTGCCAAGTCA 1892
 Db 1878 TTCTCCTGCTCATCAGGAGATCTCAGAGGCTCAGAGCTCAGAGCTGCTGCCAAGTCA 1937
 QY 1893 CACAGCTAGTGAAGACAGAGCAGTTTCACTGTGTTGACTTAAGCTCAGTCTCTCT 1952
 Db 1938 CACAGCTAGTGAAGACAGAGCAGTTTCACTGTGTTGACTTAAGCTCAGTCTCTCT 1997
 QY 1953 CCACTACCCCAACACAGCTGTGTCACCAAAAGTCTCCCAAAAGAGAGAGATG 2012
 Db 1998 CCACTACCCCAACACAGCTGTGTCACCAAAAGTCTCCCAAAAGAGAGAGATG 2057
 QY 2013 GATTTTTC--TTGAGGATGACATCTGGAATTAAGTCAAACTTAATTCACATCCCTC 2070
 Db 2058 GATTTTTC--TTGAGGATGACATCTGGAATTAAGTCAAACTTAATTCACATCCCTC 2117
 QY 2071 TAAAGTAACTACTGTTAGGAAGAGAGTGTCTCAAGTGTGGGAGCCCTCTCT 2130
 Db 2118 TAAAGTAACTACTGTTAGGAAGAGAGTGTCTCAAGTGTGGGAGCCCTCTCT 2177
 QY 2131 AATGAGACATGATTAATGACATGCTCCCTTTTGGAGTTGATTAAGTAACTTTGAAG 2190
 Db 2178 AATGAGACATGATTAATGACATGCTCCCTTTTGGAGTTGATTAAGTAACTTTGAAG 2237
 QY 2191 GTATATGACTGAGGCTGACATACAGGTTAACTGCAAGAAACAGTACTTAAGTAACTGAG 2250
 Db 2238 GTATATGACTGAGGCTGACATACAGGTTAACTGCAAGAAACAGTACTTAAGTAACTGAG 2297

QY 2251 GCGAGATTATTAATGAATTTGGCAAAATCACTTAGCAGCACTGAAGCAATTATCA 2310
 Db 2298 GCGAGATTATTAATGAATTTGGCAAAATCACTTAGCAGCACTGAAGCAATTATCA 2357
 QY 2311 CCACTGAGAGAAATCAAAACGAGAGAGGCTGTGTGAACATGTTGATTAATGCACTG 2370
 Db 2358 CCACTGAGAGAAATCAAAACGAGAGAGGCTGTGTGAACATGTTGATTAATGCACTG 2417
 QY 2371 CGAACACTGAACCTTAAGGCACTCCCAAAATGATGTTTCAAGTGTGCACTGTGTC 2430
 Db 2418 CGAACACTGAACCTTAAGGCACTCCCAAAATGATGTTTCAAGTGTGCACTGTGTC 2477
 QY 2431 ACCATGATTCATCCAGAGTCTTAAAGTTGAAGTGCATGATTTGATTAAGATGCT 2490
 Db 2478 ACCATGATTCATCCAGAGTCTTAAAGTTGAAGTGCATGATTTGATTAAGATGCT 2537
 QY 2491 TTTCTTGAATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2550
 Db 2538 TTTCTTGAATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2597
 QY 2551 CTTCAACTGC 2560
 Db 2598 CTTCAACTGC 2607

RESULT 22
 AEX72014
 ID AEX72014 standard; DNA; 2608 BP.
 AC AEX72014;
 XX
 DT 12-NOV-2003 (first entry)
 XX
 DE DNA encoding human tumour endothelial marker TEM 4.
 XX
 KW Human: endothelial cell; EC; tumour endothelial cell; TEM; NEM;
 KW Tumour endothelial marker; normal endothelial marker; PEM;
 KW pan-endothelial marker; polycystic kidney disease; psoriasis;
 KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
 KW neovascularization; immune response; cytoskeletal; antidiabetic; gene;
 KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic; ds.
 XX
 OS Homo sapiens.
 XX
 PN MO200283874-A2.
 PD
 XX 24-OCT-2002.
 PF 10-APR-2002; 2002MO-US08253.
 PR 11-APR-2001; 2001US-282850P.
 PR 06-FEB-2002; 2002US-354262P.
 XX
 PA (UYUO) UNIV JOHNS HOPKINS.
 PI Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
 XX
 DR MPI; 2003-093016/08.
 DR F-PSDB; ABUS4442.
 XX
 PT New purified human transmembrane protein, designated as tumour
 PT endothelial marker (TEM) 3, useful for detecting, diagnosing or
 PT treating tumours, polycystic kidney disease, diabetic retinopathy,
 PT rheumatoid arthritis or psoriasis -
 XX
 PS Disclosure; Page 158-160; 374pp; English.
 XX
 CC The present invention relates to a novel method for the isolation of
 CC endothelial cells (ECs), and the identification of genes expressed in
 CC normal and tumour ECs. Tumour endothelial marker (TEM), normal
 CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
 CC identified in human ECs. The human EC marker proteins and the
 CC polynucleotide sequences encoding them are useful for detecting.


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QY 2131 AATGAGCAATGATATGACACTGTCCTCTTTGGAGTTGATTAAGCTTTGAAG 2190
XX
XX 2178 AATGAGCAATGATATGACACTGTCCTCTTTGGAGTTGATTAAGCTTTGAAG 2237
Db
QY 2191 GTATATGACTAGAGGTAGCATATACCTGACAGAAAGTACTAGTATTTAG 2250
XX
XX 2238 GTATATGACTAGAGGTAGCATATACCTGACAGAAAGTACTAGTATTTAG 2297
Db
QY 2251 GCGGAGATTTAATGAATTTTGGAAAATCACTTAGCAGCACTGAAGCAATTATCAA 2310
XX
XX 2298 GCGGAGATTTAATGAATTTTGGAAAATCACTTAGCAGCACTGAAGCAATTATCAA 2357
Db
QY 2311 CCACCTGAGAAAATCAACCGAGAGGGCTGTGTGAACATGTTGTAATATCCGACTG 2370
XX
XX 2358 CCACCTGAGAAAATCAACCGAGAGGGCTGTGTGAACATGTTGTAATATCCGACTG 2417
Db
QY 2371 CGAAGCACTGAACTCAGCCCACTCCACAATGATGTTTCAGTGTGATGAGCTGGCC 2430
XX
XX 2418 CGAAGCACTGAACTCAGCCCACTCCACAATGATGTTTCAGTGTGATGAGCTGGCC 2477
Db
QY 2431 ACCATGATTCATCCAGAGTTCTTAAAGTTTAAAGTTGACATATGATTAAGCATGCT 2490
XX
XX 2478 ACCATGATTCATCCAGAGTTCTTAAAGTTTAAAGTTGACATATGATTAAGCATGCT 2537
Db
QY 2491 TTCTTGAGTTTAAATTAATGATTAATGAATAGTTGATTAAGCAATGAATGAATCA 2550
XX
XX 2538 TTCTTGAGTTTAAATTAATGATTAATGAATAGTTGATTAAGCAATGAATGAATCA 2597
Db
QY 2551 CTTCAACTGC 2560
XX
XX 2598 CTTCAACTGC 2607
Db

```

RESULT 23

AAV38798 ID AAV38798 standard; cDNA; 2490 BP.

AAV38798 AC AAV38798;

XX 09-NOV-1998 (first entry)

DT XX Homo sapiens cerebellum and embryo specific protein gene.

XX XX CESP; cerebellum and embryo specific protein; restenosis;

XX XX myocardial infarction; arrhythmia; heart disease;

XX XX atherosclerosis; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 73..1125

XX FT FT /*tag= a

XX FT FT /product= cerebellum and embryo specific protein

XX FT sig_peptide 73..133

XX FT /*tag= b

XX PN WO9827932-A2.

XX PD 02-JUL-1998.

XX PF 18-DEC-1997; 97W0-US23518.

XX PR 20-DEC-1996; 96US-0033870.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Soppet DR;

XX DR MPI; 1998-377366/32.

XX DR P-PSDB; AAW62395.

XX PT New isolated cerebellum and embryo specific polypeptide - used to develop products for treating e.g. coronary restenosis, myocardial

```

PT infarction, heart disease and artery or venous thrombosis
XX
XX Claim 2; Fig 1; 77p; English.
XX
CC The sequence is that encoding cerebellum and embryo specific protein
CC (CESP). CESP is involved in: (i) the regulation of collateral
CC circulation (particularly in the heart), coronary artery restenosis
CC following a revascularisation procedure, apoptosis in myocytes; (ii) the
CC modulation of myocyte development in the developing heart; (iii)
CC regulation of circulating blood volume, vascular tone, blood pressure and
CC cardiac output, diuresis, natriuresis; (iv) facilitation of transudation
CC of plasma water to the interstitium, and (v) inhibition of the release
CC or action of hormones such as aldosterone, angiotensin II, endothelins,
CC renin and vasopressin. The products can be used in the diagnosis and
CC treatment of CESP related disorders, e.g. coronary restenosis following
CC coronary revascularisation, coronary artery thrombus or occlusion,
CC myocardial infarction, atrial and/or ventricular arrhythmias, heart
CC block, hereditary medial necrosis of small coronary arteries,
CC cardiomyopathy, arrhythmogenic right ventricular dysplasia, athero-
CC sclerotic heart disease, venous thrombosis or Reynaud's syndrome.
XX
XX Sequence 2490 BP; 606 A; 629 C; 679 G; 576 T; 0 other;
SQ

```

Query Match 85.2%; Score 2204; DB 19; Length 2490;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2434; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

```

QY 126 GCGGCGCGCTGCGCGGCGGAGAGATGACAGCGGCTTGGGCGCACTGCTGTGCGCTG 185
Db 46 GCGGCGCGCTGCGCGGCGGAGAGATGACAGCGGCTTGGGCGCACTGCTGTGCGCTG 105
QY 186 CTGCTGCGCGCGCGGCTGCCCAAGCGGCCCGCGCTCCGACGCGGCACTTGGCTCCA 245
Db 106 CTGCTGCGCGCGCGGCTGCCCAAGCGGCCCGCGCTCCGACGCGGCACTTGGCTCCA 165
QY 246 GTCAAGCCCGCGCGGCTCTCACTACCCGACAGAGAGGCCACCTCAATGATGTTTC 305
Db 166 GTCAAGCCCGCGCGGCTCTCACTACCCGACAGAGAGGCCACCTCAATGATGATGTTTC 225
QY 306 CGGAGGTTGAGGAATGATGAGAGACAGCAGCAAAATTTGGCGAGCGCGGTGAAGAG 365
Db 226 CGGAGGTTGAGGAATGATGAGAGACAGCAGCAAAATTTGGCGAGCGCGGTGAAGAG 285
QY 366 ATGAGGCGAAGAGAGCTGCTGCTAAAGCATCATCAAGAGTGAACCTGGCAACTTACT 425
Db 286 ATGAGGCGAAGAGAGCTGCTGCTAAAGCATCATCAAGAGTGAACCTGGCAACTTACT 345
QY 426 CCGAGCTATCAATGAGACCAACAGACAGAGAGGTTGAATAATTCATCCATGTG 485
Db 346 CCGAGCTATCAATGAGACCAACAGACAGAGAGGTTGAATAATTCATCCATGTG 405
QY 486 CACCGAATTTCAAAATTAACCAACCAAGACTGCAAAATGCTCTTTTCAGAGACA 545
Db 406 CACCGAATTTCAAAATTAACCAACCAAGACTGCAAAATGCTCTTTTCAGAGACA 465
QY 546 GTTATCAATCTGTGGAGACGAAAGAGCAGAAAGAGCCACGAGTCATCCAGAGAG 605
Db 546 GTTATCAATCTGTGGAGACGAAAGAGCAGAAAGAGCCACGAGTCATCCAGAGAG 525
QY 606 GACTGTGGGCCAGCATGTAATCCAGTTTGGCAGCTTCCAGTACACTTCCAGCCATGC 665
Db 526 GACTGTGGGCCAGCATGTAATCCAGTTTGGCAGCTTCCAGTACACTTCCAGCCATGC 585
QY 666 CCGGCGCGAGAGATGCTCTGACCCGCGGACAGTGAATGCTGTGGAGACCAAGCTGTGTC 725
Db 666 CCGGCGCGAGAGATGCTCTGACCCGCGGACAGTGAATGCTGTGGAGACCAAGCTGTGTC 645
QY 726 TGGGGTCACTGACCAAAATGCGCACACGAGGCGAGCAATGGGACCATCTGTGCAACAG 785
Db 646 TGGGGTCACTGACCAAAATGCGCACACGAGGCGAGCAATGGGACCATCTGTGCAACAG 705
QY 786 AGGAGCTGCGAGCGCGGCGCTGTGCTGCTTCCAGAGAGGCTGCTGTTCCTGTGTGC 845

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Db AGGAGTCCAGCGGGGCTGTGTCTGTCTCCAGAGAGCCCTGTGTCTCCTGTGTG 765
 QY AACACCCCTGCGCCGCGAGAGCTTTGCAATGACCCCGCCAGCCGGCTTGTGACCTC 905
 Db AACACCCCTGCGCCGCGAGAGCTTTGCAATGACCCCGCCAGCCGGCTTGTGACCTC 905
 Db AACACCCCTGCGCCGCGAGAGCTTTGCAATGACCCCGCCAGCCGGCTTGTGACCTC 825
 QY ATCACTGTGAGAGCTGTAGAGCTGTAGAGCTGTAGAGCTGTAGAGCTGTAGAGCT 965
 Db ATCACTGTGAGAGCTGTAGAGCTGTAGAGCTGTAGAGCTGTAGAGCTGTAGAGCT 885
 QY CTCTGCGAGCCCGCCAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1025
 Db CTCTGCGAGCCCGCCAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 945
 QY CGTAGACCAAGATGAGAGAGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1085
 Db CGTAGACCAAGATGAGAGAGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1005
 QY AGCTTCATGAG 1065
 Db AGCTTCATGAG 1065
 QY ATGAGCGCTGGGGGAGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1205
 Db ATGAGCGCTGGGGGAGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1125
 QY ATCTGAGACAGAGCTGT 1265
 Db ATCTGAGACAGAGCTGT 1185
 QY GTGCTTTAG 1325
 Db GTGCTTTAG 1245
 QY GTGCTTTAG 1385
 Db GTGCTTTAG 1305
 QY CTTCACATCTGT 1445
 Db CTTCACATCTGT 1365
 QY CCTGTGTCAGATTTATGT 1505
 Db CCTGTGTCAGATTTATGT 1425
 QY ATGCTTTGATTAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1565
 Db ATGCTTTGATTAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1485
 QY ATGCTTTGATTAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1625
 Db ATGCTTTGATTAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1545
 QY CAACCAATGATTTTCCAG 1685
 Db CAACCAATGATTTTCCAG 1605
 QY GTTGCAGATGAAATTTTGT 1745
 Db GTTGCAGATGAAATTTTGT 1665
 QY GCTGAGCTCTACCTTGT 1805
 Db GCTGAGCTCTACCTTGT 1725
 QY CAGCAAGCTGT 1865
 Db CAGCAAGCTGT 1785
 QY GAGACTGCAAGCTGT 1925
 Db GAGACTGCAAGCTGT 1845

QY GTTGTGACTTAAGCTAGTGTCTCTCTCACTACCCACACAGCACTGTGTGCCAATA 1985
 Db GTTGTGACTTAAGCTAGTGTCTCTCTCACTACCCACACAGCACTGTGTGCCAATA 1905
 QY AGTGTCTCCCAAG 2043
 Db AGTGTCTCCCAAG 1965
 QY AAGGTCAAACTAATCTCACTACCCCTCAAAAGTAATCACTGTAGGACAGAGTGT 2103
 Db AAGGTCAAACTAATCTCACTACCCCTCAAAAGTAATCACTGTAGGACAGAGTGT 2025
 QY CTCAAGT 2163
 Db CTCAAGT 2085
 QY TGGCAGT 2223
 Db TGGCAGT 2145
 QY GCAGAAACAGTACTTAGGTAAATTTGAGGCGAGATTAATAAGAAATTTGCCAAATCAC 2283
 Db GCAGAAACAGTACTTAGGTAAATTTGAGGCGAGATTAATAAGAAATTTGCCAAATCAC 2205
 QY TTAGCAGCACTGAGAGCAATTAATCAACAGTGTGAGAAATCAACAGGAGGGCTGT 2343
 Db TTAGCAGCACTGAGAGCAATTAATCAACAGTGTGAGAAATCAACAGGAGGGCTGT 2265
 QY GTGAAACATGT 2403
 Db GTGAAACATGT 2325
 QY TGTGTTCAGGT 2463
 Db TGTGTTCAGGT 2385
 QY AGTGCACATGATTTGATTAAGATGATGATGATGATGATGATGATGATGATGATGAT 2523
 Db AGTGCACATGATTTGATTAAGATGATGATGATGATGATGATGATGATGATGATGAT 2445
 QY TTGCATTTGAAATCAAGATTAATCACTTCACTGC 2560
 Db TTGCATTTGAAATCAAGATTAATCACTTCACTGC 2482

RESULT 24
 AAI69309
 ID AAI69309 standard; DNA; 2479 BP.
 AC AAI69309;
 XX
 DT 11-FEB-2002 (first entry)
 XX
 DE Human DKK-3 DNA.
 XX
 KW DKK-3; detection; schizophrenia; neuroleptic; vaccine; gene therapy;
 KM neuralgic defect; neuropsychiatric disorder; human; ds.
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT CDS 38..1090
 FT FT /tag= a
 XX /product= "DKK-3"
 XX
 XX MO200163295-A2.
 XX
 XX PD 30-AUG-2001.
 XX
 XX 26-FEB-2001; 2001WO-1B00259.
 XX
 XX 24-FEB-2000; 2000GB-0004412.
 PR

PR 24-FEB-2000; 2000GB-0004415.
 PR 15-MAR-2000; 2000GB-0006285.
 PR 24-NOV-2000; 2000GB-0028734.
 PR 28-NOV-2000; 2000US-0724391.
 PR 08-DEC-2000; 2000GB-0030050.
 PR 12-DEC-2000; 2000US-0254830.
 PR 28-DEC-2000; 2000US-0750395.
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX
 XX Herath HMC, Parekh RB, Rohlf C, Patel TP;
 DR WPI; 2001-570652/64.
 DR P-PSDB; AAG80271.
 PT Diagnosing and monitoring Schizophrenia by detecting the presence of
 PT Schizophrenia Associated Features and Schizophrenia Associated Protein
 PT Isoforms in samples of cerebrospinal fluid -
 XX
 XX Claim 5a; Fig 2; 91pp; English.
 CC This invention describes a novel method for detecting the presence of
 CC schizophrenia associated features (SFS) and schizophrenia associated
 CC protein isoforms (SPIs) in samples, e.g. by electrophoresis, immunoassay
 CC or hybridisation assay, for diagnosing and monitoring schizophrenia,
 CC studying the effectiveness of treatments and for identifying potential
 CC therapeutic agents. The products of the invention have neuroleptic
 CC activity and can be used in vaccines or for gene therapy. The method (I)
 CC is used: (1) for screening or diagnosis of schizophrenia and the relative
 CC abundance of at least 1 chosen feature correlates with the presence or
 CC absence of schizophrenia and for monitoring the effect of therapy
 CC administered to a subject with schizophrenia and the relative abundance
 CC of at least 1 chosen feature which correlates with the severity of
 CC schizophrenia. The expression and activity of the SFS, SPIs and related
 CC molecules (e.g. secondary messengers) are studied to diagnose
 CC schizophrenia, monitor the progress of the disorder and the effectiveness
 CC of treatment and as targets to identify and produce potential therapeutic
 CC agents for the treatment of schizophrenia. The paucity of detectable
 CC neuronal defects distinguishes neuropsychiatric disorders such as
 CC schizophrenia from neurological disorders, where manifestations of
 CC anatomical and biochemical changes have been identified in many cases.
 CC Consequently the identification and characterisation of cellular and/or
 CC molecular causative defects and neuropathies are necessary for improved
 CC treatment of neuropsychiatric disorders. This sequence encodes the human
 CC DKX-3 protein described in the method of the invention.
 CC
 XX
 SQ Sequence 2479 BP; 625 A; 618 C; 668 G; 567 T; 1 other;
 Query Match 81.4%; Score 2104; DB 22; Length 2479;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2434; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Db 309 TCCTCAGCTATCATGATGAGCCAAACACAGACACGAAGTTGAATATATACCATCCATG 368
 QY 484 TGCACCGAGAAATTTCAAGATTAACCAACACAGACTGAGCAAAATGGTCTTTAGAGA 543
 Db 369 TGCACCGAGAAATTTCAAGATTAACCAACACAGACTGAGCAAAATGGTCTTTAGAGA 428
 QY 544 CAGTTATCATCTGTGGGAGACGAAGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 603
 Db 429 CAGTTATCATCTGTGGGAGACGAAGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 488
 QY 604 AGGACTGTGGGCGCCAGCATGTAATGCGAGTTTGCAGCTTCCAGTACCTGCGACCAT 663
 Db 489 AGGACTGTGGGCGCCAGCATGTAATGCGAGTTTGCAGCTTCCAGTACCTGCGACCAT 548
 QY 664 GCGGGGGCCAGAGAGATGCTGTGACCCGGGACAGTGAAGTGTGGAAGACAGCTGTGTG 723
 Db 549 GCGGGGGCCAGAGAGATGCTGTGACCCGGGACAGTGAAGTGTGGAAGACAGCTGTGTG 608
 QY 724 TCTGGGCTCACTGCACCAAAATGGCCACCGGGGAGCAATGGGACCATCTGTGACACC 783
 Db 609 TCTGGGCTCACTGCACCAAAATGGCCACCGGGGAGCAATGGGACCATCTGTGACACC 668
 QY 784 AAGAGGACCCAGCCGCGGCTGTGCTGCTTCCAGAGAGGCTGTGCTGCTGCTGCTGCT 843
 Db 669 AAGAGGACCCAGCCGCGGCTGTGCTGCTTCCAGAGAGGCTGTGCTGCTGCTGCTGCT 728
 QY 844 GCACACCCCTGCGCGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 903
 Db 729 GCACACCCCTGCGCGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 788
 QY 904 TCATACCTGAGAGCTGAGAGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 963
 Db 789 TCATACCTGAGAGCTGAGAGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 848
 QY 964 TCTTTCAGAGCCCGCCAGACCCAGAGCTGTGATGTGTGCAAGCCGACTTGTGGGGA 1023
 Db 849 TCTTTCAGAGCCCGCCAGACCCAGAGCTGTGATGTGTGCAAGCCGACTTGTGGGGA 908
 QY 1024 GCGGTACCAAGATGGGAGATCTGCTCCAGAGAGGTCCTCCCATGATGATGAAGTTG 1083
 Db 909 GCGGTACCAAGATGGGAGATCTGCTCCAGAGAGGTCCTCCCATGATGATGAAGTTG 968
 QY 1084 GCAGCTTCAATGAGAGAGTGCAGAGAGAGTGAAGAGTGAAGAGAGTGAAGAGTGAAG 1143
 Db 969 GCAGCTTCAATGAGAGAGTGCAGAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 1028
 QY 1144 AGATGGCGCTGGGGAGGCTGCGGCTGCGCGCTGCACTGCTGGAGGGGAAGATTT 1203
 Db 1029 AGATGGCGCTGGGGAGGCTGCGGCTGCGCGCTGCACTGCTGGAGGGGAAGATTT 1088
 QY 1204 AGATTCGACCAAGCTGTGGGTGATGTGCAATAGCTAATTTATTTTCCAGGT 1263
 Db 1089 AGATTCGACCAAGCTGTGGGTGATGTGCAATAGCTAATTTATTTTCCAGGT 1148
 QY 1264 GTGTGCTTTAAGGCGTGGCTGACCAAGCTTCTTCTAATCTTCTTCCAGTAAAGTTTC 1323
 Db 1149 GTGTGCTTTAAGGCGTGGCTGACCAAGCTTCTTCTAATCTTCTTCCAGTAAAGTTTC 1208
 QY 1324 CCTTGGCTTGAAGAGATGAGGTGTGTGATTTGTTCAGCTCCCGAGGCTGTCTCA 1383
 Db 1209 CCTTGGCTTGAAGAGATGAGGTGTGTGATTTGTTCAGCTCCCGAGGCTGTCTCA 1268
 QY 1384 GGCCTTCAAGCTGTGTGCTTGGAGAGTCAAGGAGGTTAACTGCAGAGACAGTTTGC 1443
 Db 1269 GGCCTTCAAGCTGTGTGCTTGGAGAGTCAAGGAGGTTAACTGCAGAGACAGTTTGC 1328
 QY 1444 ACCCTGTCCAGATTAATGGCTCTTGTGCTTCAACAGTTGGAGACAGCGTTTGTCT 1503
 Db 1329 ACCCTGTCCAGATTAATGGCTCTTGTGCTTCAACAGTTGGAGACAGCGTTTGTCT 1388
 QY 1504 ACATGCTTGTATTAATTTTGAAGGAGAGATGGAACAAATGTGAGTCTCCCTCTGA 1563

Db 1389 ACATGCTTTGATTAATGTTTGAAGGGAGAGATGAAACAATGTGAGTCTCCCTCTGA 1448
 Qy 1564 TTGTTTGGGGAAATGTGAGAAAGAGTGCCTGCTTTCGAAAATCACTACCTGGCAAAA 1623
 Db 1449 TTGTTTGGGGAAATGTGAGAAAGAGTGCCTGCTTTCGAAAATCACTACCTGGCAAAA 1508
 Qy 1624 TGCAACAAGAAATTTTCCACGAGTCTTCCATGGGGATAGCTAGTGTGCTTCAG 1683
 Db 1509 TGCAACAAGAAATTTTCCACGAGTCTTCCATGGGGATAGCTAGTGTGCTTCAG 1568
 Qy 1684 CTGTTGACATGAAATGTTCTGTTCACTGACCTGATTAATGTTTATTCACGACAGT 1743
 Db 1569 CTGTTGACATGAAATGTTCTGTTCACTGACCTGATTAATGTTTATTCACGACAGT 1628
 Qy 1744 TTGCTCAGCTCTTACCTGTCGACGAGGAGCATTTTCATTCACAGATCAATTCCTCT 1803
 Db 1629 TTGCTCAGCTCTTACCTGTCGACGAGGAGCATTTTCATTCACAGATCAATTCCTCT 1688
 Qy 1804 CTCAGCAGCTGAGGAGGAGGATCATTTGTTCTCTGTCATCAGGATCTCAGAGCT 1863
 Db 1689 CTCAGCAGCTGAGGAGGAGGATCATTTGTTCTCTGTCATCAGGATCTCAGAGCT 1748
 Qy 1864 CAGAGACTGACAGCTGCTTGGCCAACTCACAAGCTAGTGAAGACCGAGAGCTTTTATC 1923
 Db 1749 CAGAGACTGACAGCTGCTTGGCCAACTCACAAGCTAGTGAAGACCGAGAGCTTTATC 1808
 Qy 1924 TGGTTGACTCTTAAGCTCACTGCTCTCTCAGTACCCACACAGGCTTGTGCGACCA 1983
 Db 1809 TGGTTGACTCTTAAGCTCACTGCTCTCTCAGTACCCACACAGGCTTGTGCGACCA 1868
 Qy 1984 AAAGTGTCTCCCAAAAGAGAGAGAAATGGGATTTTTC--TTGAGGATGACATCTGGAA 2041
 Db 1869 AAAGTGTCTCCCAAAAGAGAGAGAAATGGGATTTTTC--TTGAGGATGACATCTGGAA 1928
 Qy 2042 TTAAAGTCAAACTAATCTCATCCCTCTTAAAGTAACTAGTGAAGACAGCAGT 2101
 Db 1929 TTAAAGTCAAACTAATCTCATCCCTCTTAAAGTAACTAGTGAAGACAGCAGT 1988
 Qy 2102 TTCTCAGTGTGGGAGGAGGCTCTTCTTAATGAAGACATGATTAATGAATTTGCAATC 2161
 Db 1989 TTCTCAGTGTGGGAGGAGGCTCTTCTTAATGAAGACATGATTAATGAATTTGCAATC 2048
 Qy 2162 TTGGGAGTGTGATTAATGATTAATGAAAGTATGATGAGCTGATGATGATGATGATGAT 2221
 Db 2049 TTGGGAGTGTGATTAATGATTAATGAAAGTATGATGAGCTGATGATGATGATGATGAT 2108
 Qy 2222 CTGCAAGAAACAGTACTTAATGATTAATGAGGCGAGATTAATGAATTTGCAAAATC 2281
 Db 2109 CTGCAAGAAACAGTACTTAATGATTAATGAGGCGAGATTAATGAATTTGCAAAATC 2168
 Qy 2282 ACTTAGCAGCAACCTGAAGCAATTAATCAACAGTGAAGAAATCAACAGGAGGAGCT 2341
 Db 2169 ACTTAGCAGCAACCTGAAGCAATTAATCAACAGTGAAGAAATCAACAGGAGGAGCT 2228
 Qy 2342 GTGTGAACATGTTGTAATGAGCACTGCAACACTGAACTCTACGCACTCCCAAAAT 2401
 Db 2229 GTGTGAACATGTTGTAATGAGCACTGCAACACTGAACTCTACGCACTCCCAAAAT 2288
 Qy 2402 GATGTTTTCAGTGTGATGAGTGTGCGACCATGATTAATCCAGGTTTAAAGTTT 2461
 Db 2289 GATGTTTTCAGTGTGATGAGTGTGCGACCATGATTAATCCAGGTTTAAAGTTT 2348
 Qy 2462 AAAGTTCAGCATGATTAATGAAGCACTGTTTCTTGAATTTAAATTAATGAATGAATGA 2521
 Db 2349 AAAGTTCAGCATGATTAATGAAGCACTGTTTCTTGAATTTAAATTAATGAATGAATGA 2408
 Qy 2522 AGTTGATTTAAGAAATCAAGCTAAATCACTTCAACTGC 2560
 Db 2409 AGTTGATTTAAGAAATCAAGCTAAATCACTTCAACTGC 2447

RESULT 25
 AAV07906

ID AAV07906 standard; cDNA; 2479 BP.
 AC AAV07906;
 DT 18-JAN-1999 (first entry)
 XX
 DE Human cysteine-rich secreted protein CRSP-1 cDNA.
 KW CRSP-1; cysteine-rich secreted protein 1; tumour; cancer; leukaemia;
 KW tissue repair; wound healing; infection; Parkinson's disease;
 KW Alzheimer's disease; Huntington's chorea; multiple sclerosis;
 KW amyotrophic lateral sclerosis; pontine myelinolysis;
 KW human immunodeficiency associated myelopathy; bulbar palsy;
 KW spinal muscular atrophy; primary lateral sclerosis; poliomyelitis;
 KW Fazio-Londe syndrome; Charcot-Marie-Tooth disease; therapy;
 KW diagnosis; drug screening; human; CRSP-1; TANGO 59;
 KW signal transduction; cell differentiation; cell proliferation; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 38..1090
 FT /tag= a
 FT /note= "claimed fragment"
 FT sig_peptide 38..106
 FT /tag= b
 FT /note= "putative signal peptide sequence may span nucleotides 38-94, 38-100 or 38-106"
 FT mat_peptide 107..1087
 FT /tag= b
 FT /note= "putative mature protein sequence may span nucleotides 95-1087, 101-1087 or 107-1087"
 PN W09846755-A1.
 XX
 PD 22-OCT-1998.
 XX
 PF 16-APR-1998; 98WO-US07894.
 XX
 PR 20-JAN-1998; 98US-0008902.
 PR 16-APR-1997; 97US-0843704.
 PR 17-APR-1997; 97US-0842898.
 PR 15-JAN-1998; 98US-0071589.
 XX
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 XX
 PI McCarthy SA;
 PT
 DR P-PSDB; AAW73016.
 DR
 XX
 PT New isolated cysteine-rich secreted proteins - used to develop
 PT products for treating, e.g. hyperproliferative disorders, cancers,
 PT wounds, infectious lesions, degenerative lesions or demyelating
 PT diseases
 XX
 PS Claim 1; Page 89-91; 142pp; English.
 XX
 CC This full-length cDNA clone, the coding region for which is also
 CC claimed and is deposited as ATCC 98634, codes for novel human
 CC cysteine-rich secreted protein 1 (CRSP-1, see AAW73016), also
 CC referred to as CRSP-1 and TANGO 59. A partial cDNA was isolated
 CC using a signal sequence trap method from human foetal brain tissue
 CC cDNA. This partial clone was then used to isolate the full-length
 CC cDNA. CRSP-1 is expressed in a tissue-specific manner, with
 CC highest expression in brain, heart and spinal cord. CRSP-1 was
 CC used to identify human CRSP-2, CRSP-3, CRSP-4 and CRSP-like-1
 CC cDNAs (see AAV07906-10). The CRSPs have at least 1 of the following
 CC activities: (i) modulation of cellular signal transduction, either
 CC in vitro or in vivo (e.g. antagonism of the activity of members of
 CC the wnt family of secreted proteins or suppression of wnt-dependent
 CC signal transduction); (ii) regulation of communication between cells

QY	1744	TTGCTCAGCTCCTACCTCTGTCGCGCAGGGGACACATTTTCATATCCAAAGATCAATTCCTCT	1803
Db	1629	TTGCTCAGCTCCTACCTCTGTCGCGCAGGGGACACATTTTCATATCCAAAGATCAATTCCTCT	1688
QY	1804	CTCAGCACACGCTGGGGAGGGGGTTCATTTTCTCTCTGTCCTACAGGATCTCAGAGCT	1863
Db	1689	CTCAGCACACGCTGGGGAGGGGGTTCATTTTCTCTCTGTCCTACAGGATCTCAGAGCT	1748
QY	1864	CAGAGACTGCGAAGCTGCTTGGCCCAAGTACACACCTGTGTAACAACAAGACAGTTTCATC	1923
Db	1749	CAGAGACTGCGAAGCTGCTTGGCCCAAGTACACACCTGTGTAACAACAAGACAGTTTCATC	1806
QY	1924	TGGTTTGACTCTAAGCTCAGTGTCTCTCCATCCACACACAGCTTGGTGCCACCA	1983
Db	1809	TGGTTTGACTCTAAGCTCAGTGTCTCTCCATCCACACACAGCTTGGTGCCACCA	1866
QY	1984	AAAGTCTCTCCCAAAAGGAGAGATGGGATTTTTCTTGGAGGATGACACTCTGGAA	2041
Db	1869	AAAGTCTCTCCCAAAAGGAGAGATGGGATTTTTCTTGGAGGATGACACTCTGGAA	1928
QY	2042	TTAAGGTCAAACTAATTTCTCACATCCCTCTAAAGTAACTACTGTGTAAGAACAGAGTG	2103
Db	1929	TTAAGGTCAAACTAATTTCTCACATCCCTCTAAAGTAACTACTGTGTAAGAACAGAGTG	1988
QY	2102	TTCTCACAGTGTGGGGCAGCCGCTCTTAATGAAAGCAATGATATTGACACTGTCCCTC	2167
Db	1989	TTCTCACAGTGTGGGGCAGCCGCTCTTAATGAAAGCAATGATATTGACACTGTCCCTC	2046
QY	2162	TTTGGCAGTTGCAATTAGTAAGTGAAGGATATGACTGAGGGTGGCATACAGGTTAC	2223
Db	2049	TTTGGCAGTTGCAATTAGTAAGTGAAGGATATGACTGAGGGTGGCATACAGGTTAC	2106
QY	2222	CTGCAGAAAACAGTACTTAGTATTTGAGGGCGAGATTAATAAGAAATTTGCAAAATC	2281
Db	2109	CTGCAGAAAACAGTACTTAGTATTTGAGGGCGAGATTAATAAGAAATTTGCAAAATC	2168
QY	2282	ACTTACACCAACTGAAGCAATTTATCAACACGTGAGAAATTCAAACCGAGCAGGGCT	2344
Db	2169	ACTTACACCAACTGAAGCAATTTATCAACACGTGAGAAATTCAAACCGAGCAGGGCT	2222
QY	2342	GTTGTGAAAATGGTTGTATATATGACACCTGCACAACCTACGCCACTGCACAAAT	2401
Db	2229	GTTGTGAAAATGGTTGTATATATGACACCTGCACAACCTACGCCACTGCACAAAT	2288
QY	2402	GATGTTTTCAAGGTGTCACTGACCTGTTGCCACCATGATTCATCCAGAGTTCTTAAAGTTT	2461
Db	2289	GATGTTTTCAAGGTGTCACTGACCTGTTGCCACCATGATTCATCCAGAGTTCTTAAAGTTT	2346
QY	2462	AAAGTTGCACATGATGTGTAAGACATGCTTCTTGAATTTAAATATGATTAACATA	2523
Db	2349	AAAGTTGCACATGATGTGTAAGACATGCTTCTTGAATTTAAATATGATTAACATA	2406
QY	2522	AGTTGCATTTAGAAATCAAGCATTAATCACTTCAACTGC	2560
Db	2409	AGTTGCATTTAGAAATCAAGCATTAATCACTTCAACTGC	2447
RESULT 26			
AAAT5128			
ID	AAAT5128	standard; cDNA; 2479 BP.	
XX	AAAT5128;		
XX	AAAT5128;		
DT	15-JAN-2001	(first entry)	
DE	cDNA encoding a human Dickkopf (Dkk)-3 protein.		
XX	Human; Dickkopf-3 protein; Dkk-3 protein; Soggy protein; optic disorder;		
KW	cysteine-rich secreted protein; glaucoma; conjunctivitis; brain disorder;		
KW	Alzheimer's disease; epilepsy; amnesia; inflammation; pulmonary disorder;		
KW	skeletal muscle disorder; Goodpasture's syndrome;		
KW	cardiovascular disorder; hyperproliferative disorder; cancer; ss.		
XX			

OS	Homo sapiens.
XX	
XX	
FT	Key
FT	Location/Qualifiers
CD	38..1090
FT	/tag= a
FT	/product= "Dickkopf (Dkk)-3 protein"
FT	38..109
FT	/tag= b
FT	
XX	
PN	W0200052047-A2.
XX	
XX	
PD	08-SEP-2000.
XX	
XX	
PF	03-MAR-2000; 2000MO-US05452.
PR	
XX	05-MAR-1999; 99US-0263022.
XX	
PA	(MILL-) MILLENNIUM PHARM. INC.
XX	
PI	McCarthy S;
DR	WPI; 2000-579276/54.
DR	P-PSDB; AAB08874.
XX	
PS	Claim 2; Fig 1A-B; 208pp; English.
XX	
CC	The present sequence encodes a human Dickkopf (Dkk)-3 protein. The
CC	specification also describes Soggy (Dkk-related) sequences. Dkk is a
CC	cysteine-rich secreted protein. The Dkk nucleic acids and proteins are
CC	useful as modulating agents in regulating cellular processes. They are
CC	particularly useful in treating subjects having a disorder characterized
CC	by aberrant expression or activity of Dkk such as optic disorders
CC	(glaucoma, conjunctivitis), brain disorders (Alzheimer's disease,
CC	epilepsy, amnesia), inflammation, skeletal muscle disorders, pulmonary
CC	disorders (Goodpasture's syndrome), cardiovascular disorders, and
CC	hyperproliferative disorders (cancer). The Dkk proteins and nucleic
CC	acids may also be used for research purposes, such as for chromosome
CC	mapping, tissue typing and in screening assays to identify modulators.
XX	
SQ	Sequence 2479 BP; 627 A; 619 C; 665 G; 567 T; 1 other;
Query Match	75.4%; Score 1951; DB 21; Length 2479;
Best Local Similarity	99.7%; Pred. No. 0;
Matches 2431; Conservative	0; Mismatches 6; Indels 2; Gaps 1;
OY	124 GGGGCGGCGGTGAGGGCGCAGACCGGAGATGCAGCGGCTTGAGGGCCACCCTGGCTGCC 183
Db	9 GGGGCGGCGGTGAGGGCGCAGACCGGAGATGCAGCGGCTTGAGGGCCACCCTGGCTGCC 68
OY	184 TGCTGTGTCGCGCGCGGTCCCA CGGCCCCCGCGCGCTTCCAGCGGACTTCGACTC 243
Db	69 TGCTGTGTCGCGCGCGGTCCCA CGGCCCCCGCGCGCTTCCAGCGGACTTCGACTC 128
OY	244 CAGTTCAAGCCCGCGCTTCAAGCTACCCGCAAGAGAGAGGCCACCTCATATGAGATG 303
Db	129 CAGTTCAAGCCCGCGCTTCAAGCTACCCGCAAGAGAGAGGCCACCTCATATGAGATG 188
OY	304 TCCGCGAGGTTGAAGAAGCTGCTTAAGATCATCAGAAAGTGAACCTGGCAAATTAC 423
Db	189 TCCGCGAGGTTGAAGAAGCTGCTTAAGATCATCAGAAAGTGAACCTGGCAAATTAC 248
OY	364 AGATGAGGCGAAGAAAGCTCTGCTTAAGATCATCAGAAAGTGAACCTGGCAAATTAC 423
Db	249 AGATGAGGCGAAGAAAGCTCTGCTTAAGATCATCAGAAAGTGAACCTGGCAAATTAC 308
OY	424 CTCCAGGATTCACAATGAGCAACAACAGACAGAGAGTTGGAATATATCCATCCATG 483
Db	309 CTCCAGGATTCACAATGAGCAACAACAGACAGAGAGTTGGAATATATCCATCCATG 368

QY 484 TGACCCGGAATTCACAGATAACCAACCAACTGACCAATGGTCTTTACAGA 543
DB 369 TGCAACGGAATTCACAGATAACCAACCAACTGACCAATGGTCTTTACAGA 428
QY 544 CAGTTATCACTCTGTGGAGACGAGAGAGGACAGAGAGCCAGATGATCATACAG 603
DB 429 CAGTTATCACTCTGTGGAGACGAGAGAGGACAGAGAGCCAGATGATCATACAG 488
QY 604 AGGACTGTGGGCGCCAGATGTACTGCCAGTTGGCAGTTCCAGTACACCTGGCAGCAT 663
DB 489 AGGACTGTGGGCGCCAGATGTACTGCCAGTTGGCAGTTCCAGTACACCTGGCAGCAT 548
QY 664 GCCGGGACCAAGAGATGCTCTGACCCCGGACAGTGAATGCTGTGAGACCAAGCTGTGTG 723
DB 549 GCCGGGACCAAGAGATGCTCTGACCCCGGACAGTGAATGCTGTGAGACCAAGCTGTGTG 608
QY 724 TCTGGGCTCACTGACCAAAATGGCCACAGGGGACAGATGGGACCATCTGTGACCAACC 783
DB 609 TCTGGGCTCACTGACCAAAATGGCCACAGGGGACAGATGGGACCATCTGTGACCAACC 668
QY 784 AGAGGACTGCGCAGCCGGGGCTGTGTGCTTGTGCTTCCAGAGAGGCTGTGTCTGTGT 843
DB 669 AGAGGACTGCGCAGCCGGGGCTGTGTGCTTGTGCTTCCAGAGAGGCTGTGTCTGTGT 728
QY 844 GCACACCCCTGCGCTGTGAGAGGCGAGCTTTGTCATGACCCCGCAGCCGCTTTGACACC 903
DB 729 GCACACCCCTGCGCTGTGAGAGGCGAGCTTTGTCATGACCCCGCAGCCGCTTTGACACC 788
QY 904 TCATCACTGTGGAGGTAGAGCTGTATGAGAGCTTGGACCGATGCTTGTGACAGTGGCC 963
DB 789 TCATCACTGTGGAGGTAGAGCTGTATGAGAGCTTGGACCGATGCTTGTGACAGTGGCC 848
QY 964 TCTCTGTGCGAGCCCGCAGCCAGCCAGCTGTGTATGTGTGCAACCCGACTTGTGTGAG 1023
DB 849 TCTCTGTGCGAGCCCGCAGCCAGCCAGCTGTGTATGTGTGCAACCCGACTTGTGTGAG 908
QY 1024 GCCCGTGAACAAGATGGGAGATCTCTGCTGCCAGAGAGTCCCGATGAGATGAAGTTG 1083
DB 909 GCCCGTGAACAAGATGGGAGATCTCTGCTGCCAGAGAGTCCCGATGAGATGAAGTTG 968
QY 1084 GCAAGCTTATGAGAGAGGTGCGCGCAGAGCTGAGAGGACCTTGAAGAGAGAGCTTGA 1143
DB 969 GCAAGCTTATGAGAGAGGTGCGCGCAGAGCTGAGAGGACCTTGAAGAGAGAGCTTGA 1028
QY 1144 AGATGGCGCTGGGGAGCGCTGCGCGCTGCGCGCTGCACTGTGGAGGGGAGAGATTT 1203
DB 1029 AGATGGCGCTGGGGAGCGCTGCGCGCTGCGCGCTGCACTGTGGAGGGGAGAGATTT 1088
QY 1204 AGATCTGAGCAAGGCTGTGGGTAGATGTGCAATGAAATAGCTAATTTATTTCCCAAGT 1263
DB 1089 AGATCTGAGCAAGGCTGTGGGTAGATGTGCAATGAAATAGCTAATTTATTTCCCAAGT 1148
QY 1264 GTGTCTTTAGCGCGTGGGCTGACCAAGGCTTCTCTCAATCTTCTTCCCAAGTATTTCC 1323
DB 1149 GTGTCTTTAGCGCGTGGGCTGACCAAGGCTTCTCTCAATCTTCTTCCCAAGTATTTCC 1208
QY 1324 CCTCTGAGCTTGAAGCATAGAGTGTGTGCAATTTGTCAGCTCCCGCAGGCTGTCTTCCA 1383
DB 1209 CCTCTGAGCTTGAAGCATAGAGTGTGTGCAATTTGTCAGCTCCCGCAGGCTGTCTTCCA 1268
QY 1384 GGCCTTCAAGTCTGGTCTTGGAGAGTCAAGCAAGGTTAACTGCAAGAGCAAGTTGGCC 1443
DB 1269 GGCCTTCAAGTCTGGTCTTGGAGAGTCAAGCAAGGTTAACTGCAAGAGCAAGTTGGCC 1328
QY 1444 ACCCTGTGCAAGATTTAGCTTGTGCTTCTCTCAACATTTGGAGACAGCCGTTTGTCT 1503
DB 1329 ACCCTGTGCAAGATTTAGCTTGTGCTTCTCTCAACATTTGGAGACAGCCGTTTGTCT 1388
QY 1504 ACATGGCTTTGATTAATTTGTTGAGGGGAGAGATGGAAACAATGTGAGTCTCCCTCTGA 1563
DB 1389 ACATGGCTTTGATTAATTTGTTGAGGGGAGAGATGGAAACAATGTGAGTCTCCCTCTGA 1448

QY 1564 TTGGTTTGGGGAAATGTGAGAGAGTGCCTGCTTGGCAATCAACTGGCAAAA 1623
DB 1449 TTGGTTTGGGGAAATGTGAGAGAGTGCCTGCTTGGCAATCAACTGGCAAAA 1508
QY 1624 TGCAACAATGAATTTTCCAGCAGAGTCTTTTCCATGGGCAATGATAGTGTGCTTCA 1683
DB 1509 TGCAACAATGAATTTTCCAGCAGAGTCTTTTCCATGGGCAATGATAGTGTGCTTCA 1568
QY 1684 CTGTTCAGATGAATAGTCTGTGCTGACCTGCATATGATGATTTATTCACAGAGTG 1743
DB 1569 CTGTTCAGATGAATAGTCTGTGCTGACCTGCATATGATGATTTATTCACAGAGTG 1628
QY 1744 TTGCTCAGTCTTACTCTGTGCGCAGGGGACGATTTTCATATCCAGATCAATCCCTCT 1803
DB 1629 TTGCTCAGTCTTACTCTGTGCGCAGGGGACGATTTTCATATCCAGATCAATCCCTCT 1688
QY 1804 CTCAGCAGACCTGGGGAGAGGGGGTCAATGTTCCTCCGTCATCCAGGGATCTCAGAGGT 1863
DB 1689 CTCAGCAGACCTGGGGAGAGGGGGTCAATGTTCCTCCGTCATCCAGGGATCTCAGAGGT 1748
QY 1864 CAGAGACTGCAAGCTGCTTGCACCAAGTCAACAGCTAGTGAAGACCAAGAGATTATC 1923
DB 1749 CAGAGACTGCAAGCTGCTTGCACCAAGTCAACAGCTAGTGAAGACCAAGAGATTATC 1808
QY 1924 TGGTTGTGACTTAAGCTCAGTGTCTCTCCACTACCCCAACCGACCTTGGTGCCACCA 1983
DB 1809 TGGTTGTGACTTAAGCTCAGTGTCTCTCCACTACCCCAACCGACCTTGGTGCCACCA 1868
QY 1984 AAAGTCTCCCAAAAAGAGAGAGATGGGATTTTCT - TTGAGGATGACATCTGGA 2041
DB 1869 AAAGTCTCCCAAAAAGAGAGAGATGGGATTTTCTTTTGAAGGATCAATCTGGA 1928
QY 2042 TTAAAGTCAACTAATTTCTCAATCCCTTAAAGTAACTCTGTAGGAACAGAGTG 2101
DB 1929 TTAAAGTCAACTAATTTCTCAATCCCTTAAAGTAACTCTGTGTAGGAACAGAGTG 1988
QY 2102 TTCTCAGTGTGGGGCAGCCGCTCTCTTAATGAAGACATATATTGACACTGCTCCTC 2161
DB 1989 TTCTCAGTGTGGGGCAGCCGCTCTCTTAATGAAGACATATATTGACACTGCTCCTC 2048
QY 2162 TTTTGCAGTTGCATTAATTTCTCAATCCCTTAAAGTAACTCTGTAGGAACAGAGTG 2221
DB 2049 TTTTGCAGTTGCATTAATTTCTCAATCCCTTAAAGTAACTCTGTAGGAACAGAGTG 2108
QY 2222 CTGCAAGAACAGTACTAGTATTTGTAGGGCAGAGATTATTAATGAATTTGCAAAATC 2281
DB 2109 CTGCAAGAACAGTACTAGTATTTGTAGGGCAGAGATTATTAATGAATTTGCAAAATC 2168
QY 2282 ACTTAGCAGCACTGAAGCAATTTATCAACACAGTGAAGAAATCAACCGAGCAGGGCT 2341
DB 2169 ACTTAGCAGCACTGAAGCAATTTATCAACACAGTGAAGAAATCAACCGAGCAGGGCT 2228
QY 2342 GTGTGAAGATGGTGTATATAGCGACTGCGAAGCTGAACCTTAGCCACTCCCAAT 2401
DB 2229 GTGTGAAGATGGTGTATATAGCGACTGCGAAGCTGAACCTTAGCCACTCCCAAT 2288
QY 2402 GATGTTTCAAGTGTCAAGAGCTGTGGCCACATGATTCATCCAGAGTCTTAAAGTT 2461
DB 2289 GATGTTTCAAGTGTCAAGAGCTGTGGCCACATGATTCATCCAGAGTCTTAAAGTT 2348
QY 2462 AAAGTGCACATGATGTATAGCAATGCTTCTTTGAGTTTAAATTAATGATTAACATA 2521
DB 2349 AAAGTGCACATGATGTATAGCAATGCTTCTTTGAGTTTAAATTAATGATTAACATA 2408
QY 2522 AGTTGATTTAGAAATCAAGCATTAATCAACTTCAACTGC 2560
DB 2409 AGTTGATTTAGAAATCAAGCATTAATCAACTTCAACTGC 2447

RESULT 27
AB281839
ID AB281839 standard; DNA; 2124 BP.
XX

AC AB281839;
 XX 11-JUN-2003 (first entry)
 XX DE DKX-2 nucleic acid sequence.
 XX DKX-2; stem cell; stem-loop RNA; antianaemic; cerebroprotective;
 XX neuroprotective; neurotropic; antiparkinsonian; cardiac;
 XX hepatotropic; antidiabetic; vulnerary; gene therapy; gene; ds.
 XX Unidentified.
 OS
 XX WO2003012082-A2.
 XX 13-FEB-2003.
 XX PD 25-JUL-2002; 2002MO-GB03409.
 XX PF 26-JUL-2001; 2001GB-0018223.
 XX (AXOR-) AXORDIA LTD.
 XX PA Andrews P, Walsh J, Gokhale P;
 XX PI WPI; 2003-278398/27.
 XX DR
 XX XX
 XX PT Modulating the differentiation state of a stem cell, useful for
 XX treating e.g. pernicious anemia, stroke, cirrhosis, diabetes or a
 XX neurodegenerative disease, comprises contacting a stem cell with a stem
 XX loop RNA
 XX
 PS Claim 7; Fig 49; 85pp; English.
 XX
 XX The present sequence is the nucleic acid sequence of DKX-2.
 XX The invention relates to a method of modulating the differentiation
 XX state of a stem cell, such as an embryonic stem cell, embryonic
 XX germ cell, embryonal carcinoma cell, haematopoietic stem cell,
 XX muscle stem cell, nerve stem cell, skin dermal sheath stem cell,
 XX liver stem cell or teratocarcinoma cell. The method involves
 XX contacting the stem cell with a stem-loop RNA molecule or a nucleic
 XX acid molecule or vector encoding the stem-loop RNA, where the
 XX nucleic acid is preferably derived from one of the nucleic acid
 XX sequences in AB281794-844, including the present sequence, and may
 XX encode a cell surface receptor expressed by a stem cell, or a ligand.
 XX The RNA molecule, the nucleic acid molecule or the vector is useful
 XX for promoting the differentiation of stem cells and for providing
 XX differentiated cells/tissues for the treatment of diseases in which
 XX cell/tissues are destroyed by the disease. These diseases include
 XX pernicious anaemia, stroke, neurodegenerative diseases such as
 XX Parkinson's disease and Alzheimer's disease, coronary heart disease,
 XX cirrhosis, diabetes, or nerve damage as a consequence of trauma
 XX (e.g. replacement of spinal cord tissue) (claimed).
 XX
 XX Sequence 2124 BP; 528 A; 516 C; 558 G; 521 T; 1 other;
 XX
 XX Query Match 70.4%; Score 1821; DB 25; Length 2124;
 XX Best Local Similarity 99.9%; Pred. No. 0;
 XX Matches 2121; Conservative 0; Mismatches 0; Indels 3; Gaps 2;

Db 181 TGGGCCGAGCATGTAAGTCCAGATTGGCCAGTTCCAGTACACCTGCCAGCATGCCGGG, 240
 QY 671 CCAGAGATGCTCTGCAACCCGGGACAGTGAAGTGTGGAGAACAGCTGTGTGGGG 730
 Db 241 CCAGAGATGCTCTGCAACCCGGGACAGTGAAGTGTGGAGAACAGCTGTGTGGGG 300
 QY 731 TCATGCAACCAAAATGGCCACCAAGGGGACAGATGGAGACATCTGTGCAACCAAGAGGA 790
 Db 301 TCATGCAACCAAAATGGCCACCAAGGGGACAGATGGAGACATCTGTGCAACCAAGAGGA 360
 QY 791 CTGCCAGCCGGGGCTGTGCTGTGCTTCCAGAGAGGCTGTGTCCCTGTGTGCAACC 850
 Db 361 CTGCCAGCCGGGGCTGTGCTGTGCTTCCAGAGAGGCTGTGTCCCTGTGTGCAACC 420
 QY 851 CCGTCCCTGAGAGGAGCGAGCTTTTGCATGACCCCGCCAGCCGGCTTGTGACCTCATCAC 910
 Db 421 CCGTCCCTGAGAGGAGCGAGCTTTTGCATGACCCCGCCAGCCGGCTTGTGACCTCATCAC 480
 QY 911 CTGGAGCTTAAGCTGTATGAGAGCTTGAACCATGCTTGTGTGCAAGTGGCTCTCTG 970
 Db 481 CTGGAGCTTAAGCTGTATGAGAGCTTGAACCATGCTTGTGTGCAAGTGGCTCTCTG 540
 QY 971 CCAGCCCAACAGCAGAGCTGTGTATGTGTGCAACCCGACTTGTGTGGAGCCGTGA 1030
 Db 541 CCAGCCCAACAGCAGAGCTGTGTATGTGTGCAACCCGACTTGTGTGGAGCCGTGA 600
 QY 1031 CCAGATGGGAGATCTGTCTGCTCCAGAGAGGTCCCGATGATGATGAATTTGGACGTT 1090
 Db 601 CCAGATGGGAGATCTGTCTGCTCCAGAGAGGTCCCGATGATGATGAATTTGGACGTT 660
 QY 1091 CATGAGAGAGGTGCGCCAGAGAGCTGAGAGACCTGAGAGAGCCCTGAAGAGATGGC 1150
 Db 661 CATGAGAGAGGTGCGCCAGAGAGCTGAGAGACCTGAGAGAGCCCTGAAGAGATGGC 720
 QY 1151 GCTGGGAGAGCTGTGAGCTGCGCGCTGCTGCACTGTGGAGAGGAAAGATTGATGTG 1210
 Db 721 GCTGGGAGAGCTGTGAGCTGCGCGCTGCTGCACTGTGGAGAGGAAAGATTGATGTG 780
 QY 1211 GACCAAGCTGTGGGAGATGTGCAATAGAAATAGTAATTTATTTCCAGAGTGTGCT 1270
 Db 781 GACCAAGCTGTGGGAGATGTGCAATAGAAATAGTAATTTATTTCCAGAGTGTGCT 840
 QY 1271 TTAGGCGTGGGCTGACAGAGCTTCTTCTACATCTTCTCCAGTAAGTTCCCTCTGG 1330
 Db 841 TTAGGCGTGGGCTGACAGAGCTTCTTCTACATCTTCTCCAGTAAGTTCCCTCTGG 900
 QY 1331 CTGACAGCATGAGGTGTGTGCAATTTGTAGCTCCCGCAGGCTTCTCCAGGCTTCA 1390
 Db 901 CTGACAGCATGAGGTGTGTGCAATTTGTAGCTCCCGCAGGCTTCTCCAGGCTTCA 960
 QY 1391 CAGTCTGTGCTTGGAGAGTCAAGCAGAGTTAACTGACAGAGCATGTTGCCACCCCTG 1450
 Db 961 CAGTCTGTGCTTGGAGAGTCAAGCAGAGTTAACTGACAGAGCATGTTGCCACCCCTG 1020
 QY 1451 TCCAAATATTGGCTGCTTGTGCTTCTTACCAATTTGGAGAGAGCCGCTTGTCTCATGSC 1510
 Db 1021 TCCAAATATTGGCTGCTTGTGCTTCTTACCAATTTGGAGAGAGCCGCTTGTCTCATGSC 1080
 QY 1511 TTTGATTAATTTGTTAGAGGAGAGATGGAACAATGTGAGTCTCCCTCTGATTTGTTT 1570
 Db 1081 TTTGATTAATTTGTTAGAGGAGAGATGGAACAATGTGAGTCTCCCTCTGATTTGTTT 1140
 QY 1571 TGGGAAATGTGGAGAAAGTGCCTGCTTTGGCAACATCAACTGGGAAAAATGGCAACA 1630
 Db 1141 TGGGAAATGTGGAGAAAGTGCCTGCTTTGGCAACATCAACTGGGAAAAATGGCAACA 1200
 QY 1631 AATGAATTTTCCAGCAATTTCTTCCATGGGCAATGTAAGTGTGCTTCAAGCTGTTC 1690
 Db 1201 AATGAATTTTCCAGCAATTTCTTCCATGGGCAATGTAAGTGTGCTTCAAGCTGTTC 1260
 QY 1691 AGATGAATTTCTGTTTCACTGCTGATTAATGTGTTTATTCATCCAGCAATGTTGCTCA 1750
 Db 1261 AGATGAATTTCTGTTTCACTGCTGATTAATGTGTTTATTCATCCAGCAATGTTGCTCA 1320

QY 731 TCACGACCAAAATGCGCCACGAGGGGAGCAATGGGACCATCTGTGACCAACGAGGGA 790
DB 301 TCACGACCAAAATGCGCCACGAGGGGAGCAATGGGACCATCTGTGACCAACGAGGGA 360
QY 791 CTGCGCAGCGGGGCTGTGTGTGCTTCCAGAGAGGCTGTGTGCTTCCGTGTGTGACACC 850
DB 361 CTGCGCAGCGGGGCTGTGTGTGCTTCCAGAGAGGCTGTGTGCTTCCGTGTGTGACACC 420
QY 851 CCGGCCCGGAGGAGGAGCTTGGCATGACCCCGAGCGGCTTCTGGAACCTATCAG 910
DB 421 CCGGCCCGGAGGAGGAGCTTGGCATGACCCCGAGCGGCTTCTGGAACCTATCAG 480
QY 911 CTGCGAGCTAGAGCTGTATGAGAGCTTGAACCGATGCTGTGTGAGAGTGTCTGTG 970
DB 481 CTGCGAGCTAGAGCTGTATGAGAGCTTGAACCGATGCTGTGTGAGAGTGTCTGTG 540
QY 971 CCAAGCCCAACGACAGCTGTGTATGTGTGCAAGCGGACCTGTGTGGGAGCGGTGA 1030
DB 541 CCAAGCCCAACGACAGCTGTGTATGTGTGCAAGCGGACCTGTGTGGGAGCGGTGA 600
QY 1031 CCAAGATGGGAGATCTGTGTGCTGACAGAGAGTCCCGATGATGATGAAATTGGCAGCTT 1090
DB 601 CCAAGATGGGAGATCTGTGTGCTGACAGAGAGTCCCGATGATGATGAAATTGGCAGCTT 660
QY 1091 CATGAGAGAGGTGTGCGCAGAGCTGTGAGAGACCTGTGAGAGAGAGCTGTGAGAGATGAGC 1150
DB 661 CATGAGAGAGGTGTGCGCAGAGCTGTGAGAGACCTGTGAGAGAGAGCTGTGAGAGATGAGC 720
QY 1151 GCTGGGGAGAGCTGTGCGCTGCGCCGCTGTGACCTGTGTGGAGGGAGAGATTTAGATCTG 1210
DB 721 GCTGGGGAGAGCTGTGCGCTGCGCCGCTGTGACCTGTGTGGAGGGAGAGATTTAGATCTG 780
QY 1211 GACCAAGCTGTGTGTATGATGTGCAATGAAATAGCTAATTTATTTCCCGAGGTGTGTCT 1270
DB 781 GACCAAGCTGTGTGTATGATGTGCAATGAAATAGCTAATTTATTTCCCGAGGTGTGTCT 840
QY 1271 TTAGGCGTGGGCTGACAGAGCTTCTTCTCATCTTCTTCCAGTAGATTCCCTCTG 1330
DB 841 TTAGGCGTGGGCTGACAGAGCTTCTTCTCATCTTCTTCCAGTAGATTCCCTCTG 900
QY 1331 CTGACAGCATGAGGTGTGTGCAATTTGTCAAGTCTCCCGAGGTGTGTCTCCAGGCTTCA 1390
DB 901 CTGACAGCATGAGGTGTGTGCAATTTGTCAAGTCTCCCGAGGTGTGTCTCCAGGCTTCA 960
QY 1391 CAGCTGTGTGTGGGAGAGTCAAGGAGGTAAATCGACAGAGAGCTTTGCCACCCCTG 1450
DB 961 CAGCTGTGTGTGGGAGAGTCAAGGAGGTAAATCGACAGAGAGCTTTGCCACCCCTG 1020
QY 1451 TCCAGATTATGAGTGTGTGCTTCTCTACCAAGTTGGCAGAGCGGTTGTCTTACATGTC 1510
DB 1021 TCCAGATTATGAGTGTGTGCTTCTCTCTACCAAGTTGGCAGAGCGGTTGTCTTACATGTC 1080
QY 1511 TTTGATTAATTTGTGAGAGGAGAGATGGAACAATGTGAGTCTCCCTGATGTGTT 1570
DB 1081 TTTGATTAATTTGTGAGAGGAGAGATGGAACAATGTGAGTCTCCCTGATGTGTT 1140
QY 1571 TGGGGAATGTGAGAGAGTGCCTGCTTGCACCAACATCAACCTGGCAAAAATGACACA 1630
DB 1141 TGGGGAATGTGAGAGAGTGCCTGCTTGCACCAACATCAACCTGGCAAAAATGACACA 1200
QY 1631 AATGAATTTTCCAGCAGTCTTCTTCCATGGGCAATGTAACCTGTGCTTCAAGTGTGTC 1690
DB 1201 AATGAATTTTCCAGCAGTCTTCTTCCATGGGCAATGTAACCTGTGCTTCAAGTGTGTC 1260
QY 1691 AGATGAATGTGTCTGTCAACCTGATTAATGTTTATTCATCCAGCAGTGTGTGTC 1750
DB 1261 AGATGAATGTGTCTGTCAACCTGATTAATGTTTATTCATCCAGCAGTGTGTGTC 1320
QY 1751 GCTCTTACCTGTGTGCGCAGAGGAGATTTTCAATCCCAAGTCAATTCCTCTTCAACA 1810
DB 1321 GCTCTTACCTGTGTGCGCAGAGGAGATTTTCAATCCCAAGTCAATTCCTCTTCAACA 1380
QY 1811 CAGCTGGGAGGGGATGTGTCTCTCTGTCTCATCAAGGATCTCAGAGG-CTCAGAGA 1869

DB 1381 CAGCTGGGAGGGGATGTGTCTCTCTGTCTCATCAGGAGATCTCAGAGNCTCAGAGA 1440
QY 1870 CTGCAAGCTCTTGGCCCAAGTGTCAACAGCTAGTGAAGACAGAGAGCTTCTCTGTTG 1929
DB 1441 CTGCAAGCTCTTGGCCCAAGTGTCAACAGCTAGTGAAGACAGAGAGCTTCTCTGTTG 1500
QY 1930 TGACTCTAAGCTCAAGTCTCTCTCTCACTACCCCAACAGCTTGTGTGCAACCAAAAGT 1989
DB 1501 TGACTCTAAGCTCAAGTCTCTCTCTCACTACCCCAACAGCTTGTGTGCAACCAAAAGT 1560
QY 1990 CTCCCAAAAGAGAGAGAGATGGGATTTTTC--TTGAGGATGACACTGTGAATTAAG 2047
DB 1561 CTCCCAAAAGAGAGAGATGGGATTTTTC--TTGAGGATGACACTGTGAATTAAG 1620
QY 2048 TCAAACTAATTCATCACTCCCTCTTAAAGTAACTACTGTGAGACAGAGTGTCTCA 2107
DB 1621 TCAAACTAATTCATCACTCCCTCTTAAAGTAACTACTGTGAGACAGAGTGTCTCA 1680
QY 2108 CAGTGTGGGAGAGCCGCTCTCTTAATGAAGCATGATTAATGACACTGTCCCTTGGC 2167
DB 1681 CAGTGTGGGAGAGCCGCTCTCTTAATGAAGCATGATTAATGACACTGTCCCTTGGC 1740
QY 2168 AGTTCATTAGTAACTTTGAAGGATATGACTGAGGCTAGCATACAGTTAACTTAC 2227
DB 1741 AGTTCATTAGTAACTTTGAAGGATATGACTGAGGCTAGCATACAGTTAACTTAC 1800
QY 2228 AAACAGTACTTAAGTAAATTTGAGGCGAGATTTAAATGAAATTTGCAAAATCACTAG 2287
DB 1801 AAACAGTACTTAAGTAAATTTGAGGCGAGATTTAAATGAAATTTGCAAAATCACTAG 1860
QY 2288 CAGCACTGAAGACATTAATCAACAGTGTGAGAAATCAAAACGAGAGGCTGTGTGA 2347
DB 1861 CAGCACTGAAGACATTAATCAACAGTGTGAGAAATCAAAACGAGAGGCTGTGTGA 1920
QY 2348 AACATGTTGTATATGAGACTGTGGAACATGAACTTACCCCACTCCCAAAATGAGT 2407
DB 1921 AACATGTTGTATATGAGACTGTGGAACATGAACTTACCCCACTCCCAAAATGAGT 1980
QY 2408 TTCAGATGATGAGCTGTGCAACATGATTAATTCAGAGTCTTAAAGTTAAAGT 2467
DB 1981 TTCAGATGATGAGCTGTGCAACATGATTAATTCAGAGTCTTAAAGTTAAAGT 2040
QY 2468 GCACATGATTTATTAAGCATGCTTCTTGTGATTTAAATTAATTAATTAAGTTC 2527
DB 2041 GCACATGATTTATTAAGCATGCTTCTTGTGATTTAAATTAATTAATTAAGTTC 2100
QY 2528 ATTGAAATCAAGCATTAATCAC 2551
DB 2101 ATTGAAATCAAGCATTAATCAC 2124

RESULT 29
ABX75346
ID ABX75346 standard; cDNA; 2124 BP.
XX AC ABX75346;
XX DT 25-MAR-2003 (first entry)
XX DE Human cDNA encoding secreted frizzled related protein 4.
XX XX
XX Gene; Notch; Wnt; embryonic stem cell; embryogenesis; ss;
XX differentiation; ligand; Parkinson's disease; Huntington's disease;
XX motor neuron disease; heart disease; diabetes; liver disease; human;
XX cleftosis; renal disease; AIDS; acquired immunodeficiency syndrome.
XX OS Homo sapiens.
XX PN W0200277204-A2.
XX PD 03-OCT-2002.
XX XX

PF 25-MAR-2002; 2002WO-GB01195.
 XX
 PR 23-MAR-2001; 2001GB-0007296.
 PR 23-MAR-2001; 2001GB-0007299.
 PR 17-APR-2001; 2001GB-0009346.
 XX
 PA (AXORDIA) AXORDIA LTD.
 XX
 PI Andrews P, Walsh J, Gokhale P;
 XX
 DR WPI; 2003-092852/08.
 DR P-PSDB; ABUS5919.
 XX
 PT Modulating the differentiation of embryonic stem cells by providing
 PT ligands which bind receptors in the Notch and Wnt pathways, useful for
 PT treating diseases such as Parkinson's, Huntington's, heart disease,
 PT diabetes and AIDS -
 XX
 PS Claim 18; Fig 103; 121pp; English.
 XX
 CC The invention relates to modulating the differentiation of an embryonic
 CC stem cell, comprising: (a) providing a culture of embryonic stem cells;
 CC (b) providing at least one ligand or its active binding fragment,
 CC capable of binding its cognate receptor polypeptide expressed by the
 CC embryonic stem cell; (c) forming a culture comprising embryonic stem
 CC cells and the ligand; and (d) growing the cell culture. Also included
 CC are: (1) Modulating the differentiation of embryonic stem cells,
 CC comprising: (a) providing a cell transfected with a nucleic acid molecule
 CC selected from: (i) any of 9 fully defined Wnt nucleic acid sequences;
 CC (ii) a nucleic acid molecule that hybridizes to the nucleic acid in
 CC (i), and which encodes a ligand capable of modulating embryonic stem
 CC cell differentiation, or capable of binding a Wnt receptor; or
 CC (iii) nucleic acid molecules which are degenerate as a result of the
 CC genetic code to the sequences of (i) or (ii); (b) forming a culture
 CC comprising the cell identified in (a) with an embryonic stem cell; and
 CC (c) growing the culture for the maintenance and/or differentiation of
 CC the embryonic stem cell; (2) Inhibiting the differentiation of embryonic
 CC stem cells, comprising: (a) providing at least one polypeptide or its
 CC active fragment, that are inhibitors of the Wnt signaling pathway;
 CC (b) forming a culture comprising the cell identified in (a) with an
 CC embryonic stem cell; and (c) growing the culture for the maintenance of
 CC embryonic stem cells in an undifferentiated state; or (3) Inhibiting the
 CC differentiation of embryonic stem cells, comprising: (a) providing a cell
 CC transfected with a nucleic acid molecule selected from: (i) a molecule
 CC encoding a Wnt inhibitory polypeptide; (ii) a molecule which hybridizes
 CC to the molecule of (i) and encodes a polypeptide capable of inhibiting
 CC Wnt signaling; and (iii) nucleic acid molecules which are degenerate as
 CC a result of the genetic code to the sequences of (i) or (ii); (b) forming
 CC a culture comprising the cell identified in (a) with an embryonic stem
 CC cell; and (c) growing the culture for the maintenance of embryonic stem
 CC cells in an undifferentiated state; and (4) A cell, therapeutic cell or
 CC cell culture obtainable by any of the methods cited above.
 CC The therapeutic cell of the present invention is useful in the
 CC treatment of an animal, preferably a human, comprising administering a
 CC cell composition comprising embryonic stem cells which have been
 CC induced to differentiate into at least one cell type. The cell is also
 CC useful for the manufacture of a composition for use in treatment of
 CC diseases such as Parkinson's disease, Huntington's disease, motor
 CC neuron disease, heart disease, diabetes, liver disease (e.g. cirrhosis),
 CC renal disease and AIDS (acquired immunodeficiency syndrome).
 CC The present sequence encodes a Wnt or Notch pathway protein
 CC (i.e. a ligand for the method of the invention).
 CC
 XX
 XX
 SQ Sequence 2124 BP; 528 A; 516 C; 558 G; 521 T; 1 other;
 Query Match 70.4%; Score 1821; DB 25; Length 2124;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2121; Conservative 0; Mismatches 0; Indels 3; Gaps 2;
 QY 431 CTATCATGATGAGCAACACAGACAGAGGTTGGAAATATATCATCCATGTGACCG 490
 DB 1 CTATCATGATGAGCAACACAGACAGAGGTTGGAAATATATCATCCATGTGACCG 60

QY 491 AGAATTCAAGATATACCAACACAGAGCTGACAAATGGTCTTTGAGACAGTTAT 550
 DB 61 AGAATTCAAGATATACCAACACAGAGCTGACAAATGGTCTTTGAGACAGTTAT 120
 QY 551 CACATCTGTGGAGAGCAAGAAAGGAGCAAGACAGATGATCATGACGAGAGCTG 610
 DB 121 CACATCTGTGGAGAGCAAGAAAGGAGCAAGACAGATGATCATGACGAGAGCTG 180
 QY 611 TGGGGCCAGCATGATCTGCTGAGTTGGCCAGCTTCCAGTACATCTGACGAGCTG 670
 DB 181 TGGGGCCAGCATGATCTGCTGAGTTGGCCAGCTTCCAGTACATCTGACGAGCTG 240
 QY 671 CCAGAGATCTCTGACACCCGGGACAGTGAAGTGTGGAGACAGCTGTGTCTG 730
 DB 241 CCAGAGATCTCTGACACCCGGGACAGTGAAGTGTGGAGACAGCTGTGTCTG 300
 QY 731 TCATCTGACCAAAATAGGCCACAGAGGAGAGCAATGGACCAATCTGTGCAACAGAG 790
 DB 301 TCATCTGACCAAAATAGGCCACAGAGGAGAGCAATGGACCAATCTGTGCAACAGAG 360
 QY 791 CTGCCAGCCGGGCTGTGCTGTGCTTCCAGAGAGGCTGTGCTTCCGTGTGACACC 850
 DB 361 CTGCCAGCCGGGCTGTGCTGTGCTTCCAGAGAGGCTGTGCTTCCGTGTGACACC 420
 QY 851 CTTGCCCTGTGAGAGGCGAGCTTTGCCATGACCCCGCAGCCGGCTTTGAGACTCATGC 910
 DB 421 CTTGCCCTGTGAGAGGCGAGCTTTGCCATGACCCCGCAGCCGGCTTTGAGACTCATGC 480
 QY 911 CTGGAGCTAGAGAGCTGATGAGAGCTTGGACAGTATGCTTGTGACAGTGGCTCTG 970
 DB 481 CTGGAGCTAGAGAGCTGATGAGAGCTTGGACAGTATGCTTGTGACAGTGGCTCTG 540
 QY 971 CCAAGCCCAACGCCACAGCTTGTATGTGTGCAAGCTTCTGTGAGAGAGCTTGA 1030
 DB 541 CCAAGCCCAACGCCACAGCTTGTATGTGTGCAAGCTTCTGTGAGAGAGCTTGA 600
 QY 1031 CCAAGTGTGGAGAGATCTGCTGCTCCAGAGAGGTCCCGATGATGAAATTGGACGTT 1090
 DB 601 CCAAGTGTGGAGAGATCTGCTGCTCCAGAGAGGTCCCGATGATGAAATTGGACGTT 660
 QY 1091 CATGAGAGAGGTGCGCCAGAGAGCTGAGAGAGCTTGAAGAGAGCTTGAAGAGTGC 1150
 DB 661 CATGAGAGAGGTGCGCCAGAGAGCTGAGAGAGCTTGAAGAGAGCTTGAAGAGTGC 720
 QY 1151 GCTGGGGGAGCCTGCGGGCTGCGCGCTGCTGCACTGCTGGGAGGGAGAGATTAGATCG 1210
 DB 721 GCTGGGGGAGCCTGCGGGCTGCGCGCTGCTGCACTGCTGGGAGGGAGAGATTAGATCG 780
 QY 1211 GACCAAGCTGTGGATGATGTCATAGAAATAGCTAATTTATTTCCCGAGGTGTGCT 1270
 DB 781 GACCAAGCTGTGGATGATGTCATAGAAATAGCTAATTTATTTCCCGAGGTGTGCT 840
 QY 1271 TTAGGGTGGGCTGACCAAGCTTCTTCTTCACTCTTCCAGTAAGTTCCCTCTG 1330
 DB 841 TTAGGGTGGGCTGACCAAGCTTCTTCTTCACTCTTCCAGTAAGTTCCCTCTG 900
 QY 1331 CTTGACAGCATGAGGTGTGTCATTGTTGCACTTCCCTCCAGAGCTTCTTCCAGAGCTTCA 1390
 DB 901 CTTGACAGCATGAGGTGTGTCATTGTTGCACTTCCCTCCAGAGCTTCTTCCAGAGCTTCA 960
 QY 1391 CAGTCTGTGCTTGGAGAGAGTCAAGCAGGCTTAACTGAGAGAGAGATTGGCACCCCTG 1450
 DB 961 CAGTCTGTGCTTGGAGAGAGTCAAGCAGGCTTAACTGAGAGAGAGATTGGCACCCCTG 1020
 QY 1451 TCCAGATTAATGAGCTTGTGCTTACCAAGTGTGACAGACAGCGTTGTTTCAATGAGC 1510
 DB 1021 TCCAGATTAATGAGCTTGTGCTTACCAAGTGTGACAGACAGCGTTGTTTCAATGAGC 1080
 QY 1511 TTTGATTAATTTGTTGAGGGGAGAGATGGAACAATGTGAGATCTTCCCTCTAATGCTTT 1570
 DB 1081 TTTGATTAATTTGTTGAGGGGAGAGATGGAACAATGTGAGATCTTCCCTCTAATGCTTT 1140
 QY 1571 TGGGAAATGTGGAGAGAGTCCCTGCTTGCAAAATCACTGGCAAAAATGACACA 1630

Db 1141 TGGGGAATGTGAGAGAGATGCCCCTGCTTGCACCACTGCGCAAAATGACAA 1200
QY 1631 AATGAATTTCCACGAGAGTCTTTCCATGGGCAATAGTGTGCTTCACTGCTTGC 1690
Db 1201 AATGAATTTCCACGAGAGTCTTTCCATGGGCAATAGTGTGCTTCACTGCTTGC 1260
QY 1691 AGATGAATGTGCTTCCATGACCTTCCATGATGATGATGATGATGATGATGATG 1750
Db 1261 AGATGAATGTGCTTCCATGACCTTCCATGATGATGATGATGATGATGATGATG 1320
QY 1751 GCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1810
Db 1321 GCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
QY 1811 CAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1869
Db 1381 CAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440
QY 1870 CTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1929
Db 1441 CTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
QY 1930 TGAATCTGAGCTGAGTGTCTCTCTCACTACCCCAACAGCCTTGTGTCACCAAAAGTG 1989
Db 1501 TGAATCTGAGCTGAGTGTCTCTCTCACTACCCCAACAGCCTTGTGTCACCAAAAGTG 1560
QY 1990 CTGCCCCAAAG 2047
Db 1561 CTGCCCCAAAG 1620
QY 2048 TCAAACTAATTTCTACATCCCTCTAAAGATTAATCTGTTAGAGAGAGAGAGAGAGAG 2107
Db 1621 TCAAACTAATTTCTACATCCCTCTAAAGATTAATCTGTTAGAGAGAGAGAGAGAGAG 1680
QY 2108 CAGTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2167
Db 1681 CAGTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1740
QY 2168 AGTTGCAATGTAGTACTTTGAAAGATATATGAGAGGAGTATGAGAGTATGAGAGTATG 2227
Db 1741 AGTTGCAATGTAGTACTTTGAAAGATATATGAGAGGAGTATGAGAGTATGAGAGTATG 1800
QY 2228 AAACAGTACTTATGATATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2287
Db 1801 AAACAGTACTTATGATATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1860
QY 2288 CAGCAACTGAAGCAATTAATCAACAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2347
Db 1861 CAGCAACTGAAGCAATTAATCAACAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
QY 2348 AACATGTTGTTATATGCGAGCTGCGAAGCTGAACTCTGACGCACTGCAAAATGATGTT 2407
Db 1921 AACATGTTGTTATATGCGAGCTGCGAAGCTGAACTCTGACGCACTCTCAAAATGATGTT 1980
QY 2408 TTTCAGGTGTATGAGAGCTGTTGCGACGATGATGATGATGATGATGATGATGATGATG 2467
Db 1981 TTTCAGGTGTATGAGAGCTGTTGCGACGATGATGATGATGATGATGATGATGATGATG 2040
QY 2468 GCACATGATGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2527
Db 2041 GCACATGATGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2100
QY 2528 ATTTAGGAATCAAGCATTAATCAAC 2551
Db 2101 ATTTAGGAATCAAGCATTAATCAAC 2124

RESULT 30
AAS62284
ID AAS62284 standard; cDNA; 2102 BP.
XX
AC AAS62284;

XX 14-FEB-2002 (first entry)
DT CDNA sequence #71 encoding novel human secreted protein.
XX
DE
DE
KW Human secreted protein; hyperproliferative disorder; autoimmune disorder;
KW immune deficiency disorder; blood disorder; inflammatory disorder;
KW infectious disorder; gene therapy; antimicrobial; hepatotropic;
KW immunosuppressive; antineoplastic; ss.
OS Homo sapiens.
PN MO200177291-A2.
PD 18-OCT-2001.
XX 29-MAR-2001; 2001MO-US10485.
XX 06-APR-2000; 2000US-195604P.
PR (GENY) GENETICS INST INC.
PA
XX Wong GG, Clark HF, Fecthel K, Agostino MJ, Howes SH, Resnick RJ;
PI Gultukora K, Graham JR;
XX
DR WPI; 2002-010900/01.
PT New polynucleotides encoding secreted proteins useful for treating e.g.
PT asthma, HIV and Crohn's disease -
XX
PS Claim 1; Page 112-113; 391pp; English.
XX
CC The present invention relates to the isolation of novel cDNA sequences
CC which encode human secreted proteins. The cDNA sequences have been
CC derived from a variety of human tissues. The invention also provides
CC a method for producing proteins from these polynucleotide sequences.
CC The proteins are useful for identifying compounds that modulate their
CC activity and production, and the cell is also useful for identifying
CC compounds that modulate expression of the polynucleotide sequences
CC encoding the secreted proteins. The sequences of the invention are
CC useful for treating diseases such as hyperproliferative disorders
CC (e.g. cancer), immune deficiency disorders (e.g. severe combined
CC immunodeficiency (SCID), autoimmune disorders (e.g. multiple
CC sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory
CC disorders (e.g. arthritis) and infectious disorders (e.g. hepatitis).
CC The polynucleotide sequences of the invention are also useful in gene
CC therapy. AAS62214-AAS62838 represent the cDNA sequences of the
CC invention that encode for novel human secreted proteins.
XX
SQ Sequence 2102 BP; 517 A; 510 C; 554 G; 521 T; 0 other;

Query Match 69.6%; Score 1799; DB 24; Length 2102;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2099; Conservative 0; Mismatches 0; Indels 3; Gaps 2;

QY 462 GTTGAATTAATACATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 521
Db 1 GTTGAATTAATACATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60
QY 522 GACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 581
Db 61 GACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
QY 582 AGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 641
Db 121 AGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
QY 642 TTCCAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 701
Db 181 TTCCAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 702 TGCTGTGAGAGCAAGCTGT 761

D	241	TGCTGTGGAGACCAAGCTGTGTGTCTGGAGGTCACTGACACCAAAATGGCCACCAAGGGGACG	300
Q	762	AATGGGACCAATCTGTGACAAACAGAGGAGCTGGCAAGCCGGGGCTGTGTCTGTCTTCAG	821
D	301	AATGGGACCAATCTGTGACAAACAGAGGAGCTGGCAAGCCGGGGCTGTGTCTGTCTTCAG	360
Q	822	AGAGGCTGTGTATCCCTGTGTGACACCCCTGCGCTGGAGGGCG-AGCTTTGGCATGA	880
D	361	AGAGGCTGTGTATCCCTGTGTGACACCCCTGCGCTGGAGGGCGAAGCTTTGGCATGA	420
Q	881	CCCCGCAAGCCGGTTTCTGAGCCTTATCACCTGGGACTTGAAGCTATGAGCCTTGA	940
D	421	CCCCGCAAGCCGGTTTCTGAGCCTTATCACCTGGGAGTTGAAGCTATGAGCCTTGA	480
Q	941	CCGATGCCCTTGTGCCAGTGGCCTCTCTGACAGCCCCACAGCCACAGCCTGTGTATGT	1000
D	481	CCGATGCCCTTGTGCCAGTGGCCTCTCTGACAGCCCCACAGCCTGTGTGTATGT	540
Q	1001	GTCGAAGCCCACTTGTGTGGGAGACCGGTGACAAATGGGAGATCCCTGCTGCCAAGA	1060
D	541	GTCGAAGCCCACTTGTGTGGGAGACCGGTGACAAATGGGAGATCCCTGCTGCCAAGA	600
Q	1061	GGTCCCGATGATGATGAAGTTTGACGCTTCATGAGAGAGTGGCCAGAGACTGAGGA	1120
D	601	GGTCCCGATGATGATGAAGTTTGACGCTTCATGAGAGAGTGGCCAGAGACTGAGGA	660
Q	1121	CCCTGGAGAGAGCCTTGACTGAGAGATGGGCGTGGGGAGAGCTGCGGCTGCGCGGCTGC	1180
D	661	CCCTGGAGAGAGCCTTGACTGAGAGATGGGCGTGGGGAGAGCTGCGGCTGCGCGGCTGC	720
Q	1181	ACTGCTGGAGGGGAGAGATTTTGAATCTGGACACAGCCTGTGGTAGATGTGCATAGAA	1240
D	721	ACTGCTGGAGGGGAGAGATTTTGAATCTGGACACAGCCTGTGGTAGATGTGCATAGAA	780
Q	1241	ATTACTAATTATTTCCCCAGAGTGTGTCTTAGCGGTGGGCTGACCAAGCTTCTCTTA	1300
D	781	ATTACTAATTATTTCCCCAGAGTGTGTCTTAGCGGTGGGCTGACCAAGCTTCTCTTA	840
Q	1301	CATCTCTTCCAGTAGATTTCCTCTGTGCTTGAACAGATGAGTGTGTGCATTTGTT	1360
D	841	CATCTCTTCCAGTAGATTTCCTCTGTGCTTGAACAGATGAGTGTGTGCATTTGTT	900
Q	1361	CAGCTCCCGCCAGGCTGTCTTCCAGGCTTCAAGTCTGGTGTGGGAGTCAAGCAAGG	1420
D	901	CAGCTCCCGCCAGGCTGTCTTCCAGGCTTCAAGTCTGGTGTGGGAGTCAAGCAAGG	960
Q	1421	TTAAATGACAGAGCAAGTTTGCACCCCTGTCCAGATTAATTGCTGTCTTCACCA	1480
D	961	TTAAATGACAGAGCAAGTTTGCACCCCTGTCCAGATTAATTGCTGTCTTCACCA	1020
Q	1481	GTTGGCAGACGCGGTTTGTCTTCAATGAGCTTGAATTTTGGAGGGAGAGATGGA	1540
D	1021	GTTGGCAGACGCGGTTTGTCTTCAATGAGCTTGAATTTTGGAGGGAGAGATGGA	1080
Q	1541	AACAATGTGAGTCTCCTCTGTATTTGGTGTGGGAAAATGAGAAAGTGCCTGCTT	1600
D	1081	AACAATGTGAGTCTCCTCTGTATTTGGTGTGGGAAAATGAGAAAGTGCCTGCTT	1140
Q	1601	TGCAAACTCAACTCGGCAAAATGCAACAATGAATTTTCCAGAGTCTTCCATAGG	1660
D	1141	TGCAAACTCAACTCGGCAAAATGCAACAATGAATTTTCCAGAGTCTTCCATAGG	1200
Q	1661	GCATAGGTAGCTGTGCTTCAAGCTGTGCAATGAATGTTCTGTTCACCTGCATTAAC	1720
D	1201	GCATAGGTAGCTGTGCTTCAAGCTGTGCAATGAATGTTCTGTTCACCTGCATTAAC	1260
Q	1721	ATGTGTTAATCATTCAGACAGTGTGTCAAGCTCTTAACTCTGTGCCAGGACATTTT	1780
D	1261	ATGTGTTAATCATTCAGACAGTGTGTCAAGCTCTTAACTCTGTGCCAGGACATTTT	1320
Q	1781	CATATCCAAATCAATTCCTCTCTCAGACACAGCTTGGGAGGGGGATATTGTTCTCTC	1840
D	1321	CATATCCAAATCAATTCCTCTCTCAGACACAGCTTGGGAGGGGGATATTGTTCTCTC	1380

Accession	Source	Length	Score	E-value	Annotations
QY	1841	1900	1841	1.0	GTCCATGAGGATCTCAGAGGCTCAGAGATCGAAGTGTGCTTCCCAAGTCACACACTTA
Db	1381	1440	1381	1.0	GTCATATGAGGATCTCAGAGGCTCAGAGACTGCAAGTGTGCTTCCCAAGTCACACACTTA
QY	1901	1960	1901	1.0	GTCGAAGCCAGAGACAGTTTCATCTGATGTGTGACTCTTACGCTCAGTGTCTCTCCACTACC
Db	1441	1500	1441	1.0	GTCGAAGCCAGAGACAGTTTCATCTGATGTGTGACTCTTACGCTCAGTGTCTCTCCACTACC
QY	1961	2020	1961	1.0	CCACACCAAGCCTTGCTGCTCCCAAAAAGTGTCTCCCAAAAAGGAGAGAAATGGATTTTTC
Db	1501	1560	1501	1.0	CCACACCAAGCCTTGCTGCTCCCAAAAAGTGTCTCCCAAAAAGGAGAGAAATGGATTTTTC
QY	2021	2078	2021	1.0	TTTGAGGCGATGACATCTGGAATTAAAGTCAAACTAATCTCAGATCCCTCTTAAAGTA
Db	1561	1620	1561	1.0	TTTTGAGGCGATGACATCTGGAATTAAAGTCAAACTAATCTCAGATCCCTCTTAAAGTA
QY	2079	2138	2079	1.0	AACACTGTTTAAAGAACACGACAGTGTCTCAACAGTGTGGGGCAGCGCTCTTCTAATGAA
Db	1621	1680	1621	1.0	AACACTGTTTAAAGAACACGACAGTGTCTCAACAGTGTGGGGCAGCGCTCTTCTAATGAA
QY	2139	2198	2139	1.0	CAATGATATTGACACTGTCCCTCTTTG3CAGTTGCACTTAGTAACTTTGAAAGATATATGA
Db	1681	1740	1681	1.0	CAATGATATTGACACTGTCCCTCTTTG3CAGTTGCACTTAGTAACTTTGAAAGATATATGA
QY	2199	2258	2199	1.0	CTGAGCGTAGCATACAGTTTAACTCTGCAAAAACATGACTTAGTAACTTTGAGGCGAGGA
Db	1741	1800	1741	1.0	CTGAGCGTAGCATACAGTTTAACTCTGCAAAAACATGACTTAGTAACTTTGAGGCGAGGA
QY	2259	2318	2259	1.0	TTATTAATGAAATTTTGCAAAATCACTTAGACAGCACTGAAACATTAATCAACACGCTGG
Db	1801	1860	1801	1.0	TTATTAATGAAATTTTGCAAAATCACTTAGACAGCACTGAAACATTAATCAACACGCTGG
QY	2319	2378	2319	1.0	AGAAATCAAAACCGAGCAGGCGTGTGTGAAACATGTTGTATATGCACTGCGAAACT
Db	1861	1920	1861	1.0	AGAAATCAAAACCGAGCAGGCGTGTGTGAAACATGTTGTATATGCACTGCGAAACT
QY	2379	2438	2379	1.0	GAACTTCAGCGCACTCCACAAATGATGTTTTCAAGGTGTACAGACTGTGGCACCATGTA
Db	1921	1980	1921	1.0	GAACTTCAGCGCACTCCACAAATGATGTTTTCAAGGTGTACAGACTGTGGCACCATGTA
QY	2439	2498	2439	1.0	TTCAATCCAGAGTTCTTAAAGTTTAAAGTTTGACATGATTTGTATAGCATGCTTTCTTTGA
Db	1981	2040	1981	1.0	TTCAATCCAGAGTTCTTAAAGTTTAAAGTTTGACATGATTTGTATAGCATGCTTTCTTTGA
QY	2499	2558	2499	1.0	GTTTTAATATATGATATAACATTAAGTTCATTTGAATCAAGCATTAATCACTTCAACT
Db	2041	2100	2041	1.0	GTTTTAATATATGATATAACATTAAGTTCATTTGAATCAAGCATTAATCACTTCAACT
QY	2559	2610	2559	1.0	GC 2560
Db	2101	2160	2101	1.0	GC 2102

FT	sig_peptide	/note= "putative signal peptide"
FT	1..63	
FT	*tag= b	
XX	/note= "putative signal peptide"	
XX	MO200018914-A2.	
XX	06-APR-2000.	
PD	17-SEP-1999; 99MO-US21647.	
XX	25-SEP-1998; 98US-0161241.	
PR	(AMGE-) AMGEN INC.	
PA	Bass MB, Sullivan JK, Theill LE, Wang D;	
PI	WPI; 2000-293153/25.	
DR	P-PSDB; AAY92070.	
XX	New nucleic acid molecule encoding a biologically active DKR	
PT	polypeptide, useful in treatment of cancer, e.g. mammary tumors and	
PT	stem cell tumors	
XX	Claim 1; Page 121-122; 143pp; English.	
PS	AAA08838-44 are novel mouse and human genes encoding DKR polypeptides.	
CC	The human DKR-3 open reading frame has homology to human rig-like 7-1	
CC	mRNA and to chicken lens fiber protein cleft4 gene. Human DKR-3	
CC	appears to be secreted, with a signal peptide cleavage site after either	
CC	amino acid 20 or 21.	
CC	DKR-1 is a human ortholog of dkk-1 (dickkopf-1), a novel gene identified	
CC	in Xenopus and mouse, purportedly an antagonist of wnt-8 signaling.	
CC	DKR-2, -3 and -4 are each related to DKR-1 by their cysteine pattern.	
CC	DKR-1 is also involved in morphogenesis in the developing embryo, and	
CC	therefore a growth factor, by inference DKR polypeptides are also	
CC	growth factors. The DKR polypeptides are useful for treating cancer, wnt	
CC	e.g. mammary tumors, stem cell tumors, or other cancers in which the wnt	
CC	and/or sonic hedgehog (Shh) signal transduction pathways are activated.	
CC	They can also be used to enhance tissue differentiation, such as bone	
CC	formation and hematopoietic cell formation.	
XX	Sequence 1053 BP; 234 A; 305 C; 336 G; 178 T; 0 other;	
XX		
Query Match	40.7%; Score 1053; DB 21; Length 1053;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 1053; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
QY	153 ATGCAGAGGCTTGAGGCGCACCTCGCTGTGCGCTGCTGCGCGCGGCTCCCAAGGCC	212
Db	1 ATGCAGAGGCTTGAGGCGCACCTCGCTGTGCGCTGCTGCGCGGCGGCTCCCAAGGCC	60
QY	213 CCGCGCGCGCTCCGAGCGCGACCTTGCGCTCAATGAAAGCCCGGCGCTTCAGCTAC	272
Db	61 CCGCGCGCGCTCCGAGCGCGACCTTGCGCTCAATGAAAGCCCGGCGCTTCAGCTAC	120
QY	273 CCGGAGGAGAGGCGCACCTCGCATGAGATGTCCGCGAGGTTGAGAACTGATGAGAGAC	332
Db	121 CCGGAGGAGAGGCGCACCTCGCATGAGATGTCCGCGAGGTTGAGAACTGATGAGAGAC	180
QY	333 ACGCAGACCAAAATTTGGCGAGCGCGGTGGAAGAGATGAGAGGAGAAAGTGTGCTTAA	392
Db	181 ACGCAGACCAAAATTTGGCGAGCGCGGTGGAAGAGATGAGAGGAGAAAGTGTGCTTAA	240
QY	393 GCAATCAACGAATGGAACCTGGGAAACTTAAGTCCGACATTCACATGAGACCAACACA	452
Db	241 GCAATCAACGAATGGAACCTGGGAAACTTAAGTCCGACATTCACATGAGACCAACACA	300
QY	453 GACACGAAGTTGGAATTAATACATTCATGTCGACCGAGAAATTCACAGATACCAAC	512
Db	301 GACACGAAGTTGGAATTAATACATTCATGTCGACCGAGAAATTCACAGATACCAAC	360
QY	513 AACCAACTGGAACAAATGGTCTTTTCAGAGACAGTTATCAATCTGTGGAGACGAAAGAA	572

[illegible]

QY 885 GCGAGCGGCTTGTGACCTCATCAGCTGGAGAGCTGATGAGCTTGGACGA 944
 DB 121 GCGAGCGGCTTGTGACCTCATCAGCTGGAGAGCTGATGAGCTTGGACGA 180
 QY 945 TGGCCTTGTGACAGTGGAGCTTGTGACAGCTTGTGACAGCTTGTGAC 1004
 DB 181 TGGCCTTGTGACAGTGGAGCTTGTGACAGCTTGTGACAGCTTGTGAC 240
 QY 1005 AAGCCGACCTTGTGAGGAGCTTGTGACAGCTTGTGACAGCTTGTGAC 1064
 DB 241 AAGCCGACCTTGTGAGGAGCTTGTGACAGCTTGTGACAGCTTGTGAC 300
 QY 1065 CCGCATAGTATGAGTGGAGCTTGTGACAGCTTGTGACAGCTTGTGAC 1124
 DB 301 CCGCATAGTATGAGTGGAGCTTGTGACAGCTTGTGACAGCTTGTGAC 360
 QY 1125 G 1125
 DB 361 G 361

RESULT 35
 ID AAS80820 standard; cDNA; 439 BP.
 XX AAS80820;
 AC AAS80820;
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #16624.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX Homo sapiens.
 OS WO200175067-A2.
 PN 11-OCT-2001.
 PD 30-MAR-2001; 2001WO-US08631.
 PF 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI: 2001-639362/73.
 XX P-PSDB; ABG16633.
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 XX
 PS Claim 1; SEQ ID No 16624; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences, (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (II) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS84197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 439 BP; 69 A; 128 C; 124 G; 118 T; 0 other;
 Query Match 11.7%; Score 303; DB 23; Length 439;
 Best Local Similarity 100.0%; Pred. No. 3,7e-108;
 Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 274 GCGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 333
 DB 303 GCGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 244
 QY 334 GCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 393
 DB 243 GCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 184
 QY 394 CATCATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 453
 DB 183 CATCATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 124
 QY 454 ACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 513
 DB 123 ACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 64
 QY 514 ACCAGAGCTGGAGCAATGCTTTTTCAGAGACAGTTATACATCTCTGGAGACGAGAG 573
 DB 63 ACCAGAGCTGGAGCAATGCTTTTTCAGAGACAGTTATACATCTCTGGAGACGAGAGAG 4
 QY 574 GCA 576
 DB 3 GCA 1

RESULT 36
 ID ABEK84291/c
 XX ABEK84291 standard; cDNA; 2569 BP.
 AC ABEK84291;
 DT 14-AUG-2002 (first entry)
 XX
 DE Human cDNA differentially expressed in granulocytic cells #662.
 XX
 KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
 KW viral infection; parasitic infection; protozoal infection;
 KW fungal infection; sterile inflammatory disease; psoriasis;
 KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
 KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
 KW adult respiratory distress syndrome; inflammatory bowel disease;
 KW Crohn's disease; ulcerative colitis; periodontal disease;
 KW granulocyte activation; chronic inflammation; allergy.
 XX
 OS Homo sapiens.
 XX
 PN WO200228999-A2.
 PD 11-APR-2002.
 PF 03-OCT-2001; 2001WO-US30821.
 PR 03-OCT-2000; 2000US-237189P.
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

DR WPI, 2002-435328/46.
 XX Detecting granulocyte activation by detecting differential expression
 PT of genes associated with granulocyte activation, which serves as
 PT diagnostic markers that is useful for monitoring disease states and
 PT drug toxicity
 XX
 XX
 PS Claim 1, SEQ ID No 862, 114pp; English.

The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by CC DNA chip analysis as given in the specification, and comparing CC the expression level to an expression level in an unactivated CC GC, where differential expression of Gs is indicative of GCA. CC Also included are modulating (M2) Gs by contacting GC with an agent CC that alters the expression of at least one gene in Gs; (2) screening (M3) CC for an agent capable of modulating GCA or an inflammation (especially CC chronic) in a tissue, an allergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease using the CC gene expression profile; (3) detecting (M4) an inflammation (especially CC chronic) in a tissue, an allergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease, by detecting the CC level of expression in a sample of the tissue of gene(s) from Gs, where CC the level of expression of the gene is indicative of inflammation; CC (4) treating (M5) an inflammation (especially chronic) or in a tissue, CC an allergic response in a subject, exposure of a subject to a pathogen CC or sterile inflammatory disease, by contacting a tissue having CC inflammation with an agent that modulates the expression of gene(s) CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for CC modulating Gs; M3 is useful for screening an agent capable of modulating CC GCA preferably in an inflammation in a tissue; M4 is useful for CC detecting an inflammation (especially chronic) in a tissue, an allergic CC response in a subject, exposure of a subject to a pathogen or sterile CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis, CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal CC reperfusion injury, ARDS, adult respiratory distress syndrome, CC inflammatory bowel disease, Crohn's disease, ulcerative colitis, CC peritoneal disease, also bacterial infection, viral infection, and CC parasitic infection, protozoal infection, fungal infection, and M5 is CC useful for treating one of the above conditions. The present CC sequence represents a gene differentially expressed in granulocytes. CC Note: The sequence data for this patent did not form part CC of the printed specification, but was obtained in electronic CC format directly from WIPO at CC ftp.wipo.int/pub/published_pct_sequences.

Sequence 2569 BP; 685 A; 601 C; 537 G; 740 T; 6 other;

Query Match 11.4%; Score 294; DB 24; Length 2569;

Best Local Similarity 100.0%; Pred. No. 9.1e-105; Indels 0; Gaps 0;

Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2267 GAAATTTGCAAAATCACTTACGACGAACTGAAGCAATTTATCAACGCTGAGAAAATC 2326
 DB 2568 GAAATTTGCAAAATCACTTACGACGAACTGAAGCAATTTATCAACGCTGAGAAAATC 2509
 QY 2327 AAACCGAGCGGGCTGTGTGAACATGTTGTAATATGCACTGCGAAGCACTGAACCTGA 2386
 DB 2508 AAACCGAGCGGGCTGTGTGAACATGTTGTAATATGCACTGCGAAGCACTGAACCTGA 2449
 QY 2387 CGCCACTCCACAAATGATGTTTCAGGTGTCATGAGCTGTGGCCACCATGATTTATCCA 2446
 DB 2448 CGCCACTCCACAAATGATGTTTCAGGTGTCATGAGCTGTGGCCACCATGATTTATCCA 2389
 QY 2447 GAGTTCTTAAAGTTAAAGTTGACATGATTTGTAATAGCAATGCTTCTTGGAGTTTAA 2505
 DB 2388 GAGTTCTTAAAGTTAAAGTTGACATGATTTGTAATAGCAATGCTTCTTGGAGTTTAA 2329
 QY 2507 TTATGTATTAACATAGTTGATTTAGAAATCAAGCAATAATCACTTCAACTGC 2560
 DB 2328 TTATGTATTAACATAGTTGATTTAGAAATCAAGCAATAATCACTTCAACTGC 2275

RESULT 37

AAV52114
 ID AAV52114 standard; cDNA; 557 BP.

AC AAV52114;

DT 09-NOV-1998 (first entry)

XX Homo sapiens CESP gene related EST clone.

DE CESP; cerebellum and embryo specific protein; restenosis;

KW myocardial infarction; arrhythmia; heart disease;

XX atherosclerosis; expressed sequence tag; ds.

OS Homo sapiens.

XX W09827932-A2.

XX 02-JUL-1998.

XX 18-DEC-1997; 97WO-US23518.

XX 20-DEC-1996; 96US-0033870.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Soppet DR,

XX WPI, 1998-377366/32.

XX New isolated cerebellum and embryo specific polypeptide - used to

PT develop products for treating e.g. coronary restenosis, myocardial

PT infarction, heart disease and artery or venous thrombosis

PS Disclosure, Page 55; 77pp; English.

XX The sequence is that of an EST clone related to the cerebellum and

CC embryo specific protein (CESP) gene.

CC Sequence 557 BP; 112 A; 160 C; 176 G; 106 T; 3 other;

Query Match 11.3%; Score 292; DB 19; Length 557;

Best Local Similarity 99.6%; Pred. No. 6.7e-104;

Matches 462; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 583 GCCACAGTGATCATCATGACAGAGACTGTGGGCCCAAGCATGTCTGCAACGTTGCCAGCT 642
 DB 1 GCCACAGTGATCATCATGACAGAGACTGTGGGCCCAAGCATGTCTGCAACGTTGCCAGCT 60
 QY 643 TCACGTACACCTGCGCAGCATGCGGGGCGAGAGATGCTTGCACCGGGAGAGTGA 702
 DB 61 TCACGTACACCTGCGCAGCATGCGGGGCGAGAGATGCTTGCACCGGGAGAGTGA 120
 QY 703 GCTGTGAGACCAAGCTGTGTCTGTGGGCTCACTGACCAAAATGGCCACAGGGGACGA 762
 DB 121 GCTGTGAGACCAAGCTGTGTCTGTGGGCTCACTGACCAAAATGGCCACAGGGGACGA 180
 QY 763 ATGGACCATCTGTGACAAACAGAGGAGCTGCGAGGCTGTGCTGCTCTCCAGA 822
 DB 181 ATGGACCATCTGTGACAAACAGAGGAGCTGCGAGGCTGTGCTGCTCTCCAGA 240
 QY 823 GAGGCTGTGCTCTGCTGTGTGACACACCTGCGCGGTGAGAGGCGAGCTTTGCCATGAC 882
 DB 241 GAGGCTGTGCTCTGCTGTGTGACACACCTGCGCGGTGAGAGGCGAGCTTTGCCATGAC 299
 QY 883 CGGCGAGCGGCTTGTGACCTCATCACTGAGAGCTAGAGCTGATGAGACTTGGACC 942
 DB 300 CGGCGAGCGGCTTGTGACCTCATCACTGAGAGCTAGAGCTGATGAGACTTGGACC 359
 QY 943 GATGCCCTTTGTCAGAGTGGCTCTTGTGACAGCCCAAGCCCAAGCCCAAGCTGTGTATGTGT 1002
 DB 360 GATGCCCTTTGTCAGAGTGGCTCTTGTGACAGCCCAAGCCCAAGCCCAAGCTGTGTATGTGT 419

QY 1003 GCACCCGACCTTCGTGGGAGCCGTGACCAAGATGGGAGATC 1046
DB 420 GCAAGCCGACCTTCGTGGGAGCCGTGACCAAGATGGGAGATC 463

RESULT 38

ID AAA45500 standard; DNA; 266 BP.

AC AAA45500;

DT 10-SEP-2001 (first entry)

DE Human REIC related DNA sequence SEQ ID 5.

KW REIC; reduced expression in immortalised cells; cancer; tumour;
KM proliferation inhibitor; viral infection; human; ds.

OS Homo sapiens.

PN WO200138528-A1.

PD 31-MAY-2001.

PF 30-AUG-2000; 2000WO-JP05879.

PR 19-NOV-1999; 99JP-0330604.

PA (HISM) HISAMITSU PHARM CO LTD.

PI Namba M, Tsuji T;

PI WPI; 2001-367688/38.

PT Cell proliferation inhibiting protein REIC and polynucleotide encoding
PT it for diagnosis and therapy of cancer and as an antiviral agent -

PS Disclosure; Page 61; 66pp; Japanese.

CC This invention relates to a protein designated REIC (reduced expression
CC in immortalised cells) which inhibits proliferation. REIC shows reduced
CC or suppressed expression in immortalised cells such as cancer cells. The
CC invention includes DNA and protein sequences for REIC. The protein is
CC useful for the treatment and diagnosis of a wide range of benign and
CC malignant tumours and of viral infections (including HIV, influenza,
CC hepatitis and Epstein-Barr virus). The present sequence represents human
CC DNA related to REIC.

SQ Sequence 266 BP; 64 A; 76 C; 60 G; 66 T; 0 other;

Query Match 9.6%; Score 248; DB 22; Length 266;

Best Local Similarity 100.0%; Pred. No. 9.7e-87;

Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1775 CATTTCATATCCAAAGATCAATTCCTCTCTCAGACAGCTGGGAGGGGTCATTGTT 1834

DB 1 CATTTCATATCCAAAGATCAATTCCTCTCTCAGACAGCTGGGAGGGGTCATTGTT 60

QY 1835 CTCCTCGTCATCAGGATCTCAGAGGCTCAGAGCTGCAAGCTGCTGCCCAAGTCACA 1894

DB 61 CTCCTCGTCATCAGGATCTCAGAGGCTCAGAGCTGCAAGCTGCTGCCCAAGTCACA 120

QY 1895 CAGTAGTAGAGACCAAGACAGTTCATCTGTTGACTCTTAAGCTCAGTGTCTCTCC 1954

DB 121 CAGTAGTAGAGACCAAGACAGTTCATCTGTTGACTCTTAAGCTCAGTGTCTCTCC 180

QY 1955 ACTACCCCAACACAGCTTGTGGCCACCAAAAGTCTCCCAAAGGAAGGAATGGGA 2014

DB 181 ACTACCCCAACACAGCTTGTGGCCACCAAAAGTCTCCCAAAGGAAGGAATGGGA 240

QY 2015 TTTTCTT 2022

DB 241 TTTTCTT 248

RESULT 39

ID AAA41559 standard; cDNA; 247 BP.

AC AAA41559;

DT 21-AUG-2000 (first entry)

DE Human secreted expressed sequence tag SEQ ID NO:299.

KW Human; mouse; xenopus; rat; secreted expressed sequence tag; SEST;
KM expressed sequence tag; EST; probe; chemokine; proliferative;
KM immunomodulatory; haematopoietic; chemokine; analgesic; haemostatic;
KM thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;
KM antiviral; antidiabetic; antiasclerotic; vulnary; antiparkinsonian;
KM anticancer; osteoprotective; neuroprotective; nocotropic; antiproliferative;
KM cerebroprotective; anticonvulsant; antidepressant; gene therapy;
KM vaccine; autoimmune disorder; multiple sclerosis; allergic condition;
KM insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
KM lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
KM central nervous system disorder; Alzheimer's disease; stroke;
KM Parkinson's disease; Huntington's disease; coagulation disorder;
KM hemophilia; thrombosis; inflammatory disorder; Crohn's disease;
KM tumour; infection; depression; psoriasis; ss.

OS Homo sapiens.

PN WO200021990-A1.

PD 20-Apr-2000.

PF 15-OCT-1999; 99WO-US24205.

PR 15-OCT-1998; 98US-0104435.

PA (GEMY) GENETICS INST INC.

PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M;

PI WPI; 2000-317937/27.

PT Isolated polynucleotides, and encoded proteins, comprising secreted
PT expressed sequence tags (SESTs), useful for treating various disorders
PT such as autoimmune, infectious, and central nervous system disorders -
PS Claim 1; Page 238; 61pp; English.

CC AAA41261 to AAA43419 represent specifically claimed secreted expressed
CC sequence tags (SESTs), isolated from human, mouse, xenopus and rat
CC tissue sources. The SESTs can have a range of activities depending on
CC the tissues they were isolated from. The activities include:
CC chemokine; proliferative; immunomodulatory; haematopoietic;
CC chemokine; analgesic; haemostatic; thrombolytic; antiinflammatory;
CC cytostatic; antibacterial; antifungal; antiviral; antidiabetic;
CC antiasclerotic; vulnary; anticancer; osteoprotective; neuroprotective;
CC nocotropic; antiparkinsonian; antiproliferative; cerebroprotective;
CC anticonvulsant; antidepressant. The SESTs can be used for gene
CC therapy and in vaccines. The SESTs are useful as probes for the
CC identification and isolation of full-length cDNAs and genomic DNA
CC molecules which correspond to the SESTs. Proteins encoded by the SESTs
CC are useful in assays for determining biological activity and raising
CC antibodies. They may be useful for treatment of autoimmune disorders
CC (multiple sclerosis, insulin dependent diabetes), allergic conditions
CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
CC osteoporosis, osteoarthritis, central nervous system disorders
CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
CC disorders (hemophilia, thrombosis), inflammatory disorders (Crohn's
CC disease), tumours, bacterial, fungal or viral infections, depression and
CC psoriasis. AAA43420 to AAA43425 represent linker variants which are given
CC in the exemplification of the present invention.


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XX Sequence 247 BP; 75 A; 50 C; 58 G; 64 T; 0 other;
Query Match 8.5%; Score 219; DB 21; Length 247;
Best Local Similarity 100.0%; Pred. No. 1,9e-75;
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2038 GGATTTAAGCTCAAACTAATTTCTACACCCCTCTAAAGAAAGTAACTGTGTGAAGAACGC 2097
DB 22 GGATTTAAGCTCAAACTAATTTCTACACCCCTCTAAAGAAAGTAACTGTGTGAAGAACGC 81
QY 2098 AGTGTTCACACAGTGTGGGCGACGCCCTCTCTATGAAGACATGATATTGCACTGTC 2157
DB 82 AGTGTTCACACAGTGTGGGCGACGCCCTCTCTATGAAGACATGATATTGCACTGTC 141
QY 2158 CCTCTTTGGCAGTGGATTAAGTAACTTTGAAAGGTATATGACGAGGTAGCATACAGGT 2217
DB 142 CCTCTTTGGCAGTGGATTAAGTAACTTTGAAAGGTATATGACGAGGTAGCATACAGGT 201
QY 2218 TAACTTGCAAAACAGTACTTATGTAATTTGTAAGCGCGAG 2256
DB 202 TAACTTGCAAAACAGTACTTATGTAATTTGTAAGCGCGAG 240
RESULT 40
AA059652
ID AA059652 standard; cDNA; 447 BP.
XX AA059652;
XX AA059652;
AC AA059652;
XX 25-MAR-2003 (updated)
DT 16-MAR-1994 (first entry)
DE Human brain Expressed Sequence Tag EST01499.
XX Gene transcription product; genetic markers; tagging; in vivo;
KM transcription; mapping; locations; chromosomes; chromosomal; ss.
XX Homo sapiens.
XX MO9316178-A2.
XX 19-AUG-1993.
PD 12-FEB-1993; 93WO-US01294.
XX 12-FEB-1992; 92US-0837195.
PR 12-FEB-1992; 92US-0837195.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICE.
PA Adams MD, Moreno RF, Venter CJ;
XX WPI; 1993-272882/34.
DR WPI; 1993-272882/34.
XX Enriched oligonucleotides and corresp. sequences - used as
PT markers for human genes transcribed in-vivo, facilitate tagging
PT of most human genes
PS Example 4; Page 210; 500bp; English.
XX The Expressed Sequence Tag was isolated from a human brain cDNA
CC library as part of a large set of ESTs which can be used as markers
CC for human genes transcribed in vivo. They can be used to facilitate
CC tagging of most human genes, for individual or forensic identification, for mapping
CC on chromosomes, for individual or forensic identification, for mapping
CC locations of disease-associated genes, for identification of tissue
CC type, and for prepn. of antisense sequences, probes and constructs.
CC EST01499 has a "good" coding probability as evaluated using the
CC coding-region prediction program CRM. See also AA059041-Q61440.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 447 BP; 99 A; 123 C; 105 G; 118 T; 2 other;

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Query Match	8.2%;	Score 213;	DB 143;	Length 447;
Best Local Similarity	100.0%;	Pred. No. 3,7e-73;		
Matches 213;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1800	CTCTCTCAGCAGCAGCTGGGGAGGGGGGTCTATTGTCTCTCGTCATCAGGGATCTCAGA	1859
Dp	1	CTCTCTCAGCAGCAGCTGGGGAGGGGGGTCTATTGTCTCTCGTCATCAGGGATCTCAGA	60
QY	1860	GGCTCAGAGAGCTGACAGTGTCTTCCCAAGTACACAGCTAGTGAAGACACAGACAGTTT	1919
Dp	61	GGCTCAGAGAGCTGACAGTGTCTTCCCAAGTACACAGCTAGTGAAGACACAGACAGTTT	120
QY	1920	CATCTGAGTTTGACTCTTAAGCTAGTGTCTCTCCACTACCCCAACACAGCTTGTATGCC	1979
Dp	121	CATCTGAGTTTGACTCTTAAGCTAGTGTCTCTCTCCACTACCCCAACACAGCTTGTATGCC	180
QY	1980	ACCAAAAGTCTCTCCCAAAAGAGAGGAATGG	2012
Dp	181	ACCAAAAGTCTCTCCCAAAAGAGAGGAATGG	213

XX	RESULT 41
XX	AAV52117
XX	ID AAV52117 standard; cDNA, 356 BP.
XX	AAV52117;
XX	09-NOV-1998 (first entry)
XX	Homo sapiens CESP gene related EST clone.
XX	CESP; cerebellum and embryo specific protein; restenosis;
XX	myocardial infarction; arrhythmia; heart disease;
XX	atherosclerosis; expressed sequence tag; ds.
XX	Homo sapiens.
XX	NO9827932-A2.
XX	02-JUL-1998.
XX	18-DEC-1997; 97WO-US23518.
XX	20-DEC-1996; 96US-0033870.
XX	(HUMA-) HUMAN GENOME SCI INC.
XX	Ruben SM, Soppet DR;
XX	WPI; 1998-377366/32.
XX	New isolated cerebellum and embryo specific polypeptide - used to
XX	develop products for treating e.g. coronary restenosis, myocardial
XX	infarction, heart disease and artery or venous thrombosis
XX	Disclosure; Page 56-57; 77pp; English.
XX	The sequence is that of an EST clone related to the cerebellum and
XX	embryo specific protein (CESP) gene.
XX	Sequence 356 BP; 66 A; 106 C; 113 G; 67 T; 4 other;
XX	Query Match 8.0%; Score 207; DB 19; Length 356;
XX	Best Local Similarity 99.6%; Pred. No. 8.3e-71;
XX	Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0
QY	591 TGCAATCATGACGACGAGCATGTGGGCCCCAGCATGTACTGCCAGTTTGCCAGCTTCCAGTAC 650
DB	1 TGCATCATGACGACGAGCATGTGGGCCCCAGCATGTACTGCCAGTTTGCCAGCTTCCAGTAC 60
QY	651 ACCGCGACGACGATGGCCGGGGCCAGAGATGCTCTGCACCCGGGACAGTGAAGTCTGTGGA 710
DB	61 ACCGCGACGACGATGGGGGGCCAGAGATGCTCTTGCACCCGGGACAGTGAAGTCTGTGGA 120

QY 711 GACCAAGCTGTGTGTGTGGGTCACTGCACCAAAATGCGCAGGGGCAACATGGAC 770
DB 121 GACCAAGCTGTGTGTGTGGGTCACTGCACCAAAATGCGCAGGGGCAACATGGAC 180
QY 777 ATCTGTGACACAGAGGAGGAGTCCAGCCGGGGCTGTGTGTGCTTCCAGAGAGCCCTG 830
DB 181 ATCTGTGACACAGAGGAGGAGTCCAGCCGGGGCTGTGTGTGCTTCCAGAGAGCCCTG 240
QY 831 CTGTTCCCTGTGTGACA 848
DB 241 CTGTTCCCTGTGTGACA 258
RESULT 42
AAVS2120
ID AAVS2120 standard; cDNA; 302 BP.
XX AAVS2120;
XX
XX
DT 09-NOV-1998 (first entry)
DE Homo sapiens CESP gene related EST clone.
XX
XX CESP; cerebellum and embryo specific protein; restenosis;
KM myocardial infarction; arrhythmia; heart disease;
XX atherosclerosis; expressed sequence tag; ds.
OS Homo sapiens.
XX
XX WO9827932-A2.
PN
XX
PD 02-JUL-1998.
XX
PF 18-DEC-1997; 97WO-US23518.
XX
PR 20-DEC-1996; 96US-0033870.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Ruben SM, Soppet DR;
XX
XX WPI; 1998-377366/32.
DR
XX New isolated cerebellum and embryo specific polypeptide - used to
PT develop products for treating e.g. coronary restenosis, myocardial
PT infarction, heart disease and artery or venous thrombosis
XX
PS Disclosure; Page 58; 77pp; English.
XX The sequence is that of an EST clone related to the cerebellum and
CC embryo specific protein (CESP) gene.
CC
XX Sequence 302 BP; 97 A; 77 C; 76 G; 50 T; 2 other;
SQ
Query Match 7.4%; Score 191; DB 19; Length 302;
Best Local Similarity 100.0%; Pred. No. 1.4e-64;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 358 TGGAGAGATGAGAGGAGAAAGCTGTCTTAAGCATCATGAAGTGAACCTTGCAA 417
DB 112 TGGAGAGATGAGAGGAGAAAGCTGTCTTAAGCATCATGAAGTGAACCTTGCAA 171
QY 418 ACTTACTCCAGCTATCATCAATGAGACCAACAGACAGAGAAAGTTGAAATATATACCA 477
DB 172 ACTTACTCCAGCTATCATCAATGAGACCAACAGACAGAGAAAGTTGAAATATATACCA 231
QY 478 TCCATGTGACCGAGAAATTCACAAATACCAACCAACAGACTGACAAATGCTCTTT 537
DB 232 TCCATGTGACCGAGAAATTCACAAATACCAACCAACAGACTGACAAATGCTCTTT 291
QY 538 CAGAGACAGTT 548

DB 292 CAGAGACAGTT 302
RESULT 43
AAO60267
ID AAO60267 standard; DNA; 386 BP.
XX
XX AAO60267;
AC
XX
DT 25-MAR-2003 (updated)
DT 16-MAR-1994 (first entry)
XX
XX Human brain Expressed Sequence Tag EST02264.
DE
XX Gene transcription product; genetic markers; tagging; in vivo;
XX transcription; mapping; locations; chromosomes; chromosomal; ss.
XX
XX Homo sapiens.
OS
XX WO9316178-A2.
PN
XX 19-AUG-1993.
PD
XX 12-FEB-1993; 93WO-US01294.
PF
XX 12-FEB-1992; 92US-0837195.
PR
XX (USSH) US DEPT HEALTH & HUMAN SERVICE.
PA
XX Adams MD, Moreno RF, Venter CJ;
PI
XX WPI; 1993-272862/34.
DR
XX
XX Enriched oligonucleotides and corresp. sequences - used as
PT markers for human genes transcribed in-vivo, facilitate tagging
PT of most human genes
XX
PS Example 4; Page 307-308; 500pp; English.
XX
XX The Expressed Sequence Tag was isolated from a human brain cDNA
CC library as part of a large set of ESTs which can be used as markers
CC for human genes transcribed in vivo. They can be used to facilitate
CC tagging of most human genes, for mapping locations of expressed genes
CC on chromosomes, for individual or forensic identification, for mapping
CC locations of disease-associated genes, for identification of tissue
CC type, and for prepn. of antisense sequences, probes and constructs.
CC EST02264 has a "poor" coding probability as evaluated using the
CC coding-region prediction program CRM. See also AAO59041-061440.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 386 BP; 85 A; 108 C; 95 G; 97 T; 1 other;
Query Match 6.9%; Score 178; DB 14; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.6e-59;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1835 CTCTCTGTCATCGAGGATCTCAGAGGCTCAGAGACTGCAAGCTGTTGCCCAAGTCACA 1894
DB 36 CTCTCTGTCATCGAGGATCTCAGAGGCTCAGAGACTGCAAGCTGTTGCCCAAGTCACA 95
QY 1895 CAGCTAGTGAAGACCAAGCAAGTTTCACTGTGTGACTTAAGCTAGAGCTCTCTCC 1954
DB 96 CAGCTAGTGAAGACCAAGCAAGTTTCACTGTGTGACTTAAGCTAGAGCTCTCTCC 155
QY 1955 ACTACCCACACAGAGCTTGTGTCACCAAAAGTCTCCCAAAAGAGAGAAATGG 2012
DB 156 ACTACCCACACAGAGCTTGTGTCACCAAAAGTCTCCCAAAAGAGAGAAATGG 213
RESULT 44
AAV38808
ID AAV38808 standard; cDNA; 480 BP.
XX

AC	AAV38808;
XX	
DT	09-NOV-1998 (first entry)
DE	Homo sapiens CESP gene related clone HHPDB95R.
XX	
KM	CESP; cerebellum and embryo specific protein; restenosis;
KW	myocardial infarction; arrhythmia; heart disease;
KW	atherosclerosis; de.
XX	
OS	Homo sapiens.
XX	
PN	MO9827932-A2.
PD	02-JUL-1998.
XX	
PF	18-DEC-1997; 97MO-US23518.
PR	20-DEC-1996; 96US-0033870.
PA	(HUMA-) HUMAN GENOME SCI INC.
PI	Ruben SM, Soppet DR;
DR	WPI; 1998-377366/32.
XX	
PT	New isolated cerebellum and embryo specific polypeptide - used to
PT	develop products for treating e.g. coronary restenosis, myocardial
PT	infarction, heart disease and artery or venous thrombosis
PS	Disclosure; Page 53-54; 77pp; English.
XX	
CC	The sequence is that of a cDNA clone related to extensive portions
CC	of the coding region of the cerebellum and embryo specific protein
CC	(CESP) gene. CESP is involved in: (i) the regulation of collateral
CC	circulation (particularly in the heart), coronary artery restenosis
CC	following a revascularisation procedure, apoptosis in myocytes; (ii) the
CC	regulation of myocyte development in the developing heart; (iii) the
CC	regulation of circulating blood volume, vascular tone, blood pressure and
CC	cardiac output, diuresis, natriuresis; (iv) facilitation of transudation
CC	of plasma water to the interstitium; and (v) inhibition of the release
CC	or action of hormones such as aldosterone, angiotensin II, endothelins,
CC	renin and vasopressin. The products can be used in the diagnosis and
CC	treatment of CESP related disorders, e.g. coronary restenosis following
CC	coronary revascularisation, coronary artery thrombus or occlusion,
CC	myocardial infarction, atrial and/or ventricular arrhythmias, heart
CC	block, hereditary medial necrosis of small coronary arteries,
CC	cardiomyopathy, arrhythmogenic right ventricular dysplasia, athero-
CC	sclerotic heart disease, venous thrombosis or Reynaud's syndrome.
SX	
SX	Sequence 480 BP; 124 A; 107 C; 111 G; 111 T; 27 other:
	Query Match 6.5%; Score 169; DB 19; Length 480;
	Best Local Similarity 100.0%; Pred. No. 4.8e-56;
	Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	353 CGCGGTGGAAGAGATGGAGGCAGAAGAGCTCTGCTTAAGCATATCAGAAGTGAACCT 412
Dd	64 CGCGGTGGAAGAGATGGAGGCAGAAGAGCTCTGCTTAAGCATATCAGAAGTGAACCT 123
OY	413 GGCAAACTTACTCCAGCTATCACATATGAGCAAACACAGACAGAAAGTTGGAAATTA 472
Dd	124 GGCAAACTTACTCCAGCTATCACATATGAGCAAACACAGACAGAAAGTTGGAAATTA 183
OY	473 TACCATTCATGTGCACCAGAAATTCCACAAGATAACCAACCAACCGAGACT 521
Dd	184 TACCATTCATGTGCACCAGAAATTCCACAAGATAACCAACCAACCGAGACT 232
	RESULT 45
	AAO60722/c
XX	ID AAO60722 standard; cDNA; 337 BP.

AC	AA060722;
XX	
DT	25-MAR-2003 (updated)
DT	16-MAR-1994 (first entry)
XX	
DE	Human brain Expressed Sequence Tag EST00846.
XX	
KW	Gene transcription product; genetic markers; tagging; in vivo; transcription; mapping; locations; chromosomes; chromosomal; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO9316178-A2.
PD	19-AUG-1993.
XX	
PF	12-FEB-1993; 93WO-US01294.
XX	
PR	12-FEB-1992; 92US-0837195.
XX	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICE.
PI	Adams MD, Moreno RF, Venter CJ;
DR	WPI; 1993-272882/34.
XX	
PT	Enriched oligonucleotides and corresp. sequences - used as markers for human genes transcribed in-vivo, facilitate tagging of most human genes
PS	Example 4; Page 379; 500pp; English.
XX	
CC	The Expressed Sequence Tag was isolated from a human brain cDNA library as part of a large set of ESTs which can be used as markers for human genes transcribed in vivo. They can be used to facilitate tagging of most human genes, for mapping locations of expressed genes on chromosomes, for individual or forensic identification, for mapping locations of disease-associated genes, for identification of tissue type, and for prepn. of antisense sequences, probes and constructs. CC EST00846 has a "poor" coding probability as evaluated using the CC coding-region prediction program CRM. See also AA059041-Q61440. CC (Updated on 25-MAR-2003 to correct PN field.) XX
SQ	Sequence 337 BP; 91 A; 69 C; 78 G; 92 T; 7 other;
Query Match	6 1%; Score 157; DB 14; Length 337;
Best Local Similarity	100.0%; Pread. NO. 2.4e-51;
Matches 157; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1866 GAGACTGCAAGCTGGTTCGCCAAGTCACACAGCTAGTGAGAGACCAGACAGTTTCATCTG 1928
DB	337 GAGACTGCAGAAGTGTGTTCCCAAGTCACACAGCTAGTGAGAGACCAGACAGTTTCATCTG 278
OY	1926 GTTGGAGCTCAAGCTCAGTGTCTCTCCATCACCCCCAGACAGCTTGAGCCACCAA 1985
DB	277 GTTGGAGCTCAAGCTCAGTGTCTCTTCATCACCCCCAGACAGCTTGAGCCACCAA 218
OY	1986 AGTGCTCCCAAAAAGAGAGAGAAATGGATTTCCTT 2022
DB	217 AGTGCTCCCAAAAAGAGAGAGAAATGGATTTCCTT 181
RESULT 46	
AAVS2119	
ID	AAVS2119 standard; CDNA, 298 BP.
XX	
AC	AAVS2119;
XX	
DT	09-NOV-1998 (first entry)
XX	
DE	Homo sapiens CESP gene related EST clone.
XX	
KX	CESP, cerebellum and embryo specific protein; resequencis;

KW myocardial infarction; arrhythmia; heart disease;
 KW atherosclerosis; expressed sequence tag; ds.
 XX Homo sapiens.
 OS WO9827932-A2.
 XX 02-JUL-1998.
 PD 18-DEC-1997; 97WO-US23518.
 PF 20-DEC-1996; 96US-0033870.
 PR (HUMA-) HUMAN GENOME SCI INC.
 XX Ruben SM, Soppet DR;
 PI WPI; 1998-377366/32.
 DR New isolated cerebellum and embryo specific polypeptide - used to
 PT develop products for treating e.g. coronary restenosis, myocardial
 PT infarction, heart disease and artery or venous thrombosis
 PS Disclosure; Page 57; 77pp; English.
 XX The sequence is that of an EST clone related to the cerebellum and
 CC embryo specific protein (CESP) gene.
 XX Sequence 298 BP; 55 A; 68 C; 98 G; 75 T; 2 other;
 SQ

Query Match 6.0%; Score 155; DB 19; Length 298;
 Best Local Similarity 99.5%; Pred. No. 1.4e-50;
 Matches 205; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1180 CACTGCTGGGAGGAGAGATTAGATCTGACACGAGCTGTGATGATGCAATAGA 1239
 DB 93 CACTGCTGGGAGGAGAGATTAGATCTGACACGAGCTGTGATGATGCAATAGA 152
 OY 1240 AATAGCTAATTTATTTCCCGAGGTGTGCTTTAGGCGTGGCTGACAGGCTTTCTTCT 1299
 DB 153 AATAGCTAATTTATTTCCCGAGGTGTGCTTTAGGCGTGGCTGACAGGCTTTCTTCT 212
 OY 1300 ACATCTTCTTCCCGAGTGTGCTTCCCTCTGAGCATGAGCATGAGTGTGATTTGT 1359
 DB 213 ACATCTTCTTCCCGAGTGTGCTTCCCTCTGAGCATGAGCATGAGTGTGATTTGT 272
 OY 1360 TCAGCTCCCCCAGGCTGTCTCCAGG 1385
 DB 273 TCAGCTCCCCCAGGCTGTCTCCAGG 298

RESULT 47
 AAV52127
 ID AAV52127 standard; cDNA; 344 BP.
 XX AAV52127;
 AC AAV52127;
 XX 09-NOV-1998 (first entry)
 DT Homo sapiens CESP gene related EST clone.
 DE Homo sapiens CESP gene related EST clone.
 KW CESP; cerebellum and embryo specific protein; restenosis;
 KW myocardial infarction; arrhythmia; heart disease;
 KW atherosclerosis; expressed sequence tag; ds.
 OS Homo sapiens.
 XX WO9827932-A2.
 XX 02-JUL-1998.
 PD 18-DEC-1997; 97WO-US23518.
 PF 18-DEC-1997; 97WO-US23518.

PR 20-DEC-1996; 96US-0033870.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Ruben SM, Soppet DR;
 PI WPI; 1998-377366/32.
 DR New isolated cerebellum and embryo specific polypeptide - used to
 PT develop products for treating e.g. coronary restenosis, myocardial
 PT infarction, heart disease and artery or venous thrombosis
 PS Disclosure; Page 60-61; 77pp; English.
 XX The sequence is that of an EST clone related to the cerebellum and
 CC embryo specific protein (CESP) gene.
 XX Sequence 344 BP; 60 A; 106 C; 108 G; 68 T; 2 other;
 SQ

Query Match 5.9%; Score 153; DB 19; Length 344;
 Best Local Similarity 100.0%; Pred. No. 8.4e-50;
 Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 713 CCAGCTGTGTCTCTGCGGTCACTGACCAAAATGGCCACGAGGGCAGCAATGGGACCAT 772
 DB 1 CCAGCTGTGTCTCTGCGGTCACTGACCAAAATGGCCACGAGGGCAGCAATGGGACCAT 60
 OY 773 CTGTGACAACAGAGAGGACTGCGCAGCGGCGTGTGCTGTGCTTCCAGAGAGGCTGCT 832
 DB 61 CTGTGACAACAGAGAGGACTGCGCAGCGGCGTGTGCTGTGCTTCCAGAGAGGCTGCT 120
 OY 833 GTTCCCTGTGTGCAACCCCTGCGCGTGTGAGGG 865
 DB 121 GTTCCCTGTGTGCAACCCCTGCGCGTGTGAGGG 153

RESULT 48
 AAV52126
 ID AAV52126 standard; cDNA; 236 BP.
 XX AAV52126;
 AC AAV52126;
 XX 09-NOV-1998 (first entry)
 DT Homo sapiens CESP gene related EST clone.
 DE Homo sapiens CESP gene related EST clone.
 KW CESP; cerebellum and embryo specific protein; restenosis;
 KW myocardial infarction; arrhythmia; heart disease;
 KW atherosclerosis; expressed sequence tag; ds.
 OS Homo sapiens.
 XX WO9827932-A2.
 XX 02-JUL-1998.
 PD 18-DEC-1997; 97WO-US23518.
 PF 20-DEC-1996; 96US-0033870.
 PR (HUMA-) HUMAN GENOME SCI INC.
 XX Ruben SM, Soppet DR;
 PI WPI; 1998-377366/32.
 DR New isolated cerebellum and embryo specific polypeptide - used to
 PT develop products for treating e.g. coronary restenosis, myocardial
 PT infarction, heart disease and artery or venous thrombosis
 PS Disclosure; Page 60; 77pp; English.
 XX The sequence is that of an EST clone related to the cerebellum and

CC embryo specific protein (CESP) gene.
XX
SQ Sequence 236 BP, 68 A; 60 C; 62 G; 44 T; 2 other;
Query Match 5.8%; Score 151; DB 19; Length 236;
Best Local Similarity 99.5%; Pred. No. 5.3e-49;
Matches 201; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 463 TTGGAATATATACATCATGTGACCGAGAAATTCACAGATTAACCAACAGACAGCTG 522
DB 1 TTGGAATATATACATCATGTGACCGAGAAATTCACAGATTAACCAACAGACAGCTG 60
QY 523 GACAAATGCTCTTTTCAGAGACAGTATCATCTGTGAGACGAGAGAGGACAGAGGA 582
DB 61 GACAAATGCTCTTTTCAGAGACAGTATCATCTGTGAGAGAGAGAGAGAGAGAGN 120
QY 583 GCCACGAGTGCATCATGACGAGAGACTGTGGGCCGACATGTACTGSCCAGTTGCCAGCT 642
DB 121 GCCACGAGTGCATCATGACGAGAGACTGTGGGCCGACATGTACTGSCCAGTTGCCAGCT 180
QY 643 TCCAGTACACCTGCGCAGCCATG 664
DB 181 TCCAGTACACCTGCGCAGCCATG 202
RESULT 49
AAV3807
ID AAV38807 standard; cDNA; 384 BP.
XX
XX AAV38807;
XX
DT 09-NOV-1998 (first entry)
XX
DE Homo sapiens CESP gene related clone HFB155Ra.
XX
XX CESP; cerebellum and embryo specific protein; restenosis;
KM myocardial infarction; arrhythmia; heart disease;
KM atherosclerosis; ds.
XX
OS Homo sapiens.
XX
XX WO9827932-A2.
PN
XX
XX 02-JUL-1998.
PD
XX
XX 18-DEC-1997; 97MO-US23518.
PF
XX
XX 20-DEC-1996; 96US-0033870.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Ruben SM, Soppet DR;
PI
XX
XX WPI; 1998-377366/32.
DR
XX
XX
PT New isolated cerebellum and embryo specific polypeptide - used to
PT develop products for treating e.g. coronary restenosis, myocardial
PT infarction, heart disease and artery or venous thrombosis
XX
XX
PS Disclosure; Page 53; 77pp; English.
XX
XX The sequence is that of a cDNA clone related to extensive portions
CC of the coding region of the cerebellum and embryo specific protein
CC (CESP) gene. CESP is involved in: (i) the regulation of collateral
CC circulation (particularly in the heart), coronary artery restenosis
CC following a revascularisation procedure, apoptosis in myocytes; (ii) the
CC modulation of myocyte development in the developing heart; (iii) the
CC regulation of circulating blood volume, vascular tone, blood pressure and
CC cardiac output, diuresis, natriuresis; (iv) facilitation of transudation
CC of plasma water to the interstitium; and (iv) inhibition of the release
CC or action of hormones such as aldosterone, angiotensin II, endothelins,
CC renin and vasopressin. The products can be used in the diagnosis and
CC treatment of CESP related disorders, e.g. coronary restenosis following

CC coronary revascularisation, coronary artery thrombus or occlusion,
CC myocardial infarction, atrial and/or ventricular arrhythmias, heart
CC block, hereditary medial necrosis of small coronary arteries,
CC cardiomyopathy, arrhythmogenic right ventricular dysplasia, athero-
CC sclerotic heart disease, venous thrombosis or Reynaud's syndrome.
SQ Sequence 384 BP; 73 A; 87 C; 106 G; 106 T; 12 other;
Query Match 5.7%; Score 148; DB 19; Length 384;
Best Local Similarity 100.0%; Pred. No. 7.3e-48;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1178 TGCACTGCTGGAGGAGAGAGATTAGATCTGACACGAGCTGGTAAATGTGCAATA 1237
DB 59 TGCACTGCTGGAGGAGAGAGATTAGATCTGACACGAGCTGGTAAATGTGCAATA 118
QY 1238 GAATAGCTAATTAATTTCCCGAGGTGTGCTTTAGACGAGGCTGACAGGCTTCTTC 1297
DB 119 GAATAGCTAATTAATTTCCCGAGGTGTGCTTTAGACGAGGCTGACAGGCTTCTTC 178
QY 1298 CTACATCTTCTTCCAGTAAGTTTCCCC 1325
DB 179 CTACATCTTCTTCCAGTAAGTTTCCCC 206
RESULT 50
AAV56832
ID AAV56832 standard; cDNA; 432 BP.
XX
XX AAV56832;
XX
XX
AC AAV56832;
XX
XX
DT 14-JUL-1999 (first entry)
XX
XX Human phdkk-3 cDNA.
DE
XX
XX Signal pathway; wnt; inhibitor; secreted glycoprotein; receptor;
KM therapy; diagnosis; treatment; cancer; breast; carcinoma; melanoma;
KM colon; cell proliferation; differentiation; ss.
XX
XX
OS Homo sapiens.
XX
XX WO9922000-A1.
PN
XX
XX 06-MAY-1999.
PD
XX
XX 27-OCT-1998; 98MO-DE03155.
PF
XX
XX 27-OCT-1997; 97DE-1047418.
PR
XX
XX (DEMR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA
XX
XX Glinka A, Niehrs C;
PI
XX
XX WPI; 1999-303017/25.
DR
XX
XX
PT Protein that inhibits wnt signalling
PT
PS Claim 4a; Fig 2; 39pp; German.
XX
XX
XX This invention describes an inhibitory protein of the wnt signalling
CC pathway (which comprises secreted glycoproteins and their associated
CC receptors). The products of the invention are useful as therapeutic
CC and diagnostic agents, e.g. to treat cancer (e.g. carcinoma of breast
CC and colon, or melanoma) and for studying processes associated with wnt
CC signalling (cell proliferation and differentiation). Primers derived
CC from the nucleic acid of the invention are used to detect the expression
CC of the gene. AAV56827-X26833 are sequences used in the method of the
CC invention.
SQ
XX
XX Sequence 432 BP, 102 A; 131 C; 135 G; 64 T; 0 other;
SQ
Query Match 5.6%; Score 144; DB 20; Length 432;
Best Local Similarity 100.0%; Pred. No. 2.6e-46;

C	78	571	737	13	EQ185014	151	463	17.9	1211	13	BU169105
	79	568	967	13	BQ123550	C	462	17.9	467		AA779346
	80	553	563	9	AU279954	C	152	17.8	462	9	AA704905
	81	562	903	13	BU147482	C	154	17.7	459	9	AM022551
	82	561	21.7	854	13	BQ988374	C	155	456	14	CB306212
	83	558	21.6	851	13	BQ77657	C	156	456	17.6	526
	84	555	21.5	947	13	BQ685825	C	157	455	17.6	689
	85	555	21.5	971	13	BQ150570	C	158	452	17.5	455
	86	551	21.3	972	13	BQ50627	C	159	451	17.4	580
	87	550	21.3	934	13	BQ686834	C	160	451	17.4	534
	88	545	21.1	853	13	BQ30977	C	161	451	17.4	534
	89	544	21.0	685	13	BQ701274	C	162	451	17.4	788
	90	544	21.0	902	13	BQ18697	C	163	447	17.3	915
	91	541	20.9	930	13	BQ685322	C	164	446	17.2	724
	92	540	20.9	607	13	BQ388481	C	165	446	17.2	457
	93	540	20.9	607	13	BQ683488	C	166	445	17.2	456
	94	540	20.9	814	10	BQ674624	C	167	441	17.1	1201
	95	539	20.8	862	13	BQ691532	C	168	440	17.0	551
	96	538	20.8	596	13	BU948296	C	169	439	17.0	443
	97	537	20.8	893	12	BU50000	C	170	439	17.0	443
	98	537	20.8	962	13	BU49818	C	171	438	16.9	456
	99	534	20.6	541	12	BQ685122	C	172	434	16.8	593
	100	534	20.6	856	13	BQ687064	C	173	433	16.7	533
	101	533	20.6	542	13	BQ091031	C	174	432	16.7	733
	102	533	20.6	822	12	BQ155372	C	175	431	16.7	932
	103	532	20.6	941	13	BQ19517	C	176	426	16.5	727
	104	531	20.5	963	13	BU80392	C	177	423	16.4	638
	105	531	20.5	1026	13	BU174087	C	178	423	16.4	710
	106	530	20.5	943	13	BQ685523	C	179	422	16.3	558
	107	528	20.4	544	9	AM022685	C	180	421	16.3	420
	108	528	20.4	933	13	BU157967	C	181	418	16.2	420
	109	518	20.0	1002	13	BQ78024	C	182	416	16.1	439
	110	516	20.0	562	13	BQ79647	C	183	416	16.1	768
	111	515	19.9	928	10	BQ326091	C	184	415	16.0	964
	112	514	19.9	541	12	BQ008298	C	185	413	16.0	465
	113	512	19.8	522	12	BQ511891	C	186	413	16.0	585
	114	512	19.8	573	13	BU948026	C	187	410	15.9	461
	115	510	19.7	1110	13	BU196372	C	188	407	15.7	443
	116	508	19.6	508	14	CA95058	C	189	404	15.6	416
	117	507	19.6	1046	13	BQ670374	C	190	403	15.6	1007
	118	505	19.5	1118	13	BU190780	C	191	400	15.5	400
	119	504	19.5	520	13	BQ639623	C	192	399	15.5	409
	120	504	19.5	675	13	BQ396230	C	193	399	15.4	407
	121	502	19.4	1154	13	BU174766	C	194	399	15.4	595
	122	501	19.4	922	13	BQ689655	C	195	397	15.4	542
	123	495	19.1	546	12	BQ531088	C	196	396	15.3	959
	124	494	19.1	494	10	BQ724383	C	197	395	15.3	401
	125	492	19.0	923	13	BQ692841	C	198	394	15.2	396
	126	491	19.0	666	10	BQ679946	C	199	394	15.2	398
	127	490	18.9	958	13	BU185705	C	200	392	15.2	506
	128	489	18.9	776	12	BQ599926	C	201	392	15.2	901
	129	488	18.9	555	13	BQ327344	C	202	390	15.1	391
	130	488	18.9	728	9	AL046185	C	203	387	15.0	1018
	131	486	18.8	551	9	AL046185	C	204	385	14.9	925
	132	484	18.7	601	12	BQ689547	C	205	383	14.8	390
	133	484	18.7	617	13	BU683972	C	206	383	14.8	409
	134	484	18.7	635	9	AL134570	C	207	383	14.8	411
	135	482	18.6	587	14	CB045353	C	208	382	14.8	435
	136	480	18.6	499	14	CB045352	C	209	382	14.8	524
	137	480	18.6	543	14	CA438305	C	210	380	14.7	403
	138	479	18.5	516	13	BU145154	C	211	380	14.7	565
	139	478	18.5	654	14	CB156678	C	212	378	14.6	678
	140	477	18.4	495	9	AM301027	C	213	376	14.5	883
	141	477	18.4	889	10	BQ680337	C	214	373	14.4	723
	142	476	18.4	478	9	AL194005	C	215	372	14.4	429
	143	474	18.3	613	14	CB121677	C	216	371	14.3	371
	144	472	18.3	965	13	BU180395	C	217	371	14.3	435
	145	471	18.2	671	12	BQ1835184	C	218	370	14.3	440
	146	469	18.1	966	9	AL534481	C	219	369	14.2	596
	147	465	18.0	465	9	BF057318	C	220	367	14.2	670
	148	463	17.9	601	12	BQ145074	C	221	362	14.0	508
	149	463	17.9	947	13	BU149991	C	222	361	14.0	410
	150	463	17.9	992	13	BU163532	C	223	361	14.0	547

C 370	155	6.0	308	9	A1929307	aus9909.x	443	67	2.6	517	12	BM006523	BM006523 603615481
C 371	153	5.9	344	14	R14945	Y994G06.r1	444	65	2.5	156	14	Z19902	Z19902 HSA4A4ZT P
C 372	153	5.9	412	14	T33827	BEST58418.Hu	445	65	2.5	1113	12	BM007075	BM007075 603615481
C 373	151	5.8	203	14	Z38477	HSC0C082 n	446	63	2.4	800	14	CB311336	CB311336 AGENCOURT
C 374	151	5.8	236	14	T08793	BEST06685 in	447	59	2.3	190	14	Z20312	Z20312 HSA4BWX5 P
C 375	150	5.8	403	14	AA98511	am75e01.s	448	54	2.1	529	14	BQ426205	BQ426205 UMN3BA11-
C 376	148	5.7	267	10	BF954624	RC6-NN116	449	54	2.0	151	14	R57834	R57834 FS953 Fetal
C 377	147	5.7	359	9	A1249686	qx50G12.x	450	53	1.9	233	14	T03598	T03598 IBS68 Infant
C 378	147	5.7	253	12	BM684732	UI-E-EJ1-	451	48	1.9	123	12	BM482687	BM482687 PM2-CT080
C 379	147	5.7	325	9	AM190135	x159G04.x	452	47	1.8	86	9	AA911546	AA911546 oe77n12.s
C 380	147	5.7	473	14	N26110	yx90G01.s1	453	46	1.8	331	14	L48824	L48824 HUM060625P
C 381	146	5.6	146	9	AA844276	a194e04.s	454	45	1.7	150	10	BF076133	BF076133 225627 MA
C 382	141	5.5	750	12	BM007284	603615062	455	45	1.7	121	12	BM482966	BM482966 536073 MA
C 383	140	5.4	359	9	AA226979	z118G10.r	456	45	1.7	161	12	BM482970	BM482970 536073 MA
C 384	139	5.4	309	14	T32418	BST48217.Hu	457	45	1.7	144	12	BM482687	BM482687 535672 MA
C 385	139	5.4	426	9	AM078717	xb32h05.x	458	45	1.7	350	9	AU231600	AU231600 AU231600
C 386	136	5.3	238	14	T31076	BST27168.Hu	459	45	1.7	560	13	BO091916	BO091916 UMN17C01
C 387	131	5.1	314	14	Z20942	HSAADDERK P	460	45	1.7	576	13	BO091454	BO091454 UMN 17C02
C 388	129	5.0	361	14	T30528	HSAADDERK P	461	44	1.7	582	14	CB586647	CB586647 UMN3BA11-
C 389	127	4.9	491	10	BE812829	RCO-AN006	462	43	1.7	383	12	BM006880	BM006880 603615361
C 390	124	4.8	187	9	AM794562	RC6-UM001	463	42	1.6	640	12	BM006880	BM006880 603615361
C 391	124	4.8	300	14	N86855	LI235F.Huma	464	41	1.6	477	12	BG988742	BG988742 MR2-HT116
C 392	123	4.8	396	14	T33817	BST59369.Hu	465	39	1.5	379	9	AL631296	AL631296 AL631296
C 393	122	4.7	424	14	H18461	YM433F04.s1	466	38	1.5	245	14	C14023	C14023 C14023 Clon
C 394	120	4.6	349	12	BI497458	dfl36h02.	467	35	1.4	268	14	BO960784	BO960784 AGENCOURT
C 395	119	4.6	124	14	Z19631	HSAAADXT J	468	35	1.4	295	9	AA807015	AA807015 oc29h09.s
C 396	118	4.6	148	9	A1351552	qf06F08.x	469	35	1.4	255	9	AA807015	AA807015 oc29h09.s
C 397	117	4.5	1058	13	BU941114	AGENCOURT	470	35	1.4	576	9	A1673820	A1673820 lc03902.x
C 398	116	4.5	218	9	AA031480	2k16B05.s	471	35	1.4	1010	14	CD117119	CD117119 AGENCOURT
C 399	116	4.5	221	9	AA322156	EST24750	472	35	1.4	1056	10	BF678927	BF678927 602153554
C 400	115	4.4	160	12	BI496658	dfl27a09.	473	34	1.4	1239	12	BM560285	BM560285 AGENCOURT
C 401	114	4.4	255	12	BM665688	UI-E-CL1-	474	34	1.3	222	10	BI775230	BI775230 467635 MA
C 402	113	4.4	334	12	BC945256	PMO-AN008	475	34	1.3	232	10	BE752573	BE752573 204995 MA
C 403	112	4.3	351	10	BE812783	RCO-AN006	476	34	1.3	337	10	BF601715	BF601715 266750 MA
C 404	111	4.3	255	10	CO5172	Huma	477	34	1.3	439	9	AV734888	AV734888 AV734888
C 405	111	4.3	210	14	CO5296	CO5296.Huma	478	34	1.3	611	14	CB448740	CB448740 702900 MA
C 406	110	4.3	225	14	F09872	HSC37E102 n	479	34	1.3	1370	12	BM924462	BM924462 AGENCOURT
C 407	110	4.3	118	9	A1146938	cy24c09.s	480	34	1.3	148	9	A1251982	A1251982 qv57d12.x
C 408	110	4.3	174	14	T18925	G12048t.Tes	481	33	1.3	171	9	A1733956	A1733956 qv57d12.x
C 409	110	4.3	263	14	T30923	BST4807.Hu	482	33	1.3	177	9	A1732863	A1732863 qv57d12.x
C 410	109	4.2	216	14	Z19623	HSAADDERK P	483	33	1.3	184	9	A1345889	A1345889 LB66d05.y
C 411	107	4.1	279	14	Z42237	HSC0C081 n	484	33	1.3	184	9	A1345909	A1345909 LB66d05.x
C 412	107	4.1	664	12	BQ021491	UI-H-DH1-	485	33	1.3	219	9	A1141711	A1141711 oc08H02.x
C 413	105	4.1	247	9	AA424460	zv82h04.r	486	33	1.3	230	12	BI976333	BI976333 485174 MA
C 414	103	4.0	175	14	T65270	yc79c10.r1	487	33	1.3	243	9	A1345202	A1345202 lb67501.x
C 415	101	3.9	166	10	BC923349	naef79h03.	488	33	1.3	294	12	BM541506	BM541506 AGENCOURT
C 416	99	3.8	163	13	BQ772965	CV1-FM016	489	33	1.3	320	9	AA479635	AA479635 26635 MAR
C 417	99	3.8	647	12	BM006260	603614924	490	33	1.3	324	11	BC018964	BC018964 HOMO_SAPI
C 418	95	3.7	605	13	BO807940	NISC_KK12	491	33	1.3	336	9	AA222318	AA222318 mm19H09.r
C 419	94	3.6	335	14	W45085	zc20c09.r1	492	33	1.3	351	9	AA768369	AA768369 oc17c05.s
C 420	94	3.6	330	9	AA360054	EST69206	493	33	1.3	384	9	A1097316	A1097316 qd35b03.x
C 421	93	3.6	451	10	BE812783	RCO-AN006	494	33	1.3	397	14	CA910323	CA910323 PCS05676F
C 422	93	3.6	491	10	BE812829	RCO-AN006	495	33	1.3	478	14	CB344206	CB344206 CA48EN000
C 423	92	3.6	404	12	BI034315	BM-NN022	496	33	1.3	478	9	A1378748	A1378748 lc38f05.x
C 424	91	3.5	742	10	BE807724	601497757	497	33	1.3	486	14	CB344266	CB344266 CA48EN000
C 425	90	3.5	91	12	BG829903	602764307	498	33	1.3	486	14	CB344266	CB344266 CA48EN000
C 426	90	3.5	183	10	BF944464	RC6-NN116	499	33	1.3	505	14	CB344044	CB344044 CA48EN000
C 427	90	3.5	189	14	T65229	yc79c10.r1	500	33	1.3	587	14	CA666143	CA666143 wtk1-PK00
C 428	89	3.4	328	14	CB927787	12822015	501	33	1.3	587	14	CA666143	CA666143 wtk1-PK00
C 429	89	3.4	397	14	RS3311	yg79d06.r1-	502	33	1.3	587	14	CA666143	CA666143 wtk1-PK00
C 430	87	3.4	398	14	CO1001	HUM0000386	503	33	1.3	587	14	CA666143	CA666143 wtk1-PK00
C 431	84	3.2	179	14	Z19659	HSAADDERK P	504	33	1.3	587	14	CA666143	CA666143 wtk1-PK00
C 432	84	3.2	303	14	RS8671	G4596.Fetal	505	33	1.3	587	14	CA666143	CA666143 wtk1-PK00
C 433	82	3.2	181	9	AA376024	EST88391	506	33	1.3	587	14	CA666143	CA666143 wtk1-PK00
C 434	81	3.1	458	9	A1394169	cg6h03.x	507	33	1.3	587	14	CA666143	CA666143 wtk1-PK00
C 435	81	3.1	708	14	CB311290	AGENCOURT	508	33	1.3	587	14	CA666143	CA666143 wtk1-PK00
C 436	81	3.1	796	14	CB308228	AGENCOURT	509	33	1.3	587	14	CA666143	CA666143 wtk1-PK00
C 437	79	3.1	185	10	BE718313	BM-NN106	510	33	1.3	587	14	CA666143	CA666143 wtk1-PK00
C 438	79	3.1	185	10	BE718313	BM-NN106	511	33	1.3	587	14	CA666143	CA666143 wtk1-PK00
C 439	76	2.9	139	10	BG058190	nat21h06.	512	33	1.3	587	14	CA666143	CA666143 wtk1-PK00
C 440	71	2.7	439	9	A1929384	PMO-AN008	513	33	1.3	587	14	CA666143	CA666143 wtk1-PK00
C 441	70	2.7	438	9	BG945204	FM0-AN008	514	33	1.3	587	14	CA666143	CA666143 wtk1-PK00
C 442	69	2.7	1455	12	BM006928	603615632	515	33	1.3	587	14	CA666143	CA666143 wtk1-PK00

ALIGNMENTS

RESULT 1
LOCUS BQ690088
DEFINITION AGENCOURT 8034033 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6208328
5', mRNA sequence.
ACCESSION BQ690088
VERSION BQ690088.1 GI:21815404
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 936)
 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LNCM2365 row: n column: 09
 High quality sequence stop: 686.
 Location/Qualifiers

FEATURES
 source
 1..936
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6208256"
 /issue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

BASE COUNT 186 a 234 c 275 g 240 t 1 others
 ORIGIN

Query Match 30.4%; Score 786; DB 13; Length 936;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 886; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

849 CCCCTGCCCGGAGAGGAGAGCTTGGCATGACCCCGACCGGCTTCTGACCTTCATC 908
 1 CCCCTGCCCGGAGAGGAGAGCTTGGCATGACCCCGACCGGCTTCTGACCTTCATC 60
 909 ACCTGGAGAGCTGATGAGAGCTTGGAGAGCTTGGAGAGCTTGGAGAGCTTGGAG 968
 61 ACCTGGAGAGCTGATGAGAGCTTGGAGAGCTTGGAGAGCTTGGAGAGCTTGGAG 120
 969 TGGCAG 1028
 121 TGGCAG 180
 1029 GACCAAGATGGAG 1088
 181 GACCAAGATGGAG 240
 1089 TTCTAG 1148
 241 TTCTAG 300
 1149 GCGCTGGAG 1208
 301 GCGCTGGAG 360
 1209 TGGACAG 1268
 361 TGGACAG 420
 1269 CTTTAG 1328
 421 CTTTAG 480

QY 1329 GGCTTGACAGATGAG 1388
 DB 481 GGCTTGACAGATGAG 540
 QY 1389 CACAGCTGAG 1448
 DB 541 CACAGCTGAG 600
 QY 1449 TGTCCAGATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1508
 DB 601 TGTCCAGATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 QY 1509 GCTTGAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1568
 DB 661 GCTTGAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 QY 1569 TTTGGGAG 1628
 DB 721 TTTGGGAG 780
 QY 1629 CAATGAATTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1688
 DB 781 CAATGAATTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 QY 1689 GAGATGAATTTTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1736
 DB 841 GAGATGAATTTTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 888

RESULT 2
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 AGENCOURT 8034028 NIH_MGC_110 Homo sapiens CDNA clone IMAGE:6208256
 5', mRNA sequence.
 B0690888
 B0690888.1 GI:21816204
 EST.
 Homo sapiens (human)
 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LNCM2365 row: k column: 09
 High quality sequence stop: 698.
 Location/Qualifiers

FEATURES
 source

1..951
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6208256"
 /issue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

BASE COUNT 191 a 239 c 276 g 244 t 1 others

ORIGIN

Query Match 30.1%; Score 778; DB 13; Length 951;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 878; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

849 CCCCTGCCCTGGAGGCGAGCTTTGCCATGACCCCGCAGCCGCTTGGACCTATC 908
 1 CCCCTGCCCTGGAGGCGAGCTTTGGCATGACCCCGCAGCCGCTTGGACCTATC 60

909 ACCTGGAGAGTAAAGCTGTATGAGCCTTGGACCTATGCTTGTCTCCAGTGGCTCTC 968
 61 ACCTGGAGAGTAAAGCTGTATGAGCCTTGGACCTATGCTTGTCTCCAGTGGCTCTC 120

969 TGGCAGCCCAACAGCCACAGCTGTATGAGCCTTGGACCTATGCTTGTCTCCAGTGGCTCTC 1028
 121 TGGCAGCCCAACAGCCACAGCTGTATGAGCCTTGGACCTATGCTTGTCTCCAGTGGCTCTC 180

1029 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGCTCCCGATGATGAAAGTTGGACCT 1088
 181 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGCTCCCGATGATGAAAGTTGGACCT 240

1089 TTCAATGAGAGAGGAGGAGAGCTGTATGAGCCTTGGACCTATGCTTGTCTCCAGTGGCTCTC 1148
 241 TTCAATGAGAGAGGAGGAGAGCTGTATGAGCCTTGGACCTATGCTTGTCTCCAGTGGCTCTC 300

1149 GCGCTGGGAGAGCTTGGCTGCCCGCGCTGCACTGCTGGAGAGGAGAGATTTAGATC 1208
 301 GCGCTGGGAGAGCTTGGCTGCCCGCGCTGCACTGCTGGAGAGGAGAGATTTAGATC 360

1209 TGAACCGAGCTGTGGGAGAGTGGCAATAGAAATAGCTATTTATTTCCCGAGTGGTGC 1268
 361 TGAACCGAGCTGTGGGAGAGTGGCAATAGAAATAGCTATTTATTTCCCGAGTGGTGC 420

1269 CTTTGGAGCTGTGGGAGAGCTTCTCTTCCAGTAACTTTCCCGAGTGGTGC 1328
 421 CTTTGGAGCTGTGGGAGAGCTTCTCTTCCAGTAACTTTCCCGAGTGGTGC 480

1329 GCGCTGGAGAGCTTGGCTGCCCGCGCTGCACTGCTGGAGAGGAGAGATTTAGATC 1388
 481 GCGCTGGAGAGCTTGGCTGCCCGCGCTGCACTGCTGGAGAGGAGAGATTTAGATC 540

1389 CACAGTGTGTGTGGGAGAGTGGCAATAGAAATAGCTATTTATTTCCCGAGTGGTGC 1448
 541 CACAGTGTGTGTGGGAGAGTGGCAATAGAAATAGCTATTTATTTCCCGAGTGGTGC 600

1449 TGTCCAGATTAATGGCTGTCTTGTCTTACCAAGTGGCAAGAGCTTGTCTTACATG 1508
 601 TGTCCAGATTAATGGCTGTCTTGTCTTACCAAGTGGCAAGAGCTTGTCTTACATG 660

1509 GCTTGAATTAATGGTGTGGGAGAGAGATGAAACAAATGAGAGTCTCCCTGTGATGGT 1568
 661 GCTTGAATTAATGGTGTGGGAGAGAGATGAAACAAATGAGAGTCTCCCTGTGATGGT 720

1569 TTTGGGAGAAATGTGGAGAGAGTGGCTGTCTTGGCAACATCAACTGGCAAAATGCA 1628
 721 TTTGGGAGAAATGTGGAGAGAGTGGCTGTCTTGGCAACATCAACTGGCAAAATGCA 780

1629 CAATGAATTTTCCAGCAGTCTTCCATGAGGAGATGAGAGCTGTGAGCTTGTGAGCTGT 1688
 781 CAATGAATTTTCCAGCAGTCTTCCATGAGGAGATGAGAGCTGTGAGCTTGTGAGCTGT 840

1689 GCAGATGAATGTCTGTCTACCTGTGATTAACATGTGTTT 1728
 841 GCAGATGAATGTCTGTCTACCTGTGATTAACATGTGTTT 880

RESULT 3
 AL535720 977 bp mRNA linear EST 31-MAY-2003
 LOCUS AL535720 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 DEFINITION CS0DF016VJ11 5-PRIME, mRNA sequence.

ACCESSION AL535720 GI:1260722
 VERSION AL535720.2
 KEYWORDS EST
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Li, W.-B., Gruber, C., Jesses, J., and Polayes, D.
 TITLE 1 (bases 1 to 977)
 JOURNAL Full-length cDNA libraries and normalization
 Unpublished

COMMENT
 On Feb 13, 2001 this sequence version replaced gi:12799213.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6027.r For more information about this cluster, see
 http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DF016CE06P1c;cluster=6027.r. Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Parady Avenue Genoscope sequence ID: CS0DF016CE06P1.

FEATURES
 source
 Location/Qualifiers
 1..977
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DF016VJ11"
 /tissue_type="FETAL BRAIN"
 /dev_stage="fetal"
 /clone_lib="Homo sapiens FETAL BRAIN"
 /note="Organ: brain; Vector: pCMVSPORT-6; 1st strand cDNA was primed with a NotI-0190 (dr) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

BASE COUNT 222 a 294 c 296 g 165 t

ORIGIN

Query Match 29.5%; Score 763; DB 9; Length 977;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 883; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

126 GCGCGGCTGCGGCGCGAGAGCGAGATGAGCGGCTTGGGCGCACCTGCTGCTG 185
 95 GCGCGGCTGCGGCGCGAGAGCGAGATGAGCGGCTTGGGCGCACCTGCTGCTG 154

186 CTGCTGGGCGGCGGCTGCCAGCGGCTCCGCGCTCCGAGCGGAGCTCGGCTTCA 245
 155 CTGCTGGGCGGCGGCTGCCAGCGGCTCCGCGCTCCGAGCGGAGCTCGGCTTCA 214

246 GTCAGAGCCCGGCGGCTGCTGAGCTACCGGAGAGAGCCACCTCAATGAGATGTC 305
 215 GTCAGAGCCCGGCGGCTGCTGAGCTACCGGAGAGAGCCACCTCAATGAGATGTC 274

306 CGCGAGTTGAGGAATGATGAGAGAGAGAGAGCAAAATTTGCGAGCGGCTGGAAG 365
 275 CGCGAGTTGAGGAATGATGAGAGAGAGAGAGAGCAAAATTTGCGAGCGGCTGGAAG 333

366 ATGGAGGAGAGAGAGCTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 425
 334 ATGGAGGAGAGAGAGCTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 393

426 CCCAGCTATCAAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 485
 394 CCCAGCTATCAAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 453

486 CACCGAATTTCCAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 545
 454 CACCGAATTTCCAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 513

QY		546	GTTATCACTACTGTGGGAGACGAAGAAGCGCAGAGAGGCCACGATGCATCATGACGAG	605
Db		514	GTTATCACTACTGTGGGAGACGAAGAAGCGCAGAGAGGCCACGATGCATCATGACGAG	573
QY		606	GACTGTGGGCCCAGACATGTACTGTGCAGTTTGGCCAGCTTCAGTAACCTTCCAGCACATGC	665
Db		574	GACTGTGGGCCCAGACATGTACTGTGCAGTTTGGCCAGCTTCAGTAACCTTCCAGCACATGC	633
QY		666	CGGGGCCAAGAGATGCTTCTGCACCCCGGGACAGTAGTGCTTTGGAGAACCACTGTGTCTC	725
Db		634	CGGGGCCAAGAGATGCTTCTGCACCCCGGGACAGTAGTGCTTTGGAGAACCACTGTGTCTC	693
QY		726	TGGGGTCACTGCATCAAAATATGGCCACCAGGGGCGACGATGGGACCATCTGTGACAACGAG	785
Db		694	TGGGGTCACTGCATCAAAATATGGCCACCAGGGGCGACGATGGGACCATCTGTGACAACGAG	753
QY		786	AGGAGCTGCCACCGCGGGCTGTGCTTGTCTTCCAGAGAAGGCTTGTTCCTCTGTGTGC	845
Db		754	AGGAGCTGCCACCGCGGGCTGTGCTTGTCTTCCAGAGAAGGCTTGTTCCTCTGTGTGC	813
QY		846	ACACCCCTGCCTGGCGGAGAGGCGAGCTTTGCCATGACCCCCGCGAGCTTCTGGACCTC	905
Db		814	ACACCCCTGCCTGGCGGAGAGGCGAGCTTTGCCATGACCCCCGCGAGCTTCTGGACCTC	873
QY		906	ATCACCTTGGAGCTTGAAGCCTTGATGAGCCTTTGACCCGATGCTTTGTGCCAGTGTGCTC	965
Db		874	ATCACCTTGGAGCTTGAAGCCTTGATGAGCCTTTGACCCGATGCTTTGTGCCAGTGTGCTC	933
QY		966	CTTCCGACGAGCCCGACAGCCACAGCCTGTGTATGTGTGTCAGAGCC	1009
Db		934	CTTCCGACGAGCCCGACAGCCACAGCCTGTGTATGTGTGTCAGAGCC	977
RESULT 4				
BX418715			1201 bp mRNA linear EST 15-MAY-2003	
LOCUS				
DEFINITION			BX418715 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone	
ACCESSION			CSDDP008YN12.5-PRIME, mRNA sequence.	
VERSION			BX418715	
KEYWORDS			BX418715.1 GI:307669505	
SOURCE			EST.	
ORGANISM			Homo sapiens (human)	
REFERENCE			Homo sapiens	
AUTHORS			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
TITLE			Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
JOURNAL			1 (Dates 1 to 1201)	
COMMENT			Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished	
			Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: segref@genoscope.cns.fr Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6027.r For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CSDDP008DG06QP1&cluster=6027.r. Contact : htp://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Paradise Avenue Genoscope sequence ID : CSDDP008DG06QP1.	
FEATURES				
Source			Location/Qualifiers	
			1..1201	

BASE COUNT	266 a	347 c	379 g	195 t	14 others
ORIGIN	cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."				

Query Match	29.4%	Score 760;	DB 13;	Length 1201;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 1000; Conservative	0;	Mismatches 0;	Indels 2;	Gaps 2;

QY	55	CGAGACCCGGGCGGCTCCGACGGGAGACGAGATCAATCCGACCGGACGCAATC	114
Db	67	CGAGCCCGGCGCTCCGCGGGAGCAGACGATCCATCCGGCCCGACGCAATC	126
QY	115	GGTCAGTCGAGGCGGCGCTGCGGGCGAGAGCGAGATGACGCGCTTGGGGCCACC	174
Db	127	GGTCAGATCGAGGCGGCGCTGCGGGCGAGAGCGAGATGACGCGCTTGGGGCCACC	186
QY	175	TGCTGTCCCGCTGTGTGGCGGGCGGCTCCCAAGGCCCGCGCCGCTCCGACGGCGA	234
Db	187	TGCTGTCCCGCTGTGTGGCGGGCGGCTCCCAAGGCCCGCGCCGCTCCGACGGCGA	246
QY	235	CCTCGGCTCCAGTCMAAGCCCGGCGCTGTAGCTACCCGCGAGAGAGGCCACCTCA	294
Db	247	CCTCGGCTCCAGTCMAAGCCCGGCGCTGTAGCTACCCGCA-GAGAGAGCCACCTCA	305
QY	295	ATGAGATGTTCCGCGAGAGTTGAGAAATTGATGAGAGACAGCGACCAAAATTGGCGACG	354
Db	306	ATGAGATGTTCCGCGAGAGTTGAGAACTGATGAGAGACAGCGACCAAAATTGGCGA-CG	366
QY	355	CGGTGAGAGAGATGAGAGCGAGAAAGCTGCTGAAGCATCATCGAAATGAACTGG	414
Db	365	CGGTGAGAGAGATGAGAGCGAGAAAGCTGCTGAAGCATCATCGAAATGAACTGG	424
QY	415	CAAACTTAACCTCCAGCTATCACAATTGAGACCAACAGACGAAAGTTGGAAATATA	474
Db	425	CAAACTTAACCTCCAGCTATCACAATTGAGACCAACAGACGAAAGTTGGAAATATA	484
QY	475	CCATCCATGTGTSCACCGAGAAATTCACAAGATTAACCAACACAGACTGACCAATTGCT	534
Db	485	CCATCCATGTGTSCACCGAGAAATTCACAAGATTAACCAACACAGACTGACCAATTGCT	544
QY	535	TTTCAGAGACAGTTATCACATCTGTGGGAGACGAAAGGCGAAGAGGCCAGAGTGCA	594
Db	545	TTTCAGAGACAGTTATCACATCTGTGGGAGACGAAAGGCGAAGAGGCCAGAGTGCA	604
QY	595	TCATCGACGAGAGACTGTGGGCCCGACATGTACTCCAGTTGCGAGCTCCAGTACACT	654
Db	605	TCATCGACGAGAGACTGTGGGCCCGACATGTACTCCAGTTGCGAGCTCCAGTACACT	664
QY	655	GCCAGCCATGCGGGGCGCAGAGATGCTTTCGACCCCGGAGACGTGAATGCTGTGTGAAC	714
Db	665	GCCAGCCATGCGGGGCGCAGAGATGCTTTCGACCCCGGAGACGTGAATGCTGTGTGAAC	724
QY	715	AGCTGTGTGTGGGGGTCACTGCAACAAATGGCGCACGAGGGGCGAGCAATGGACCAAT	774
Db	725	AGCTGTGTGTGGGGGTCACTGCAACAAATGGCGCACGAGGGGCGAGCAATGGACCAAT	784
QY	775	GTGACAAACAGAGGAGCTGCCAGCGGGGCTGTGTGCTTCTTCCAGAGAGGCTGTCT	834
Db	785	GTGACAAACAGAGGAGCTGCCAGCGGGGCTGTGTGCTTCTTCCAGAGAGGCTGTCT	844
QY	835	TCCCTGTGTGACACCCCTGCGCGGTGAGAGGGCGAGCTTGTGCATGACCCCGCACGCGC	894
Db	845	TCCCTGTGTGACACCCCTGCGCGGTGAGAGGGCGAGCTTGTGCATGACCCCGCACGCGC	904
QY	895	TTCTGACCTCATCACTGTGGAGCTGAGGCTGATGAGAGCTTGAACGATGCCCTTGT	954
Db	905	TTCTGACCTCATCACTGTGGAGCTGAGGCTGATGAGAGCTTGAACGATGCCCTTGT	964
QY	955	CCAGTGGGCTCTCTGCGACGCGCCACAGCCACAGGCTGTGTATGTGTGCAAGCGCACT	1014
Db	965	CCAGTGGGCTCTCTGCGACGCGCCACAGCCACAGGCTGTGTATGTGTGCAAGCGCACT	1024

QY 1015 TCGTGGGAGCCGTRACCAAGATGGGAGATCCCTGCTCCCA 1056
 Db 1025 TCGTGGGAGCCGTRACCAAGATGGGAGATCCCTGCTCCCA 1066

RESULT 5
 B0879213
 LOCUS B0879213 936 bp mRNA linear EST 16-AUG-2002
 DEFINITION AGENCOURT 8229317 lupski_dorsal_root_ganglion Homo sapiens cDNA
 clone IMAGE:6183568 5', mRNA sequence.

ACCESSION B0879213
 VERSION B0879213
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 936)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 UNPUBLISHED
 CONTACT: Robert Strausberg, Ph.D.
 EMAIL: cgabbs-rc@mail.nih.gov
 TISSUE Procurement: Dr. James R. Lupski
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: L14M13571 row: 6 column: 17
 High quality sequence stop: 708.

FEATURES
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6183568"
 /sex="male"
 /tissue_type="dorsal root ganglia"
 /dev_stage="adult, 36 yr"
 /lab_host="DH10B"
 /clone_1lb="lupski_dorsal_root_ganglion"
 /note="Vector: pCMV-SPORT6 (Life Technologies); Site 1: NotI; Site 2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCGAGCGCTCG-3' and 5'-GACTAGTCTAGATCGGAGCGGCGCCCTT(15)-3'. Size selected > 1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."

BASE COUNT 213 a 249 c 289 g 185 t

Query Match 29.3%; Score 758; DB 13; Length 936;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 758; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 401 AGAAGTGAACCTGGCAACTTACCTCCAGCTATCAACATGAGACCAACAGACGAA 460
 Db 1 AGAAGTGAACCTGGCAACTTACCTCCAGCTATCAACATGAGACCAACAGACGAA 60

QY 461 GGTGGAAATTAATCAATGATGAGACCGAGAAATTCACAAATTAACCAACACAGAC 520
 Db 61 GGTGGAAATTAATCAATGATGAGACCGAGAAATTCACAAATTAACCAACACAGAC 120

QY 521 TGGCAAAATGCTCTTTTCAGAGACAGTTATCACTGTGGAGACGAGAGAGGCGAAG 580
 Db 121 TGGCAAAATGCTCTTTTCAGAGACAGTTATCACTGTGGAGAGAGAGAGAGGCGAAG 180

QY 581 GAGCCAGAGTGCATCATCGAGAGACTGTGGGCCAGACATGTACGACATTTGCCAG 640

Db 181 GAGCCAGAGTGCATCATCGAGAGACTGTGGGCCAGACATGTACGACATTTGCCAG 240
 QY 641 CTTCAGATCACTGTCAGACCATGCGGGGCGAGAGATGCTCTGCAACCGGGACAGTGA 700
 Db 241 CTTCAGATCACTGTCAGACCATGCGGGGCGAGAGATGCTCTGCAACCGGGACAGTGA 300
 QY 701 GTGCTGAGAGACCAAGCTGTGTCTGAGGCTCACTGCACAAATGGCCACAGGGGCGAG 760
 Db 301 GTGCTGAGAGACCAAGCTGTGTCTGAGGCTCACTGCACAAATGGCCACAGGGGCGAG 360

QY 761 CAATGGACCACTGTGAGACCAACAGAGGAGCTGCCAGCGGGGCTGTGTCGCTTCCA 820
 Db 361 CAATGGACCACTGTGAGACCAACAGAGGAGCTGCCAGCGGGGCTGTGTCGCTTCCA 420

QY 821 GAGAGCTGCTGTTCCCTGTGTGACACCCCTGCGCGTGAAGGCGAGCTTGCATGA 880
 Db 421 GAGAGCTGCTGTTCCCTGTGTGACACCCCTGCGCGTGAAGGCGAGCTTGCATGA 480

QY 881 CCCCCGAGCGGCTTCTGACCTCTATCACTGAGAGCTGAGAGCTGAGAGCTTGA 940
 Db 481 CCCCCGAGCGGCTTCTGACCTCTATCACTGAGAGCTGAGAGCTTGA 540

QY 941 CCGATGCCCTTGTGCAAGTGGCTCTCTGCAAGCCCAAGCCACAGCTGTATGT 1000
 Db 541 CCGATGCCCTTGTGCAAGTGGCTCTCTGCAAGCCCAAGCCACAGCTGTATGT 600

QY 1001 GTGCAGACCACTTGTGTGGGAGCGGTGACCAAGATGGGAGATCTGCTGCCAGAGA 1060
 Db 601 GTGCAGACCACTTGTGTGGGAGCGGTGACCAAGATGGGAGATCTGCTGCCAGAGA 660

QY 1061 GGTCCCGATGATGATGAGATGGAGCTTCAATGAGAGAGTGGCAGAGCTGAGGA 1120
 Db 661 GGTCCCGATGATGATGAGATGGAGCTTCAATGAGAGAGTGGCAGAGCTGAGGA 720

QY 1121 CCTGAGAGAGGCTGACTGTGAAGAGATGGCGCTGGGGG 1158
 Db 721 CCTGAGAGAGGCTGACTGTGAAGAGATGGCGCTGGGGG 758

RESULT 6
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 LOCUS BUI49689 8049944 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6083782
 DEFINITION AGENCOURT 8049944 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6083782
 5', mRNA sequence.

ACCESSION BUI49689
 VERSION BUI49689.1 GI:22663221
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 949)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 UNPUBLISHED
 CONTACT: Robert Strausberg, Ph.D.
 EMAIL: cgabbs-rc@mail.nih.gov
 TISSUE Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: L14M2314 row: h column: 23
 High quality sequence start: 19
 High quality sequence stop: 678.

FEATURES
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 /mol_type="mRNA"
 /db_xref="taxon:9606"

/clone="IMAGE:6083782"
 /tissue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAAGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC library."

BASE COUNT 188 a 236 c 288 g 237 t
 ORIGIN

Query Match 29.1%; Score 752; DB 13; Length 949;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 802; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

848 ACCCTGCCCCGCGGAGAGGAGGAGCTTTGCCATGACCCCGCAGCCGCTTCTGACCTCAT 907
 31 ACCCTGCCCCGCGGAGAGGAGGAGCTTTGCCATGACCCCGCAGCCGCTTCTGACCTCAT 90
 908 CACCTGGAGCTAGAGCTGATGAGACCTTGGACCGATGCCCTTGTGGCAGTGCCCTCT 967
 91 CACCTGGAGCTAGAGCTGATGAGACCTTGGACCGATGCCCTTGTGGCAGTGCCCTCT 150
 968 CTGCGACCCCGACAGCCAGCCTGTGTATGTGTGCAAGCCGACCTTGTGGGAGACCG 1027
 151 CTGCGACCCCGACAGCCTGTGTATGTGTGCAAGCCGACCTTGTGGGAGACCG 210
 1028 TGACCAAGATGGGGAGATCCTGCTGCCAGAGAGTCCCGATGATGATGAAGTTGGCAG 1087
 211 TGACCAAGATGGGGAGATCCTGCTGCCAGAGAGTCCCGATGATGATGAAGTTGGCAG 270
 1088 CTTCATGAGAGAGTGGCCAGAGAGCTGGAGGACCTGGAGAGAGCTTGAAGAGAT 1147
 271 CTTCATGAGAGAGTGGCCAGAGAGCTGGAGGACCTGGAGAGAGCTTGAAGAGAT 330
 1148 GGGCGTGGGGAGACCTGGCGCTGGCCCGCTGCTGCTGCTGGAGAGGGAGAGATTTAGT 1207
 331 GGGCGTGGGGAGACCTGGCGCTGGCCCGCTGCTGCTGCTGGAGAGGGAGAGATTTAGT 390
 1208 CTGAGCAGAGCTGTGGGTGATGTGCATAGAATAAGTAAATTTATTTCCAGAGTGT 1267
 391 CTGAGCAGAGCTGTGGGTGATGTGCATAGAATAAGTAAATTTATTTCCAGAGTGT 450
 1268 GCTTTAGGGCTGGGCTGACCAAGCTTCTTCTCAATCTTCTTCCAGTAAGTTCCCTC 1327
 451 GCTTTAGGGCTGGGCTGACCAAGCTTCTTCTCAATCTTCTTCCAGTAAGTTCCCTC 510
 1328 TGCTTGACAGCATGAGGTGTGTGCATTTGTTCAGCTCCCCAGGCTTTTCTCCAGCT 1387
 511 TGCTTGACAGCATGAGGTGTGTGCATTTGTTCAGCTCCCCAGGCTTTTCTCCAGCT 570
 1388 TCACAGCTGTGTCTTGGAGAGTCAAGGAGGTTAACTGACAGAGCAAGTTTGCACCC 1447
 571 TCACAGCTGTGTCTTGGAGAGTCAAGGAGGTTAACTGACAGAGCAAGTTTGCACCC 630
 1448 CTGTCCAGATTTATTTGCTGCTTGGCTTACCAAGTTGGCAGAGAGCTTGTTCAT 1507
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 691 GCGTTGATTAATTTGTTGAGGGAGAGATGAACAATGTGAGAGTCTCCCTGATTTGG 750
 1568 TTTTGGGAGAAATGTGAGAGAGATGTGCCCTGCTTGGCAACATCAACTGGCAAAAATGA 1627
 751 TTTTGGGAGAAATGTGAGAGAGATGTGCCCTGCTTGGCAACATCAACTGGCAAAAATGA 810
 1628 ACAATGAATTTTCCACGAGTT 1650

Db 811 ACAATGAATTTTCCACGAGTT 833

RESULT 7
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 LOCUS AGNCCUR7_8076102 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6084891
 DEFINITION 5', mRNA sequence.
 ACCESSION BU196879
 VERSION BU196879.1 GI:22710863
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 985)
 NIH-MGC http://mgs.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: sgapds-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LICM2317 row: g column: 04
 High quality sequence stop: 644.
 Location/Qualifiers

FEATURES

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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6084891"
 /tissue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAAGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC library."

BASE COUNT 199 a 256 c 282 g 248 t
 ORIGIN

Query Match 28.7%; Score 741; DB 13; Length 985;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 791; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

849 CCCCTGCCCGTGGAGGGCGAGCTTTGGCATGACCCCGCAGCGGCTTCTGGAGCTCATC 908
 1 CCCCTGCCCGTGGAGGGCGAGCTTTGGCATGACCCCGCAGCGGCTTCTGGAGCTCATC 60
 909 ACTGGAGCTAGAGCTGATGAGACCTTGGACCGATGCCCTGTGTGCAAGTGGCTCTC 968
 61 ACTGGAGCTAGAGCTGATGAGACCTTGGACCGATGCCCTGTGTGCAAGTGGCTCTC 120
 969 TGGCAGCCCCCAGACCCAGAGCTGTGTATGTGTGCAAGCGACCTTCGTGGGAGGCGT 1028
 121 TGGCAGCCCCCAGACCCAGAGCTGTGTATGTGTGCAAGCGACCTTCGTGGGAGGCGT 180
 1029 GACCAAGATGGGAGATCTGCTGCCAGAGAGGTCCCGATGATGAAGTTGGCAGC 1088
 181 GACCAAGATGGGAGATCTGCTGCCAGAGAGGTCCCGATGATGAAGTTGGCAGC 240
 1089 TTCTATGAGAGAGTGGCGCCAGAGACTGGAGAGCTTGAAGAGAGCTTGAAGAGATG 1148
 241 TTCTATGAGAGAGTGGCGCCAGAGACTGGAGAGCTTGAAGAGAGCTTGAAGAGATG 300

QY 1149 GCGCTGGGGGAGCGCTGCGGCTGCGGCTGCTGCTGAGGGGAGAGATTAGATC 1208
 Db 301 GCGCTGGGGGAGCGCTGCGGCTGCGGCTGCTGCTGAGGGGAGAGATTAGATC 360
 QY 1209 TGGACCAAGGCTGTGGGTGATGTGCAATGAAATGCTAATTTATTTTCCCAAGGTGTG 1268
 Db 361 TGGACCAAGGCTGTGGGTGATGTGCAATGAAATGCTAATTTATTTTCCCAAGGTGTG 420
 QY 1269 CTTTGGGCTGGGCTGACGAGGCTTCTCTACATCTTCTCCAGTAAGTTCCCTCT 1328
 Db 421 CTTTGGGCTGGGCTGACGAGGCTTCTCTACATCTTCTCCAGTAAGTTCCCTCT 480
 QY 1329 GCGCTTGAACGATGAGGTGTGTGCTATTGTTCAAGCTCCCGAGGCTGTCTCCAGCTT 1388
 Db 481 GCGCTTGAACGATGAGGTGTGTGCTATTGTTCAAGCTCCCGAGGCTGTCTCCAGCTT 540
 QY 1389 CACAGTCTGTGCTTGGGAGAGTCAAGGAGGTTAACTGACGAGGAGTTGCGACCCC 1448
 Db 541 CACAGTCTGTGCTTGGGAGAGTCAAGGAGGTTAACTGACGAGGAGTTGCGACCCC 600
 QY 1449 TGTCCAGATTATGCTGCTTGTGCTTGTCTTACCAATTGCGACAGCCGTTGTCTACATG 1508
 Db 601 TGTCCAGATTATGCTGCTTGTGCTTGTCTTACCAATTGCGACAGCCGTTGTCTACATG 660
 QY 1509 GCTTTGATTAATTTGTTTGGGGGAGAGATGAAACAATGTGAGTCTCCCTGATTTGCT 1568
 Db 661 GCTTTGATTAATTTGTTTGGGGGAGAGATGAAACAATGTGAGTCTCCCTGATTTGCT 720
 QY 1569 TTTGGGGAATGTGGAGAGAGTGCCTGCTTGGCAACATCAACTGCGCAAAATGCAA 1628
 Db 721 TTTGGGGAATGTGGAGAGAGTGCCTGCTTGGCAACATCAACTGCGCAAAATGCAA 780
 QY 1629 CAAATGATTTT 1640
 Db 781 CAAATGATTTT 792

RESULT 8
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 5', mRNA sequence.
 ACCESSION B0689208.1 GI:21814524
 VERSION B0689208
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 1 (bases 1 to 870)
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: rgs@bbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LMNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMNL at:
 http://image.llnl.gov/
 Plate: LCM2364 row: 1 column: 04
 High quality sequence stop: 691.
 Location/Qualifiers
 1..870
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
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 /issue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"

/clone.lib="NIH MGC 110"
 /note="Organ: pancreas; Vector: pOTB7; Site: 1; XhoI;
 Site: 2; EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GCGACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH MGC Library."

BASE COUNT 170 a 217 c 267 g 216 t
 ORIGIN

Query Match 28.4%; Score 734; DB 13; Length 870;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 784; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 849 CCCTTGCCCGTGAGGAGGAGCTTGGCATGACCCCGCAGCCGCTTCTGACCTCATC 908
 Db 1 CCCTTGCCCGTGAGGAGGAGCTTGGCATGACCCCGCAGCCGCTTCTGACCTCATC 60
 QY 909 ACCTGGAGCTAGAGCTTATGAGACCTTGAACCGATGCCCTTGTGCGAGTGGCCCTCTC 968
 Db 61 ACCTGGAGCTAGAGCTTATGAGACCTTGAACCGATGCCCTTGTGCGAGTGGCCCTCTC 120
 QY 969 TGGCAGCCCGCAGAGCCAGCTGTGATGTGTGCAAGCCGACCTTGTGAGGAGCCGT 1028
 Db 121 TGGCAGCCCGCAGAGCCAGCTGTGATGTGTGCAAGCCGACCTTGTGAGGAGCCGT 180
 QY 1029 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGTCCCGATGATGATGAGTTGGACAC 1088
 Db 181 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGTCCCGATGATGATGAGTTGGACAC 240
 QY 1089 TTCTATGAGAGAGTGTGGCCAGAGCTGAGAGACTGAGAGAGGCTGACTGAGAGATG 1148
 Db 241 TTCTATGAGAGAGTGTGGCCAGAGCTGAGAGACTGAGAGAGGCTGACTGAGAGATG 300
 QY 1149 GCGCTGGGGAGGCTGCGGCTGCGGCTGCTGCACTGTGGAGGGGAGAGATTAGATC 1208
 Db 301 GCGCTGGGGAGGCTGCGGCTGCGGCTGCTGCACTGTGGAGGGGAGAGATTAGATC 360
 QY 1209 TGGACCAAGGCTGTGGGTGATGTGCAATGAAATGCTAATTTATTTTCCCAAGGTGTG 1268
 Db 361 TGGACCAAGGCTGTGGGTGATGTGCAATGAAATGCTAATTTATTTTCCCAAGGTGTG 420
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 Db 421 CTTTGGGCTGGGCTGACGAGGCTTCTCTACATCTTCTCCAGTAAGTTCCCTCT 480
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 Db 481 GCGCTTGAACGATGAGGTGTGTGCTATTGTTCAAGCTCCCGAGGCTGTCTCCAGCTT 540
 QY 1389 CACAGTCTGTGCTTGGGAGAGTCAAGGAGGTTAACTGACGAGGAGTTGCGACCCC 1448
 Db 541 CACAGTCTGTGCTTGGGAGAGTCAAGGAGGTTAACTGACGAGGAGTTGCGACCCC 600
 QY 1449 TGTCCAGATTATGCTGCTTGTGCTTGTCTTACCAATTGCGACAGCCGTTGTCTACATG 1508
 Db 601 TGTCCAGATTATGCTGCTTGTGCTTGTCTTACCAATTGCGACAGCCGTTGTCTACATG 660
 QY 1509 GCTTTGATTAATTTGTTTGGGGGAGAGATGAAACAATGTGAGTCTCCCTGATTTGCT 1568
 Db 661 GCTTTGATTAATTTGTTTGGGGGAGAGATGAAACAATGTGAGTCTCCCTGATTTGCT 720
 QY 1569 TTTGGGGAATGTGGAGAGAGTGCCTGCTTGGCAACATCAACTGCGCAAAATGCAA 1628
 Db 721 TTTGGGGAATGTGGAGAGAGTGCCTGCTTGGCAACATCAACTGCGCAAAATGCAA 780
 QY 1629 CAAAT 1633
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```

RESULT 9
BQ230646      885 bp      mRNA      linear      EST 02-MAY-2002
LOCUS         AGENCOURT 7273720 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:6016827
DEFINITION    5' mRNA sequence.
ACCESSION     BQ230646
VERSION       BQ230646.1 GI:20412046
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 885)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM13215 row: c column: 04
High quality sequence stop: 665.
Location/Qualifiers
1. 885
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6016827"
/tissue_type="epitheloid carcinoma"
/lab_host="DH10B (pmap-resistance)"
/notes="Organ: pancreas; Vector: pCMV-Sport6; Site: 1; NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
BASE COUNT    184 a      212 c      251 g      234 t      4 others
ORIGIN
Query Match    28.4%; Score 734; DB 13; Length 885;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 734; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1082 TGCGAGCTTATGAGAGAGGTGGCCAGAGCTGAGAGACCTGGAGAGAGGCTGCTGA 1141
Db 1 TGCGAGCTTATGAGAGAGGTGGCCAGAGCTGAGAGACCTGGAGAGAGGCTGCTGA 60
QY 1142 AGAGATGGCGCTGGGGAGGCTGGCGGCTGCCGCGCTGCACTGCTGGAGAGGAGAGAT 1201
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Db 121 TTAGATGTGACCAAGAGCTGTGGGTAGATGTGCAATGAATAATAGCTAATTTATTTCCCGAG 180
QY 1262 GTGTGCTTTAGAGCGTGGGCTGACCAAGAGCTTCTTCTACATCTTCTCCAGTAAGTT 1321
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Db 301 CAGGCTTCAAGTGTGCTGTGGAGAGTCAAGAGAGGTTAAATGCAAGAGAGCTTTG 360
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Db 361 CCACCCCTGTCCAGATTAATGGCTTGGCTTGTGCTTCAACAGTTGGCAGACAGCCGTTTGT 420
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Db 421 CTACATGGCTTTGATAATTTGTTGAGGGGAGAGATGAAACAATGTGAGTCTCCTCT 480
QY 1562 GATTGTTTTGGGAAATGTGGAGAAAGAGTCCCTGTTTGGCAACATCAACCTGGGAA 1621
Db 481 GATTGTTTTGGGAAATGTGGAGAAAGAGTCCCTGTTTGGCAACATCAACCTGGGAA 540
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Db 661 TGTGCTCAGCTCTTACCTCTGTGCGCAGGAGAGATTTTCAATCAATCAATTCCT 720
QY 1802 CTCTCAGCAGAGCC 1815
Db 721 CTCTCAGCAGAGCC 734

RESULT 10
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LOCUS         AGENCOURT 8304969 Lupski_sympathetic_trunk Homo sapiens cDNA clone
DEFINITION    IMAGE:6193228 5' mRNA sequence.
ACCESSION     BQ722575
VERSION       BQ722575.1 GI:21861472
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 931)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM13596 row: i column: 05
High quality sequence stop: 642.
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Directionally cloned using the following adaptors:
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5'-GACTAGTCTTGAATCGCAGCGGCGGCTT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor

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College of Medicine); available through Life Technologies."

BASE COUNT 217 a 279 c 281 g 154 t

ORIGIN

Query Match 27.7%; Score 717; DB 13; Length 931;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

142 GCAGAGCGGAGATGAGCGGCTTG3G3GCCACCTTGCTGCTGCTGCGGCGGCGG 201

1 GCAGAGCGGAGATGAGCGGCTTG3G3GCCACCTTGCTGCTGCTGCGGCGGCGG 60

202 TCCCGACGG 261

61 TCCCGACGG 120

262 CTCTGAGCTACCGCGAGAGAGAGCGCCACCTTCAATGAGATGTTCCGCGAGGTTGAGAAC 321

121 CTCTGAGCTACCGCGAGAGAGAGCGCCACCTTCAATGAGATGTTCCGCGAGGTTGAGAAC 180

322 TGATGAG 381

181 TGATGAG 240

382 CTGCTGCTAAAGCATCATCAGAGAGTGAACCTTGCGCAACTTACCTCCAGCTATCACAATG 441

241 CTGCTGCTAAAGCATCATCAGAGAGTGAACCTTGCGCAACTTACCTCCAGCTATCACAATG 300

442 AGACCAACAACAAG 501

301 AGACCAACAACAAG 360

502 AGATAACCAACAAG 561

361 AGATAACCAACAAG 420

562 GAGAGCAAG 621

421 GAGAGCAAG 480

622 TGATGAG 681

481 TGATGAG 540

682 TGTGACAG 741

541 TGTGACAG 600

742 AATAGGCAAG 801

601 AATAGGCAAG 660

802 GGTGCTGCTGCTGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 858

661 GGTGCTGCTGCTGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 717

RESULT 11

BO897953 883 bp mRNA linear EST 16-AUG-2002

LOCUS AGENCOURT 8061767 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6208520

DEFINITION 5', mRNA sequence.

ACCESSION BO897953

VERSION BO897953.1 GI:22289967

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 883)

NITH-MGC http://mgi.nci.nih.gov/

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: gsabbs@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LHC2366 row: 6 column: 09

High quality sequence stop: 684.

FEATURES

Location/Qualifiers

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/clone_lib="NIH MGC 110"

/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;

Site 2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCAAGAG(G). Library constructed by

Ling Hong in the laboratory of Gerald M. Rubin (University

of California, Berkeley) using Zap-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH MGC Library."

BASE COUNT 178 a 220 c 263 g 222 t

ORIGIN

Query Match 27.6%; Score 715; DB 13; Length 883;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

849 CCCCTGCGGAG 908

1 CCCCTGCGGAG 60

909 ACCTGGAGCTAAGAGCTGATGAGAGCTTGTGACCGATGCCCTTGTGCGAGTGCCTTC 968

61 ACCTGGAGCTAAGAGCTGATGAGAGCTTGTGACCGATGCCCTTGTGCGAGTGCCTTC 120

969 TGGCAGGCCACAGCCACAGCTGATGATGATGATGATGATGATGATGATGATGATG 1028

121 TGGCAGGCCACAGCCACAGCTGATGATGATGATGATGATGATGATGATGATGATG 180

1029 GACCAAGATGGAGAGATCTGCTGCCAGAGAGCTCCCGATGATGATGATGATGATG 1088

181 GACCAAGATGGAGAGATCTGCTGCCAGAGAGCTCCCGATGATGATGATGATGATGATG 240

1089 TTCAATGAG 1148

241 TTCAATGAG 300

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301 GCGCTGGAGAGAGAGCTGCGGCTGCCCGGCTGCACTGCTGGAGAGAGAGATTAGATC 360

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421 CTTTAGGCGTGGGCTGACAGAGCTTCTTCTAATCTTCTTCCAGTAAGTTTCCCTCT 480

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481 GCGCTTACAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 540

1389 CACAGCTGATGCTTGGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1448

Db 541 CACAGTCTGCTGCTGGAGAGTCAAGGAGGTAACTGACAGAGCATTTGGCCACCCC 600
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 QY 1509 GCTTTGATATTTGTTGGAGGGAGAGATGAAACATGTGAGTCTCCCTCTGATTGAT 1568
 Db 661 GCTTTGATATTTGTTGGAGGGAGAGATGAAACATGTGAGTCTCCCTCTGATTGAT 720
 QY 1569 TTTGGGAAATGTGAGAAAGTGCCTGCTTTGCAACATCAACC 1614
 Db 721 TTTGGGAAATGTGAGAAAGTGCCTGCTTTGCAACATCAACC 766
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 DEFINITION 5', mRNA sequence.
 ACCESSION BUI62929
 VERSION BUI62929
 KEYWORDS EST, mRNA sequence, GI:22676839
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1065)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
 Plate: LLCM2139 row: P column: 03
 High quality sequence stop: 647.
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 /note="Organ: pancreas; Vector: pOT87; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."
 BASE COUNT 219 a 278 c 297 g 271 t
 ORIGIN
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 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 849 CCCCCTGGGAGGGAGGAGCTTGGCATGACCCCGCAGCGGCTTGGACCTCATC 908
 Db 1 CCCCCTGGGAGGGAGGAGCTTGGCATGACCCCGCAGCGGCTTGGACCTCATC 60
 QY 909 ACTGGAGCTAGAGCTGATGAGACCTTGGACCGATGCCCTTGTGCCATGAGCTCTC 968

Db 61 ACTGGAGCTAGAGCTGATGAGACCTTGGACCGATGCCCTTGTGCCATGAGCTCTC 120
 QY 969 TGCAGAGCCCAACAGCCAGACCTGATGATGTGAGAGCCGACCTTCTGTGGAGCCGT 1028
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 QY 1209 TGAACAGAGCTGTGGATGATGTCATAGAAATAGCTAATTTATTTCCAGATGTGTG 1268
 Db 361 TGAACAGAGCTGTGGATGATGTCATAGAAATAGCTAATTTATTTCCAGATGTGTG 420
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 Db 601 TGTCCAGATTATTTGGCTGCTTTGCTCTTCCAGTTGGCAGAGCCGTTGTTCAACTG 660
 QY 1509 GCTTTGATATTTGTTGGAGGGAGAGATGAAACATGTGAGTCTCCCTCTGATTGAT 1568
 Db 661 GCTTTGATATTTGTTGGAGGGAGAGATGAAACATGTGAGTCTCCCTCTGATTGAT 720
 QY 1569 TTTGGGAAATGTGAGAAAGTGCCTGCTTTGCAACATCAACC 1614
 Db 721 TTTGGGAAATGTGAGAAAGTGCCTGCTTTGCAACATCAACC 766
 RESULT 13
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 LOCUS AGENCOURT_8061866 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6208646
 DEFINITION 5', mRNA sequence.
 ACCESSION BQ889489
 VERSION BQ889489
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 892)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
 Plate: LLCM2366 row: K column: 15

High quality sequence stop: 680.
Location/Qualifiers

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Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 179 a 223 c 269 g 221 t
ORIGIN

Query Match 27.5%; Score 711; DB 13; Length 892;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 761; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
849 CCCCTGCCCCGTGAGGCGAGCTTTGCCATGACCCGCCAGCCGCTTTGACCTCATC 908
1 CCCCTGCCCCGTGAGGCGAGCTTTGCCATGACCCGCCAGCCGCTTTGACCTCATC 60
909 ACCCTGGAGCTAGAGCTGATGAGCTTGGACCGATGCGCTTGTGACAGTGGAGCTCTC 968
61 ACCCTGGAGCTAGAGCTGATGAGCTTGGACCGATGCGCTTGTGACAGTGGAGCTCTC 120
969 TGCAGAGCCCAACAGCCAGCTGTGTATGTGTGCAAGCCAGCTTGTGAGGAGCCGT 1028
121 TGCAGAGCCCAACAGCCAGCTGTGTATGTGTGCAAGCCAGCTTGTGAGGAGCCGT 180
1029 GACCAAGATGGAGAGATCTCTGCTCCAGAGAGTCCCGCATAGATAGAGTTGGACAG 1088
181 GACCAAGATGGAGAGATCTCTGCTCCAGAGAGTCCCGCATAGATAGAGTTGGACAG 240
1089 TTCAATGAGAGAGTGTGCGCCAGAGAGCTTGGAGAGCTTGGAGAGAGCTTGAAGAGATG 1148
241 TTCAATGAGAGAGTGTGCGCCAGAGAGCTTGGAGAGAGCTTGAAGAGAGATG 300
1149 GCGCTGGAGAGCTGTGCGCGCTGCGCGCTGCACTGCTGGAGAGAGAGATTTAGATC 1208
301 GCGCTGGAGAGCTGTGCGCGCTGCGCGCTGCACTGCTGGAGAGAGAGATTTAGATC 360
1209 TGAACCAAGCTGTGAGTATGATGATAGATAATAGCTAATTTATTTCCCAAGTGTGTG 1268
361 TGAACCAAGCTGTGAGTATGATGATAGATAATAGCTAATTTATTTCCCAAGTGTGTG 420
1269 CTTTAAAGCGTGGCTGACCAAGCTTTCTTCTTCTTCTTCCCAAGTATTTCCCTCTC 1328
421 CTTTAAAGCGTGGCTGACCAAGCTTTCTTCTTCTTCTTCCCAAGTATTTCCCTCTC 480
1329 GCGCTGACAGATGAGTGTGCTGATTTGTTCACTTCCCAAGCTTCTCCAGGCTT 1388
481 GCGCTGACAGATGAGTGTGCTGATTTGTTCACTTCCCAAGCTTCTCCAGGCTT 540
1389 CACAGTCTGTGCTTGGAGAGTCAAGAGAGGTTAACTGAGAGAGAGTTTGGACATCC 1448
541 CACAGTCTGTGCTTGGAGAGTCAAGAGAGGTTAACTGAGAGAGAGTTTGGACATCC 600
1449 TGTCCAGATTTATGGCTGTGCTTGTGCTTCAACAGTTGGACAGACGCTTTGTTCAATG 1508
601 TGTCCAGATTTATGGCTGTGCTTGTGCTTCAACAGTTGGACAGACGCTTTGTTCAATG 660
1509 GCTTGAATTAATTTGTTGAGGAGAGATGAGAACTAATGTGAGATCTTCTGATTTGAT 1568
661 GCTTGAATTAATTTGTTGAGGAGAGATGAGAACTAATGTGAGATCTTCTGATTTGAT 720

QY 1569 TTGGGGAATGTGAGAGAGTCCCTGCTTTGCAACATC 1610
Db 721 TTGGGGAATGTGAGAGAGTCCCTGCTTTGCAACATC 762

RESULT 14
B0686792
LOCUS
DEFINITION
5', mRNA sequence.
ACCESSION
B0686792.1 GI:21812108
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 932)
NIH-MGC <http://mgc.ncl.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
TITLE
AUTHORS
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC
DNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
<http://image.llnl.gov>
Plate: L10M2393 row: f column: 15
High quality sequence stop: 710.

FEATURES

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/clone_lib="NIH_MGC_110"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 184 a 235 c 279 g 234 t
ORIGIN

Query Match 27.4%; Score 708; DB 13; Length 932;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 758; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 847 CACCCCTGCGGTGAGAGGCGAGCTTTGCCATGACCCCGAGCGGCTTGTGACCTCA 906
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907 TCACCTGGAGCTAGAGCTGATGAGAGCTTGAACCGATGCGCTTGTGCAAGTGGCTCC 966
Db 78 TCACCTGGAGCTAGAGCTGATGAGAGCTTGAACCGATGCGCTTGTGCAAGTGGCTCC 137
QY 967 TGTGCAAGCCCAACAGCCAGCTGTGTATGTGTGAACCGACCTTGTGGGGAAGCC 1026
Db 138 TGTGCAAGCCCAACAGCCAGCTGTGTATGTGTGAACCGACCTTGTGGGGAAGCC 197
QY 1027 GTGACCAAGATGGAGAGATCTGCTGCCAGAGAGTCCCGATGATGATGAAGTTGGCA 1086
Db 198 GTGACCAAGATGGAGAGATCTGCTGCCAGAGAGTCCCGATGATGATGAAGTTGGCA 257
QY 1087 GCTTATGAGAGAGTGTGCGCCAGAGAGCTGAGAGACTTGAAGAGAGCTGATGAAGA 1146

Db 258 GCTTCATGAGAGAGGCTGCGCCAGAGCTGAGAGACCTGAGAGAGAGCTGACTGAGAGAGA 317
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Db 318 TGGCGCTGAGAGGAGCCTGCGGCTGCGCGCCGCTCACTGCTGGAGAGGAGAGATTGAA 377
QY 1207 TCTGAGACAGAGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTATTCCCAAGGTG 1266
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RESULT 15
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DEFINITION 5', mRNA sequence.
ACCESSION BQ890463
VERSION BQ890463.1 GI:22282477
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
AUTHORS Unpublished
JOURNAL Contact: Robert Strauberg, Ph.D.
COMMENT Email: ggaaps-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LNCM2364 row: m column: 17
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Location/Qualifiers
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/clone="IMAGE:6207928"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH MGC 110"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;

Query Match 27.3% Score 706; DB 13; Length 878;
Best Local Similarity 99.98% Pred. No. 0;
Matches 756; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Note: this is a NIH MGC Library.

BASE COUNT 175 a 218 c 264 g 219 t 2 others

ORIGIN

Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).

QY 849 CCCCTGCCCCGTGAGAGGAGGAGCTTTGACATGACCCGACCGGCTTCTGACCTATC 908
Db 1 CCCCTGCCCCGTGAGAGGAGGAGCTTTGACATGACCCGACCGGCTTCTGACCTATC 60
QY 909 ACCTGGAGCTAGAGAGCTGATGAGAGCTTGAACCGATGCTTGTGCTGACAGGCTCTC 968
Db 61 ACCTGGAGCTAGAGAGCTGATGAGAGCTTGAACCGATGCTTGTGCTGACAGGCTCTC 120
QY 969 TGCCAGCCCCACAGACAGAGCTGATGATGTGCAAGCCGACCTTGTGAGAGAGCCGT 1028
Db 121 TGCCAGCCCCACAGACAGAGCTGATGATGTGCAAGCCGACCTTGTGAGAGAGCCGT 180
QY 1029 GACCAAGATGGAGAGATCTGCTGCTGCCAGAGAGGTCCCGATGATGAAGATTGGCAGC 1088
Db 181 GACCAAGATGGAGAGATCTGCTGCTGCCAGAGAGGTCCCGATGATGAAGATTGGCAGC 240
QY 1089 TTCAATGAGAGAGGTGCGGCTGAGAGAGCTGAGAGAGAGCTGACATGAAGAGATG 1148
Db 241 TTCAATGAGAGAGGTGCGGCTGAGAGAGCTGAGAGAGAGCTGACATGAAGAGATG 300
QY 1149 GCGCTGAGAGAGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 1208
Db 301 GCGCTGAGAGAGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 360
QY 1209 TGAGACAGAGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTATTCCCAAGGTG 1268
Db 361 TGAGACAGAGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTATTCCCAAGGTG 420
QY 1269 CTTTAGGCGTGGGCTGACAGAGCTTCTTCTACATCTTCTTCCAGTAAGTTCCCTCT 1328
Db 421 CTTTAGGCGTGGGCTGACAGAGCTTCTTCTACATCTTCTTCCAGTAAGTTCCCTCT 480
QY 1329 GCGTTGACAGATGAGAGTGTGCTGATTTGTCAGCTCCCGCAGGCTGCTCCAGGCTT 1388
Db 481 GCGTTGACAGATGAGAGTGTGCTGATTTGTCAGCTCCCGCAGGCTGCTCCAGGCTT 540
QY 1389 CACAGCTGTGCTGTGGAGAGATGAGAGGATTAACCTGAGAGAGAGATTGGACACCC 1448
Db 541 CACAGCTGTGCTGTGGAGAGATGAGAGGATTAACCTGAGAGAGAGATTGGACACCC 600
QY 1449 TGTCCAGATTATGCTGCTCTTGTGCTCTTCAACAGTTGGAGAGAGCGCTTGTCTACAGT 1508
Db 601 TGTCCAGATTATGCTGCTCTTGTGCTCTTCAACAGTTGGAGAGAGCGCTTGTCTACAGT 660
QY 1509 GCTTTGATTAATTGTTTGAAGGAGAGATGAGAAATGATGAGTCTCCCTGATTTGT 1568
Db 661 GCTTTGATTAATTGTTTGAAGGAGAGATGAGAAATGATGAGTCTCCCTGATTTGT 720
QY 1569 TTTGGGAAATGTGAGAAAGAGTGCCTGCTTTGCA 1605
Db 721 TTTGGGAAATGTGAGAAAGAGTGCCTGCTTTGCA 757

RESULT 16
BX391733/c 922 bp mRNA linear EST 13-MAY-2003
LOCUS BX391733 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION Clone CS01036YNI1 3-PRIME, mRNA sequence.
ACCESSION BX391733

VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
EX391733.1	GI:30611681	EST.	Homo sapiens (human)	Mammalia; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Homnidae; Homo.	1 (bases 1 to 922)	Li, W. B., Gruber, C., Jesse, J., and Polayes, D.	Full-length cDNA libraries and normalization	Unpublished
								Contact: Genoscope
								Genoscope - Centre National de Sequencage
								Bp 191 91006 EVRI cedex - France
								Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
								Library was constructed by Life Technologies, a division of
								Invitrogen. This sequence belongs to sequence cluster 6027.r For
								more information about this cluster, see
								http://www.genoscope.cns.fr/
								cgf-bin/cluster/cgf/seq=CSOBA1021ZG05_CSO1959_1&cluster=6027.r.
								Contact : Feng Liang Email : fliang@life.com URL :
								http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
								Faraday Avenue Genoscope sequence ID : CSOBA1021ZG05_CSO1959_1.
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source								1..922
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								/mol_type="mRNA"
								/db_xref="taxon:9606"
								/clone="CSOD1036YH11"
								/tissue_type="PLACENTA COT 25-NORMALIZED"
								/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
								/note="1st strand cDNA was primed with a NotI-oligo (dT)
								primer. Five prime end enriched, double-strand cDNA was
								digested with Not I and cloned into the Not I and EcoR V
								sites of the pCMSPORT 6 vector. Library was normalized."
BASE COUNT								245 a 261 c 213 g 192 t 11 others
ORIGIN								
Query Match								27.0%; Score 698; DB 13; Length 922;
Best Local Similarity								100.0%; Pred. No. 0;
Matches								698; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1117	AGGACCTTGAAGAGGAGCCTGACTGAAGAAGATGCGCTGGGGAGCCTCGGCTGCGCCG	1178					
DB	720	AGGACCTTGAAGAGGAGCCTGACTGAAGAAGATGCGCTGGGGAGCCTCGGCTGCGCCG	661					
OY	1177	CTGCACTCTGGAGAGGAGAGATTTAGATCTGAGCAGGCTGTGGTAGATGTGCAT	1238					
DB	660	CTGCACTCTGGAGAGGAGAGATTTAGATCTGAGCAGGCTGTGGTAGATGTGCAT	601					
OY	1237	AGAAATAGCTAATTTATTTCCCCAGGTGTGCTTTAGGCGTGGCTGACCAAGCTTTCTT	1296					
DB	600	AGAAATAGCTAATTTATTTCCCCAGGTGTGCTTTAGGCGTGGCTGACCAAGCTTTCTT	541					
OY	1297	CCTACATCTTCTCCAGTAAGTTTCCCTCGGCTTGACAGCATGAGTGTGTGCATT	1356					
DB	540	CCTACATCTTCTCCAGTAAGTTTCCCTCGGCTTGACAGCATGAGTGTGTGCATT	481					
OY	1357	TGTTCACTCCCCAGGCTGTTCTCAAGCTTCAACAGTGTGCTTGGAGAGTCAAGC	1418					
DB	480	TGTTCACTCCCCAGGCTGTTCTTCCAGGCTTCAACAGTGTGCTTGGAGAGTCAAGC	421					
OY	1417	AGGTTAATCTGACAGAGAGTTTGCACACCCTGTCCAGATTATTTGGCTGCTTCCCT	1478					
DB	420	AGGTTAATCTGACAGAGAGTTTGCACACCCTGTCCAGATTATTTGGCTGCTTCCCT	361					
OY	1477	ACCACTTGGCAGACAGCCGTTGTTCTACATGCGCTTGATTAATTTGTTGAGGGAGAGA	1536					
DB	360	ACCACTTGGCAGACAGCCGTTGTTCTACATGCGCTTGATTAATTTGTTGAGGGAGAGA	301					
OY	1537	TGGAAACATGTGAGAGTCTCCCTCGATTGTTGTTGGGAAATGTGAGAAAGATGCCCT	1596					
DB	300	TGGAAACATGTGAGAGTCTCCCTCGATTGTTGTTGGGAAATGTGAGAAAGATGCCCT	241					

QY	1597	GCCTTGCAGAACCAACCTGGCAAAATGCAAAATGATTTTCCAGCAGATCTTCC	1656
Db	240	GCCTTGCAGAACCAACCTGGCAAAATGCAAAATGATTTTCCAGCAGATCTTCC	181
QY	1657	ATGGGCAATAGTAAGCTGTGCTTCACCTGTGGAGATGAAATGTTCTCTACCCGTGCA	1716
Db	180	ATGGGCAATAGTAAGCTGTGCTTCACCTGTGGAGATGAAATGTTCTCTACCCGTGCA	121
QY	1717	TTACATATGTTTAAATTCATCCAGCAGAGTGTGCTCAGCTCCTACCTCTGCGCAGGACGA	1776
Db	120	TTACATATGTTTAAATTCATCCAGCAGAGTGTGCTCAGCTCCTACCTCTGCGCAGGACGA	61
QY	1777	TTTTCATATCCCAAGATCAATTTCCCTCTCTGACGACAC	1814
Db	60	TTTTCATATCCCAAGATCAATTTCCCTCTCTGACGACAC	23
RESULT 17			
BO689483		867 bp	MRNA
LOCUS			
DEFINITION	AGENCOURT_8343875 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6248433		EST 15-JUL-2002
ACCESSION	BO689483		
VERSION	BO689483.1		GI:21814799
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Unpublished		
AUTHORS	Contact: Robert Strausberg, Ph.D.		
TITLE	Email: cgaabs-remail.nih.gov		
JOURNAL	Tissue Procurement: ATCC		
COMMENT	CDNA Library Preparation: Rubin Laboratory		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.llnl.gov		
	Plate: L1CM2388 row: e column: 10		
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	/clone="IMAGE:6248433"		
	/tissue_type="ductal carcinoma, cell line"		
	/lab_host="DH10B (phage-resistant)"		
	/clone_lib="NIH MGC 110"		
	/note="Organ: pancreas; Vector: pOTB7; Site: 1; XhoI; Site: 2; EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."		
BASE COUNT	173 a	218 c	261 g
ORIGIN			
Query Match	26.8%	Score 693;	DB 13; Length 867;
Best Local Similarity	99.9%	Pred. No. 0;	
Matches 743; Conservative	0;	Mismatches 1;	Indels 0; Gaps 0;
QY	849	CCCTGACCCGCTGGAGGGGCGAGCTTGGCATATACCCCGCAGCCGCTTCTGACCTCATC	908
Db	1	CCCTGACCCGCTGGAGGGGCGAGCTTGGCATATACCCCGCAGCCGCTTCTGACCTCATC	60
QY	909	ACTGGAGAGCTAGAGCCTGATGAGCCTTGGAGCCGATGCGCTTGTGCGACAGTGGCTCTC	968

QY 661 CATGCCGGGGCCAGAGATGCTCTGCACCC 690
 DB 681 CATGCCGGGGCCAGAGATGCTCTGCACCC 710
 RESULT 19
 LOCUS BU157365 1002 bp mRNA linear EST 04-SEP-2002
 DEFINITION AGENCOURT_6937229 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:5952261
 5', mRNA sequence.
 BU157365
 ACCESSION BU157365.1 GI:22670897
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE NIH-MGC http://mgs.nci.nih.gov/
 1 (bases 1 to 1002)
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgsbds-remail.nih.gov
 Tissue Procurement: ATCC
 Tissue Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LNC2139 row: p column: 22
 High quality sequence stop: 743.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /tissue_type="ductal carcinoma, cell line"
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 /clone_1lb="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pORF7; Site_1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAAGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH-MGC library."
 BASE COUNT 204 a 258 c 288 g 252 t
 ORIGIN
 Query Match 26.7%; Score 690; DB 13; Length 1002;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 740; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 849 CCCCTGCGGTGAGAGGCGAGCTTTGCCATGACCCCGCAGCGGCTTCTGACCTATC 908
 DB 1 CCCCTGCGGTGAGAGGCGAGCTTTGCCATGACCCCGCAGCGGCTTCTGACCTATC 60
 QY 909 ACCTGGAGACTAGAGCTGATGAGAGCTTGAACCGATGCGCTTGTGCCAGTGGCTCTC 968
 DB 61 ACCTGGAGACTAGAGCTGATGAGAGCTTGAACCGATGCGCTTGTGCCAGTGGCTCTC 120
 QY 969 TGGCAGCCCCCAGCAGCAGCTGTGTATGTGTGAAACCGACCTCTGTGGGAGCCGT 1028
 DB 121 TGGCAGCCCCCAGCAGCAGCTGTGTATGTGTGAAACCGACCTCTGTGGGAGCCGT 180
 QY 1029 GACCAAGATGGGAGATCTCTGTGCGCCAGAGAGTCCCGCATGATGATGATGATGATG 1088
 DB 181 GACCAAGATGGGAGATCTCTGTGCGCCAGAGAGTCCCGCATGATGATGATGATGATG 240

QY 1089 TTGATGAGAGAGTGGCGCCAGAGCTGAGAGACCTTGAGAGAGAGGCTGATGAAAGATG 1148
 DB 241 TTGATGAGAGAGTGGCGCCAGAGCTGAGAGACCTTGAGAGAGAGGCTGATGAAAGATG 300
 QY 1149 GCAGCTGGGAGAGCTGCGGCTCGCGCTCGCGCTGCGCTGCGCTGCGGAGGAGAGATTTAGATC 1208
 DB 301 GCAGCTGGGAGAGCTGCGGCTCGCGCTCGCGCTGCGCTGCGGAGGAGAGATTTAGATC 360
 QY 1209 TGGACCAAGCTGTGGTATGATGCAATGAAATAGCTAATTTATTTCCCGAGGTGTG 1268
 DB 361 TGGACCAAGCTGTGGTATGATGCAATGAAATAGCTAATTTATTTCCCGAGGTGTG 420
 QY 1269 CTTAGACGCGGCTGACCAAGGCTTCTTCTTCAATCTTCTTCCAGTAATTTCCCTCT 1328
 DB 421 CTTAGACGCGGCTGACCAAGGCTTCTTCTTCAATCTTCTTCCAGTAATTTCCCTCT 480
 QY 1329 GAGCTTACAGCATGAGAGTGTGTGCAATTTGTGAGTCTCCCGAGGCTTCTTCCAGGCTT 1388
 DB 481 GAGCTTACAGCATGAGAGTGTGTGCAATTTGTGAGTCTCCCGAGGCTTCTTCCAGGCTT 540
 QY 1389 CACAGTCTGGTGTGGAGAGATCAGGAGGTTAACTGACAGAGCACTTGGCCACCC 1448
 DB 541 CACAGTCTGGTGTGGAGAGATCAGGAGGTTAACTGACAGAGCACTTGGCCACCC 600
 QY 1449 TGTCCAGATTTATTTGCTGCTTTCCTTACCAAGTGGCAGACAGCCGTTTCTTCAATG 1508
 DB 601 TGTCCAGATTTATTTGCTGCTTTCCTTACCAAGTGGCAGACAGCCGTTTCTTCAATG 660
 QY 1509 GCTTTGATATTTGTTGAGAGGAGAGATGAAACAGTGGAGTCCCTGATGATG 1568
 DB 661 GCTTTGATATTTTGTGAGAGGAGAGATGAAACAGTGGAGTCCCTGATGATG 720
 QY 1569 TTGGGGAAATGTGAGAGAA 1589
 DB 721 TTGGGGAAATGTGAGAGAA 741
 RESULT 20
 LOCUS BQ897122 906 bp mRNA linear EST 16-AUG-2002
 DEFINITION AGENCOURT_8074293 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6085612
 5', mRNA sequence.
 BQ897122
 ACCESSION BQ897122.1 GI:22289136
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE NIH-MGC http://mgs.nci.nih.gov/
 1 (bases 1 to 906)
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgsbds-remail.nih.gov
 Tissue Procurement: ATCC
 Tissue Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LNC2139 row: e column: 05
 High quality sequence stop: 607.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6085612"
 /tissue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NIH_MGC_110"

/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGG(5). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

BASE COUNT
ORIGIN

183 a 227 c 271 g 225 t

Query Match 26.5%; Score 685; DB 13; Length 906;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 735; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 849 CCCCTGCCGTGGAGGGGAGCTTTGGCCATGACCCCGCAGCGCGCTTCTGACCTCATC 908
D 1 CCCCTGCCGTGGAGGGGAGCTTTGGCCATGACCCCGCAGCGCGCTTCTGACCTCATC 60
QY 909 ACCTGGAGCTAGAGCTGATGAGAGCTTGAACCGATGCTTGTGCGCATGAGCTCTC 968
D 61 ACCTGGAGCTAGAGCTGATGAGAGCTTGAACCGATGCTTGTGCGCATGAGCTCTC 120
QY 969 TGGCAGCCCAACCCCAACAGCTGCTGATGATGATGATGATGATGATGATGATGATG 1028
D 121 TGGCAGCCCAACCCCAACAGCTGCTGATGATGATGATGATGATGATGATGATGATG 180
QY 1029 GACCAAGATGGAGAGATCTGCTGCCCAAGAGAGTCCCGATGATGATGATGATGATG 1088
D 181 GACCAAGATGGAGAGATCTGCTGCCCAAGAGAGTCCCGATGATGATGATGATGATGATG 240
QY 1089 TTGATGAGAGAGTGGCCAGAGAGCTGAGAGAGCTTGAAGAGAGCTGATGAGAGATG 1148
D 241 TTGATGAGAGAGTGGCCAGAGAGCTGAGAGAGCTTGAAGAGAGCTGATGAGAGATG 300
QY 1149 GCGCTGGGGAGAGCTGCGGCTGCGCGCTGCACTGCTGAGAGAGAGAGATTTAGATC 1208
D 301 GCGCTGGGGAGAGCTGCGGCTGCGCGCTGCACTGCTGAGAGAGAGAGATTTAGATC 360
QY 1209 TGGACCAAGCTGTGGGTAGATGTCATAGAAATAGCTAATTATTTCGCCAGGTGTG 1268
D 361 TGGACCAAGCTGTGGGTAGATGTCATAGAAATAGCTAATTATTTCGCCAGGTGTG 420
QY 1269 CTTTAGGCGTGGGCTGACCAAGCTTCTCTCATATTTCTCCAGTAGTTCCCTCT 1328
D 421 CTTTAGGCGTGGGCTGACCAAGCTTCTCTCATATTTCTCCAGTAGTTCCCTCT 480
QY 1329 GCGCTGACAGCATGAGGTGTGTGCAATTTGTCAGTCTCCCGAGGCTGTTCACAGCTT 1388
D 481 GCGCTGACAGCATGAGGTGTGTGCAATTTGTCAGTCTCCCGAGGCTGTTCACAGCTT 540
QY 1389 CAGAGTCTGTGCTTGGAGAGTCAAGAGAGGTTAACTGACAGAGACATTTGCCACCC 1448
D 541 CAGAGTCTGTGCTTGGAGAGTCAAGAGAGGTTAACTGACAGAGACATTTGCCACCC 600
QY 1449 TGTCCAGATTATTTGGCTTTGCTCTTACCAAGTTGGCAGACAGCGTTGTCTTCAATG 1508
D 601 TGTCCAGATTATTTGGCTTTGCTCTTACCAAGTTGGCAGACAGCGTTGTCTTCAATG 660
QY 1509 GCTTTGATTAATTTTGGAGAGAGAGATGGAACAATGTGAGTCTCCCTCTGATGTGT 1568
D 661 GCTTTGATTAATTTTGGAGAGAGAGATGGAACAATGTGAGTCTCCCTCTGATGTGT 720
QY 1569 TTTGGGAAATGTGA 1584
D 721 TTTGGGAAATGTGA 736

RESULT 21
BU174805 841 bp mRNA linear EST 04-SEP-2002
LOCUS BU174805
DEFINITION AGENCOURT 7974830 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6082014
5', mRNA sequence.

ACCESSION BU174805
VERSION BU174805.1 GI:22688776
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>
AUTHORS 1 (bases 1 to 841)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LCM2309 row: 0 column: 07
High quality sequence stop: 649.

FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6082014"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_110"

/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGG(5). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

BASE COUNT 168 a 210 c 254 g 209 t

Query Match 26.5%; Score 684; DB 13; Length 841;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 734; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 849 CCCCTGCCGTGGAGGGGAGCTTTGGCCATGACCCCGCAGCGCGCTTCTGACCTCATC 908
D 1 CCCCTGCCGTGGAGGGGAGCTTTGGCCATGACCCCGCAGCGCGCTTCTGACCTCATC 60
QY 909 ACCTGGAGCTAGAGCTGATGAGAGCTTGAACCGATGCTTGTGCGCATGAGCTCTC 968
D 61 ACCTGGAGCTAGAGCTGATGAGAGCTTGAACCGATGCTTGTGCGCATGAGCTCTC 120
QY 969 TGGCAGCCCAACCCCAACAGCTGCTGATGATGATGATGATGATGATGATGATGATG 1028
D 121 TGGCAGCCCAACCCCAACAGCTGCTGATGATGATGATGATGATGATGATGATGATG 180
QY 1029 GACCAAGATGGAGAGATCTGCTGCCCAAGAGAGTCCCGATGATGATGATGATGATG 1088
D 181 GACCAAGATGGAGAGATCTGCTGCCCAAGAGAGTCCCGATGATGATGATGATGATG 240
QY 1089 TTGATGAGAGAGTGGCCAGAGAGCTGAGAGAGCTTGAAGAGAGCTGATGAGAGATG 1148
D 241 TTGATGAGAGAGTGGCCAGAGAGCTGAGAGAGCTTGAAGAGAGCTGATGAGAGATG 300
QY 1149 GCGCTGGGGAGAGCTGCGGCTGCGCGCTGCACTGCTGAGAGAGAGAGATTTAGATC 1208
D 301 GCGCTGGGGAGAGCTGCGGCTGCGCGCTGCACTGCTGAGAGAGAGAGATTTAGATC 360
QY 1209 TGGACCAAGCTGTGGGTAGATGTCATAGAAATAGCTAATTATTTCGCCAGGTGTG 1268
D 361 TGGACCAAGCTGTGGGTAGATGTCATAGAAATAGCTAATTATTTCGCCAGGTGTG 420

QY 1269 CTTTAGGGGCTGGGCTGACACGAGCTTCTCTACATCTTCTCCAGTAGTTCCCTCT 1328
DB 421 CTTTAGGGGCTGGGCTGACACGAGCTTCTCTACATCTTCTCCAGTAGTTCCCTCT 480
QY 1329 GGCTTGACAGCATGAGAGTGTGTGATTTGTTCACTGCCAGGCTGTCTCCAGGCTT 1388
DB 481 GGCTTGACAGCATGAGAGTGTGTGATTTGTTCACTGCCAGGCTGTCTCCAGGCTT 540
QY 1389 CACAGCTGTGTGTGGAGAGTCAAGGAGGTTAACTGACAGAGAGTTGGACACCC 1448
DB 541 CACAGCTGTGTGTGGAGAGTCAAGGAGGTTAACTGACAGAGAGTTGGACACCC 600
QY 1449 TGTCCAGATTATGCTGCTTGTCTCTACACAGTTGGACAGAGCGTTGTTCTACATG 1508
DB 601 TGTCCAGATTATGCTGCTTGTCTCTACACAGTTGGACAGAGCGTTGTTCTACATG 660
QY 1509 GCTTTGATTAATTTGTTGAGGGGAGAGATGAAACAATGTGAGTCTCCCTGATTTG 1568
DB 661 GCTTTGATTAATTTGTTGAGGGGAGAGATGAAACAATGTGAGTCTCCCTGATTTG 720
QY 1569 TTTGGGGAATGTGG 1583
DB 721 TTTGGGGAATGTGG 735

RESULT 22
B0686534 877 bp mRNA linear EST 15-JUL-2002
LOCUS AGENCOURT 8034689 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6207169
DEFINITION 5', mRNA sequence.
ACCESSION B0686534
VERSION B0686534.1 GI:21811850
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@rs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LNCM2362 row: n column: 02
High quality sequence stop: 692.
Location/Qualifiers
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/organism="Homo sapiens"
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/clone="IMAGE:6207169"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_11b="NIH_MGC_110"
/note="Organ: pancreas; Vector: pORF7, Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library." 1 others

BASE COUNT 179 a 213 c 265 g 219 t 1 others
ORIGIN

Query Match 26.5%; Score 684; DB 13; Length 877;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 734; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 849 CCCCTGCCCTGGAGAGGCGAGCTTTGCGATGACACCCCGACCGGCTTCTGACCTTCATC 908
DB 1 CCCCTGCCCTGGAGAGGCGAGCTTTGCGATGACACCCCGACCGGCTTCTGACCTTCATC 60
QY 909 ACCGTGAGAGCTAGAGCCTGATGAGCCTTGAACCAATGACCTTGTGCTGACCTCTC 968
DB 61 ACCGTGAGAGCTAGAGCCTGATGAGCCTTGAACCAATGACCTTGTGCTGACCTCTC 120
QY 969 TGGCAGCCCAACAGCCCAAGCCTGTGTATGTGTGCAAGCCACTTCTGTGGGAGCCCT 1028
DB 121 TGGCAGCCCAACAGCCCAAGCCTGTGTATGTGTGCAAGCCACTTCTGTGGGAGCCCT 180
QY 1029 GACCAAGATGGGAGAGTCTGCTGCCAGAGAGTCCCGATGATGATGATGAGTGGCAGC 1088
DB 181 GACCAAGATGGGAGAGTCTGCTGCCAGAGAGTCCCGATGATGATGATGAGTGGCAGC 240
QY 1089 TTCATGAGAGAGTGTGCGCAAGAGCTGAGAGACCTGAGAGAGCCTGACTGAAGATG 1148
DB 241 TTCATGAGAGAGTGTGCGCGCAAGAGCTGAGAGACCTGAGAGAGCCTGACTGAAGATG 300
QY 1149 GCGCTGGGGAGAGCCTGCGGCTGCGCGCGCTGCACTGCTGGGAGGGAGAGATTAGATC 1208
DB 301 GCGCTGGGGAGAGCCTGCGGCTGCGCGCGCTGCACTGCTGGGAGGGAGAGATTAGATC 360
QY 1209 TGACACAGGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTATTTCCAGAGTGTG 1268
DB 361 TGACACAGGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTATTTCCAGAGTGTG 420
QY 1269 CTTTAGGCGTGGGTGACCAAGGCTTCTCTACATCTTCTCCAGTAATTTCCCTCT 1328
DB 421 CTTTAGGCGTGGGTGACCAAGGCTTCTCTACATCTTCTCCAGTAATTTCCCTCT 480
QY 1329 GAGCTTGACAGCATGAGAGTGTGTGATTTGTTCACTGCCAGGCTGTCTCCAGGCTT 1388
DB 481 GAGCTTGACAGCATGAGAGTGTGTGATTTGTTCACTGCCAGGCTGTCTCCAGGCTT 540
QY 1389 CACAGCTGTGTGTGGAGAGTCAAGGAGGTTAACTGACAGAGAGTTGGACACCC 1448
DB 541 CACAGCTGTGTGTGGAGAGTCAAGGAGGTTAACTGACAGAGAGTTGGACACCC 600
QY 1449 TGTCCAGATTATGCTGCTTGTCTCTACACAGTTGGACAGAGCGTTGTTCTACATG 1508
DB 601 TGTCCAGATTATGCTGCTTGTCTCTACACAGTTGGACAGAGCGTTGTTCTACATG 660
QY 1509 GCTTTGATTAATTTGTTGAGGGGAGAGATGAAACAATGTGAGTCTCCCTGATTTG 1568
DB 661 GCTTTGATTAATTTGTTGAGGGGAGAGATGAAACAATGTGAGTCTCCCTGATTTG 720
QY 1569 TTTGGGGAATGTGG 1583
DB 721 TTTGGGGAATGTGG 735

RESULT 23
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LOCUS AGENCOURT 8345155 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6250117
DEFINITION 5', mRNA sequence.
ACCESSION B0686811
VERSION B0686811.1 GI:21812127
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LNCM2392 row: k column: 14
 High quality sequence stop: 688.
 Location/Qualifiers

FEATURES

source

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/clone_id="NIH_MGC_110"
/note="Organ: pancreas; Vector: pOTB7; Site:1: XhoI;
Site:2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

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BASE COUNT

183 a 223 c 273 g 236 t

Query Match 26.5%; Score 684; DB 13; Length 915;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;

Matches 734; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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909 ACCCTGGAGGTAGAGCTGTATGAGACCTTGACCGATCCCTGTGCGCATGCTCCCTC 968
61 ACCCTGGAGGTAGAGCTGTATGAGACCTTGACCGATCCCTGTGCGCATGCTCCCTC 120
969 TGGCAGCCCCAGCCAGCCAGCTGTATGTATGTATGTATGTATGTATGTATGTATGTAT 1028
121 TGGCAGCCCCAGCCAGCCAGCTGTATGTATGTATGTATGTATGTATGTATGTATGTAT 180
1029 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGGTCCCGATGATGATGAGTTGGCAGC 1088
181 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGGTCCCGATGATGATGAGTTGGCAGC 240
1089 TTCTATGAGAGGTGACCCAGAGAGCTGAGAGACCTTGAGAGAGAGCTGATGAAGATG 1148
241 TTCTATGAGAGGTGACCCAGAGAGCTGAGAGACCTTGAGAGAGAGCTGATGAAGATG 300
1149 GCGCTGGGGAGAGCTTGGGCTGCCCGCCGCTGCACTGCTGGAGAGAGAGATTAGATC 1208
301 GCGCTGGGGAGAGCTTGGGCTGCCCGCCGCTGCACTGCTGGAGAGAGAGATTAGATC 360
1209 TGGACAGAGCTGTGGGTAGATGTGCAATAGAAATAGTAATTTATTTCCCAAGTGTG 1268
361 TGGACAGAGCTGTGGGTAGATGTGCAATAGAAATAGTAATTTATTTCCCAAGTGTG 420
1269 CTTTAGGCGTGGGCTGACAGAGCTTCTCTCAATCTTCTTCCCAAGTGTGCTCCCTCT 1328
421 CTTTAGGCGTGGGCTGACAGAGCTTCTCTCAATCTTCTTCCCAAGTGTGCTCCCTCT 480
1329 GCGCTGACAGATGAGGTGTGTGCAATTTGTAGAGCTCCCGCAGAGGCTTCCAGAGCTT 1388
481 GCGCTGACAGATGAGGTGTGTGCAATTTGTAGAGCTCCCGCAGAGGCTTCCAGAGCTT 540
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Db 541 CACAGTCTGTGCTTGGAGAGTCAAGCAGAGGTTAACTGACAGAGAGATTGGCACCCC 600

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Qy 1509 GCTTGTATTAATTTGTTGAGGGAGAGATGGAACAATGTGAGTCTCCCTGTATTGCT 1568

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Qy 1569 TTTGGGAAATGTGG 1583

Db 721 TTTGGGAAATGTGG 735

RESULT 24

B0690443

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LNCM2395 row: h column: 14
 High quality sequence stop: 683.
 Location/Qualifiers

FEATURES

source

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/clone_id="NIH_MGC_110"
/note="Organ: pancreas; Vector: pOTB7; Site:1: XhoI;
Site:2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

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BASE COUNT

192 a 241 c 285 g 232 t 2 others

ORIGIN

Query Match 26.5%; Score 684; DB 13; Length 952;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;

Matches 734; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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849 CCCCTGCCCTGAGAGGGGAGAGCTTTGGCATGAGCCCGCCAGCCGCTTGTGACCTCATC 908
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909 ACCCTGGAGGTAGAGCTGTATGAGACCTTGACCGATCCCTGTGCGCATGCTCCCTC 968
61 ACCCTGGAGGTAGAGCTGTATGAGACCTTGACCGATCCCTGTGCGCATGCTCCCTC 120

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QY 969 TGCCAGCCCCCAGCCAGAGAGCTGGTGTATGTGTCAAGCCGACCTTGTGGGGAGCCGT 1028
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 QY 1029 GACCAAGATGGGAGATCTCTGTCCAGAGAGTCCCGATGAGTATGAAGTTGGCAGC 1088
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 Db 421 CTTTGAAGGCTGGGCTGAGAGAGCTTCTCTACATCTTCCAGTAAAGTTCCCTCT 480
 QY 1329 GCGTTGACAGCATGAGTGTGTGTGCAATTTGTCAAGTCCCGAGGCTTTCTCAAGCTT 1388
 Db 481 GCGTTGACAGCATGAGTGTGTGTGCAATTTGTCAAGTCCCGAGGCTTTCTCAAGCTT 540
 QY 1389 CACAGCTGTGTCTTGGGAGAGTCAAGAGGAGTAACTGAGAGAGAGTGTGACACCC 1448
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 QY 1509 GCTTTGATTAATTTGTTGAGGGAGAGAGATGAGAAACAATGTGAGTCCCTGTGTTGTT 1568
 Db 661 GCTTTGATTAATTTGTTGAGGGAGAGAGATGAGAAACAATGTGAGTCCCTGTGTTGTT 720
 QY 1569 TTTGGGGAAATGTG 1583
 Db 721 TTTGGGGAAATGTG 735

RESULT 25
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 LOCUS BQ687864
 DEFINITION AGENCOURT 8346023 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6250987
 5', mRNA sequence.
 ACCESSION BQ687864
 VERSION BQ687864.1 GI:21813180
 SOURCE EST
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: c9abds-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LNCM2394 row: 0 column: 20
 High quality sequence stop: 650.

FEATURES
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 /clone_id="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pORF7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming;
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH-MGC Library." 1 others

BASE COUNT 181 a 222 c 267 g 227 t 1 others
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Query Match 26.2%; Score 678; DB 13; Length 898;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 728; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 849 CCCCCTGCGGTGGAGGGGAGAGCTTGGCATGACCCCGCAGCGGCTTGTGACCTCAGC 908
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 Db 61 ACCTGGAGAGTAGAGCTGATGAGAGCTTGAACCAATGCCCTTGTGCAATGGCTCTC 120
 QY 969 TGCCAGCCCCCAGCCAGAGAGCTGTGTATGTGTGAAGCCAGCTTGTGGGGAGAGCGT 1028
 Db 121 TGCCAGCCCCCAGCCAGAGAGCTGTGTATGTGTGAAGCCAGCTTGTGGGGAGAGCGT 180
 QY 1029 GACCAAGATGGGAGATCTCTGCTCCAGAGAGTCCCGATGAGTATGAAGTTGGCAGC 1088
 Db 181 GACCAAGATGGGAGATCTCTGCTCCAGAGAGTCCCGATGAGTATGAAGTTGGCAGC 240
 QY 1089 TTCATGGAGAGAGTGGCCAGAGAGCTGAGAGAGCTGATGAGAGAGTGTGAGAGT 1148
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 QY 1149 GCGCTGGGAGAGCTGCGGCTCCGCGCTGCACTGTGGAGGGGAAAGATTAGATC 1208
 Db 301 GCGCTGAGAGAGCTGCGGCTCCGCGCTGCACTGTGGAGGGGAAAGATTAGATC 360
 QY 1209 TGACACAGAGCTGGGTATGATGTGCAATGAAATGCTAATTTATTTCCAGAGTGTG 1268
 Db 361 TGACACAGAGCTGGGTATGATGTGCAATGAAATGCTAATTTATTTCCAGAGTGTG 420
 QY 1269 CTTTGAAGGCTGGGCTGAGAGAGCTTCTCTACATCTTCCAGTAAAGTTCCCTCT 1328
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 QY 1329 GCGTTGACAGCATGAGTGTGTGTGCAATTTGTCAAGTCCCGAGGCTTTCTCAAGCTT 1388
 Db 481 GCGTTGACAGCATGAGTGTGTGTGCAATTTGTCAAGTCCCGAGGCTTTCTCAAGCTT 540
 QY 1389 CACAGCTGTGTCTTGGGAGAGTCAAGAGGAGTAACTGAGAGAGAGCTTGTGCCACCC 1448
 Db 541 CACAGCTGTGTCTTGGGAGAGTCAAGAGGAGTAACTGAGAGAGAGCTTGTGCCACCC 600
 QY 1449 TGTCCAGATTAATGTGCTGCTTTGCTCTACAGATTTGGCAGACGCTTTGTTCAATG 1508
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 QY 1509 GCTTTGATTAATTTGTTGAGGGAGAGAGATGAGAAACAATGTGAGTCCCTGTGTTGTT 1568
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 QY 1569 TTTGGGGAA 1577

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Db      721 TTTGGGGA 729
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RESULT 26
LOCUS   BUI46060
DEFINITION AGENCOURT_8074271 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6085826
5', mRNA sequence.
ACCESSION BUI46060
VERSION   BUI46060.1 GI:22659592
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 893)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgabbs-remail.nih.gov
           Tissue Procurement: ATCC
           cDNA Library Preparation: Rubin Laboratory
           DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LNL at:
           http://image.llnl.gov
           Plate: LHCW2319 row: n column: 03
           High quality sequence stop: 644.
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               Site 2: EcoRI; cDNA made by oligo-dT priming.
               Directionally cloned into EcoRI/XhoI sites using the
               following 5' adaptor: GGCACGAG(G). Library constructed by
               Ling Hong in the Laboratory of Gerald M. Rubin (University
               of California, Berkeley) using Zap-cDNA synthesis kit
               (Stratagene) and Superscript II RT (Life Technologies).
               Note: this is a NIH MGC library."
BASE COUNT 179 a 225 c 269 g 220 t
ORIGIN
Query Match 26.1%; Score 676; DB 13; Length 893;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 726; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

849 CCCCTCCCGGAGGCGAGCTTGGCATGACCCCGCAGCCGGCTTGAACCTCATC 908
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909 ACCTGGAGCTAGAGCTGATGAGACCTTGACACCGATGCCCTTGCGCACTGCTTCC 968
Db 61 ACCTGGAGCTAGAGCTGATGAGACCTTGACACCGATGCCCTTGCGCACTGCTTCC 120

969 TGGCAGCCCCCAGCAGCAGCTGTGATGTGCGAAGCCGACCTTCGTGGGAGACCGT 1028
Db 121 TGGCAGCCCCCAGCAGCAGCTGTGATGTGCGAAGCCGACCTTCGTGGGAGACCGT 180

1029 GACCAAGATGGGAGATCTGTGCTGCCAGAGAGGTCCCGATGATGATGAAGTTGGACG 1088
Db 181 GACCAAGATGGGAGATCTGTGCTGCCAGAGAGGTCCCGATGATGATGAAGTTGGACG 240

1089 TTGATGAGAGGAGTGGGCGCAGAGCTGAGAGACTGTGAGAGGAGCTGATGAAGATG 1148

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Db      241 TTGATGAGAGAGTGTCCGCGCAGAGCTGAGAGACCTGAGAGAGACCTGACTGAAGAGATG 300
Qy      1149 GCGCTGGGAGAGCTGTGCGGCTGCGCGCTGCACTGCTGGAGGGAGAGATTATGATC 1208
Db      301 GCGCTGAGGAGAGCTGTGCGGCTGCGCGCTGCACTGCTGGAGGGAGAGATTATGATC 360
Qy      1209 TGGACAGAGCTGTGGGTGATGTGCAATAGAAATAGCTATTTATTTCCAGAGTGTG 1268
Db      361 TGGACAGAGCTGTGGGTGATGTGCAATAGAAATAGCTATTTATTTCCAGAGTGTG 420
Qy      1269 CTTTAAAGGCTGGGCTGACACAGCTTTCTTCTACATCTTCTTCCAGTAAGTTTCCCTCT 1328
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Qy      1329 GCGTTGACAGATAGAGTGTGTGATTTGTACAGTCTCCCGCAGGCTGTTCACAGCTT 1388
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Qy      1389 CACAGTCTGTGCTTGGAGAGATCAGGAGGATTAACTGACAGAGAGATTGGCACCC 1448
Db      541 CACAGTCTGTGCTTGGAGAGATCAGGAGGATTAACTGACAGAGAGATTGGCACCC 600
Qy      1449 TGTCCAGATTATTTGGCTCTTGTGCTTACACAGTGTGACAGACGCGTTTGTCTACATG 1508
Db      601 TGTCCAGATTATTTGGCTCTTGTGCTTACACAGTGTGACAGACGCGTTTGTCTACATG 660
Qy      1509 GCTTGAATATTTGTTTGAAGGAGAGAGATGAAACAATGTGAGTCTTCTCTGATTTG 1568
Db      661 GCTTGAATATTTGTTTGAAGGAGAGAGATGAAACAATGTGAGTCTTCTCTGATTTG 720
Qy      1569 TTTGGGG 1575
Db      721 TTTGGGG 727

RESULT 27
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DEFINITION AGENCOURT_8111705 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6251806
5', mRNA sequence.
ACCESSION BO691090
VERSION   BO691090.1 GI:21816406
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 901)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgabbs-remail.nih.gov
           Tissue Procurement: ATCC
           cDNA Library Preparation: Rubin Laboratory
           DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LNL at:
           http://image.llnl.gov
           Plate: LHCW2397 row: a column: 23
           High quality sequence stop: 601.
           Location/Qualifiers
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               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="IMAGE:6251806"
               /tissue_type="ductal carcinoma, cell line"
               /lab_host="DH10B (phage-resistant)"
               /clone_1lb="NIH MGC 110"
               /note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
               Site 2: EcoRI; cDNA made by oligo-dT priming."

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 Db 465 TACCTCCAGCTATGACATGAGACCAACACAGACAGAGGTTGGAATATACCATCC 524
 QY 481 ATGTGACCGAGAAATTCACAGATACCAACACAGACTGACAAATGCTCTTTTCA 540
 Db 525 ATGTGACCGAGAAATTCACAGATACCAACACAGACTGACAAATGCTCTTTTCA 584
 QY 541 AGACAGTTATCATCTGTGGAGACGAGAGGAGAGAGAGAGAGAGAGAGAGAGAG 600
 Db 585 AGACAGTTATCATCATCTGTGGAGACGAGAGGAGAGAGAGAGAGAGAGAGAGAG 644
 QY 601 AGAGAGAGCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 Db 645 AGAGAGAGCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 704
 QY 661 CATGCCGGGGCCCA 673
 Db 705 CATGCCGGGGCCCA 717

RESULT 29
 BQ888956 869 bp mRNA linear EST 16-AUG-2002
 LOCUS AGENCOURT_8049821 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6083894
 DEFINITION 5', mRNA sequence.

ACCESSION BQ888956
 VERSION BQ888956
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 869)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM2314 row: m column: 15
 High quality sequence stop: 645.

FEATURES

Location/Qualifiers
 1..869
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6083894"
 /tissue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOPB7; Site_1: XhoI;
 Site_2: EcoRI; CDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

BASE COUNT 176 a 219 c 262 g 212 t

ORIGIN

Query Match 26.0%; Score 672; DB 13; Length 869;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 849 CCCCTGCCGTGGAGGGCGAGCTTTGCCATGACCCCGCCAGCCGCTTCTGAGCTCATC 908
 Db 1 CCCCTGCCGTGGAGGGCGAGCTTTGCCATGACCCCGCCAGCCGCTTCTGAGCTCATC 960
 QY 909 ACTTGGAGCTTGAAGCTTGAAGAGCTTGGACCGATGCGCTTGTGCGAGCTCTC 968
 Db 61 ACTTGGAGCTTGAAGCTTGAAGAGCTTGGACCGATGCGCTTGTGCGAGCTCTC 120
 QY 969 TGCACGCCCCACAGCCACAGAGCTGTGTATGTGTGCAAGCCGACTTGTGGAGAGCT 1028
 Db 121 TGCACGCCCCACAGCCACAGAGCTGTGTATGTGTGCAAGCCGACTTGTGGAGAGCT 180
 QY 1029 GACCAAGATGGGAGATCTCTGCTGCCAAGAGAGCTCCCGATGAGATGAAAGTTGGACAG 1088
 Db 181 GACCAAGATGGGAGATCTCTGCTGCCAAGAGAGCTCCCGATGAGATGAAAGTTGGACAG 240
 QY 1089 TTCATGAGAGAGGTGGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1148
 Db 241 TTCATGAGAGAGGTGGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 QY 1149 GCGCTGGGGAGAGCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1208
 Db 301 GCGCTGGGGAGAGCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 QY 1209 TGGACCAAGCTGTGGGAGATGTGCAATGAAATGAAATGAAATGAAATGAAATGAAAT 1268
 Db 361 TGGACCAAGCTGTGGGAGATGTGCAATGAAATGAAATGAAATGAAATGAAATGAAAT 420
 QY 1269 CTTTAGGCGTGGGCTGACCAAGGCTTCTTCTTACATCTTCTTCCAGTAACTTCCCTCT 1328
 Db 421 CTTTAGGCGTGGGCTGACCAAGGCTTCTTCTTACATCTTCTTCCAGTAACTTCCCTCT 480
 QY 1329 GCGTTTACACATGAGGTGTGTGCAATGAAATGAAATGAAATGAAATGAAATGAAAT 1388
 Db 481 GCGTTTACACATGAGGTGTGTGCAATGAAATGAAATGAAATGAAATGAAATGAAAT 540
 QY 1389 CACAGTCTGTGTGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1448
 Db 541 CACAGTCTGTGTGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
 QY 1449 TGTCCAGATTTATGCGCTGCTTGTGCTTACAGTGGCAAGAGCGCTTGTCTACATG 1508
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 QY 1509 GCTTGAATATTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1568
 Db 661 GCTTGAATATTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 QY 1569 TTT 1571
 Db 721 TTT 723

RESULT 30
 BUI96397 1043 bp mRNA linear EST 04-SEP-2002
 LOCUS AGENCOURT_6910865 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:5952243
 DEFINITION 5', mRNA sequence.

ACCESSION BUI96397
 VERSION BUI96397
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 1043)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory

FEATURES

source

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1CM2139 row: P column: 04
 High quality sequence stop: 599.
 Location/Qualifiers
 1. 1043

BASE COUNT

207 a 264 c 308 g 263 t 1 others

ORIGIN

Query Match 26.0%; Score 672; DB 13; Length 1043;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

849 CCCCTGCCCCGAGAGGAGAGCTTGGCCATACCCCGCAGCCGCTTGGACCTATC 908
 Db 1 CCCCTGCCCCGAGAGGAGAGCTTGGCCATACCCCGCAGCCGCTTGGACCTATC 60
 909 ACCTGGGAGCTAGAGCTGATGAGACCTTGAACCGATGCCCTTGGCCAGTGGCCTCTC 968
 Db 61 ACCTGGGAGCTAGAGCTGATGAGACCTTGAACCGATGCCCTTGGCCAGTGGCCTCTC 120
 969 TGGCAGCCCCCAGACGACAGCTGATGATGTCAGACGACCTTGGGGGAGCCGT 1028
 Db 121 TGGCAGCCCCCAGACGACGCTGATGATGTCAGACGACCTTGGGGGAGCCGT 180
 1029 GACCAAGATGGGAGAGTCTGCTGCGCCAGAGAGTCCCGATGAGTATGAATTGGACG 1088
 Db 181 GACCAAGATGGGAGAGTCTGCTGCGCCAGAGAGTCCCGATGAGTATGAATTGGACG 240
 1089 TTCATGGAGAGAGTGGCCAGAGAGCTGAGAGAGCTTGGAGAGAGCTGACGAAGAAGATG 1148
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 1149 GGCCTGGGAGAGAGCTGCGCTGCGCCGCTGACATGCTGGAGGGGAGAGATTAGATC 1208
 Db 301 GGCCTGGGAGAGAGCTGCGCTGCGCCGCTGACATGCTGGAGGGGAGAGATTAGATC 360
 1209 TGGACCAAGCTGTGGTAAATGTCATTAAGAAATAGCTAATTTATTTCCCGAGGTGTG 1268
 Db 361 TGGACCAAGCTGTGGTAAATGTCATTAAGAAATAGCTAATTTATTTCCCGAGGTGTG 420
 1269 CTTTAGGCGGAGCTAGACGAGCTTCTCTACATCTTCTCCAGTAGAGTTCCCTCT 1328
 Db 421 CTTTAGGCGGAGCTAGACGAGCTTCTCTACATCTTCTCCAGTAGAGTTCCCTCT 480
 1329 GAGCTTGAACAGATGAGGTGTGTGCAATTTGTTCACTTCCCGAGGTGTGTTCACAGCTT 1388
 Db 481 GAGCTTGAACAGATGAGGTGTGTGCAATTTGTTCACTTCCCGAGGTGTGTTCACAGCTT 540
 1389 CACAGTCTGGTGTGGAGAGTCAAGGACAGGTTAACTGACAGAGAGATTGGACACCC 1448
 Db 541 CACAGTCTGGTGTGGAGAGTCAAGGACAGGTTAACTGACAGAGAGATTGGACACCC 600
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Db 601 TGTCAGATTATTTGGCTTTGCTTACAGATTGGACAGAGCCGTTTGTTCATGATG 660
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 Db 661 GCTTGAATTAATTTTGAAGGAGAGATGAAACAATGTGAGTCTTCCCTGATTTGT 720
 QY 1569 TTT 1571
 Db 721 TTT 723

RESULT 31

BUI96968 905 bp mRNA linear EST 04-SEP-2002
 LOCUS AGENCOUNT_7974356 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6082897
 DEFINITION 5', mRNA sequence.
 BUI96968
 BUI96968.1 GI:22710952

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 905)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapsb@mail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1CM2312 row: d column: 02
 High quality sequence stop: 571.
 Location/Qualifiers

FEATURES

source

1. 905
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 /db_xref="taxon:9606"
 /clone="IMAGE:6082897"
 /tissue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOTB7; Site: 1; XhoI;
 Site 2: EcoRI; CDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

BASE COUNT 189 a 223 c 271 g 222 t

ORIGIN

Query Match 25.9%; Score 671; DB 13; Length 905;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 721; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

849 CCCCTGCCCCGAGAGGAGAGCTTGGCCATGACCCCGCAGCCGCTTGGACCTATC 908
 Db 1 CCCCTGCCCCGAGAGGAGAGCTTGGCCATGACCCCGCAGCCGCTTGGACCTATC 60
 909 ACCTGGGAGCTAGAGCTGATGAGACCTTGAACCGATGCCCTTGGCCAGTGGCCTCTC 968
 Db 61 ACCTGGGAGCTAGAGCTGATGAGACCTTGAACCGATGCCCTTGGCCAGTGGCCTCTC 120
 969 TGGCAGCCCCCAGACGACAGCTGATGATGTCAGACGACCTTGGGGGAGCCGT 1028
 Db 121 TGGCAGCCCCCAGACGACGCTGATGATGTCAGACGACCTTGGGGGAGCCGT 180

QY 1029 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGTCCCCGATGATGAAAGTTGGCAGC 1088
 Db 181 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGTCCCCGATGATGAAAGTTGGCAGC 240
 QY 1089 TTCATGAGAGAGTGGCGCCAGAGCTGAGAGACCTGAGAGAGAGCTTACTGAGAGATG 1148
 Db 241 TTCATGAGAGAGTGGCGCCAGAGCTGAGAGACCTGAGAGAGAGCTTACTGAGAGATG 300
 QY 1149 GCGCTGGGGAGCTTGGCGCTGCCCGCGCTGCACTGTGGAGGGGAAAGATTGATC 1208
 Db 301 GCGCTGAGGAGAGCTTGGCGCTGCCCGCGCTGCACTGTGGAGGGGAAAGATTGATC 360
 QY 1209 TGGACCAAGCTGTGGGTAGATGTCGAAATGAAATGCTAATTATTATTTCCAGAGTGTG 1268
 Db 361 TGGACCAAGCTGTGGGTAGATGTCGAAATGAAATGCTAATTATTATTTCCAGAGTGTG 420
 QY 1269 CTTTAAAGCGTGGGCTGACCAAGGCTTCTTCCATCATCTTCTTCCAGTAAGTTCCCTCT 1328
 Db 421 CTTTAAAGCGTGGGCTGACCAAGGCTTCTTCCATCATCTTCTTCCAGTAAGTTCCCTCT 480
 QY 1329 GCGTTGACAGCATGAGAGTGTGTCATTTGTCACGCTCCCCAGGCTGTCTCCAGGCTT 1388
 Db 481 GCGTTGACAGCATGAGAGTGTGTCATTTGTCACGCTCCCCAGGCTGTCTCCAGGCTT 540
 QY 1389 CACAGCTGCTGCTTGGAGAGATCAAGGCTTAACTGACAGAGAGCTTGGCCAGCC 1448
 Db 541 CACAGCTGCTGCTTGGAGAGATCAAGGCTTAACTGACAGAGAGCTTGGCCAGCC 600
 QY 1449 TGTCCAGATTATTGGCTGCTTGGCTCTTCCAGATTGGCAGACGCCGTTTGTCTACATG 1508
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 QY 1509 GCTTATATATTGTTGAGAGGAGAGATGAAACATGTGAGTCTCCCTGTGATTGT 1568
 Db 661 GCTTATATATTGTTGAGAGGAGAGATGAAACATGTGAGTCTCCCTGTGATTGT 720
 QY 1569 TT 1570
 Db 721 TT 722

RESULT 32
 LOCUS B0691927 912 bp mRNA linear EST 15-JUL-2002
 DEFINITION AGENCOURT 8034941 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6207089
 5', mRNA sequence.
 ACCESSION B0691927
 VERSION B0691927.1 GI:21817255
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 912)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished.
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1CM2362 row: j column: 18
 High quality sequence stop: 654.
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 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dt priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAAGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC library."

BASE COUNT 180 a 228 c 270 g 231 t 3 others
 ORIGIN

Query Match 25.9%; Score 671; DB 13; Length 912;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 721; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 849 CCCCTGCCGTGAGAGGCGAGCTTGTGCATGACCCCGCAGCCGCGCTTGTGACCTCATC 908
 Db 1 CCCCTGCCGTGAGAGGCGAGCTTGTGCATGACCCCGCAGCCGCGCTTGTGACCTCATC 60
 QY 909 ACCTGGAGCTTAAGCTGATGAGAGCTTGGACCATGCTTGTGCAATGAGCTTCTC 968
 Db 61 ACCTGGAGCTTAAGCTGATGAGAGCTTGGACCATGCTTGTGCAATGAGCTTCTC 120
 QY 969 TGGCAGCCCAAGCCACAGCTGTGTATGTGTGCAAGCCGCTTGTGAGAGCGCT 1028
 Db 121 TGGCAGCCCAAGCCACAGCTGTGTATGTGTGCAAGCCGCTTGTGAGAGCGCT 180
 QY 1029 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGTCCCCGATGATGAAAGTTGGCAGC 1088
 Db 181 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGTCCCCGATGATGAAAGTTGGCAGC 240
 QY 1089 TTCATGAGAGAGTGGCGCCAGAGCTGAGAGACCTGAGAGAGAGCTTACTGAGAGATG 1148
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 QY 1209 TGGACCAAGCTGTGGGTAGATGTCGAAATGAAATGCTAATTATTATTTCCAGAGTGTG 1268
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 QY 1269 CTTTAAAGCGTGGGCTGACCAAGGCTTCTTCCATCATCTTCTTCCAGTAAGTTCCCTCT 1328
 Db 421 CTTTAAAGCGTGGGCTGACCAAGGCTTCTTCCATCATCTTCTTCCAGTAAGTTCCCTCT 480
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 QY 1389 CACAGCTGCTGCTTGGAGAGATCAAGGCTTAACTGACAGAGAGCTTGGCCAGCC 1448
 Db 541 CACAGCTGCTGCTTGGAGAGATCAAGGCTTAACTGACAGAGAGCTTGGCCAGCC 600
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 Db 601 TGTCCAGATTATTGGCTGCTTGGCTCTTCCAGATTGGCAGACGCCGTTTGTCTACATG 660
 QY 1509 GCTTATATATTGTTGAGAGGAGAGATGAAACATGTGAGTCTCCCTGTGATTGT 1568
 Db 661 GCTTATATATTGTTGAGAGGAGAGATGAAACATGTGAGTCTCCCTGTGATTGT 720
 QY 1569 TT 1570
 Db 721 TT 722

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RESULT 33
BO888730      880 bp      mRNA      linear      EST 16-AUG-2002
LOCUS         BO888730
DEFINITION    BO888730.1 GI:22280744
5', mRNA sequence.
ACCESSION     BO888730
VERSION       BO888730.1
KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     NIH-MGC http://mgi.nci.nih.gov/.
1 (bases 1 to 880)
AUTHORS       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished
COMMENT       Email: sgabs-r@mail.nih.gov.
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM2319 row: f column: 15
High quality sequence stop: 652.
Location/Qualifiers
1..880
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6086034"
/tissue_type="ductal carcinoma, cell line"
/lab_host="NIH MGC 110"
/notes="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
BASE COUNT    176 a      221 c      266 g      217 t
ORIGIN
Query Match    25.8%; Score 668; DB 13; Length 880;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 849 CCCCTGCCGTGGAGGGGCGAGCTTTGCAATGACCCGCGAGCGGCTTGTGACCTCATC 908
DB 1 CCCCTGCCGTGGAGGGGCGAGCTTTGCAATGACCCGCGAGCGGCTTGTGACCTCATC 60
QY 909 ACCGTGGAGCTAGAGCTTATGAGAGCTTGAACCGATGCTCTTGCCAGTGGCTCTCTC 968
DB 61 ACCGTGGAGCTAGAGCTTATGAGAGCTTGAACCGATGCTCTTGCCAGTGGCTCTCTC 120
QY 969 TGGCAGCCCGACAGCCAGAGCTGTGTATGTGTGCAAGCCGACCTGTGTGGGAGCCGT 1028
DB 121 TGGCAGCCCGACAGCCAGAGCTGTGTATGTGTGCAAGCCGACCTGTGTGGGAGCCGT 180
QY 1029 GACCAAGATGGGAGATCTGTGCTGCCAGAGAGTCCCGATGATGATGATGATGATGATG 1088
DB 181 GACCAAGATGGGAGATCTGTGCTGCCAGAGAGTCCCGATGATGATGATGATGATGATG 240
QY 1089 TTATATGAGAGAGTGGGAGAGAGTGGAGAGCTTGGAGAGAGAGAGAGAGAGAGAGATG 1148
DB 241 TTATATGAGAGAGTGGGAGAGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATG 300
QY 1149 GCGCTGGGGAGAGCTGCGGCTGCGCGCTGCACTGCTGGAGAGAGAGATTTAGATC 1208
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DB 301 GCGCTGAGGAGAGCTTGGGCTGCGCGCTGCGAGCTGAGAGAGAGAGATTTAGATC 360
QY 1209 TGGACAGAGCTGTGGGTAGATGTCATAGAAATGCTAATTTATTTCCCGAGGTGTG 1268
DB 361 TGGACAGAGCTGTGGGTAGATGTCATAGAAATGCTAATTTATTTCCCGAGGTGTG 420
QY 1269 CTTTAAAGCGGTGGCTGACAGAGAGCTTCTTCAATCTTCTTCCAGTAAGTTCCCTCT 1328
DB 421 CTTTAAAGCGGTGGCTGACAGAGAGCTTCTTCAATCTTCTTCCAGTAAGTTCCCTCT 480
QY 1329 GCGTTACAGAGATGAGAGTGTGTGCAATTTGTCAGTCCCGAGAGGTGTTCACAGCTT 1388
DB 481 GCGTTACAGAGATGAGAGTGTGTGCAATTTGTCAGTCCCGAGAGGTGTTCACAGCTT 540
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DB 601 TGTCCAGATTTATTTGGCTGCTTCCCTCTACAGTTGGCAGACAGCGGTTGTCTACATG 660
QY 1509 GCTTTGATATTTGTTTGGAGAGAGATGAAACATGTGAGTCTCCTCTGATTTG 1567
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RESULT 34
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LOCUS         BU191090
DEFINITION    AGENCOURT 8074903 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6086034
5', mRNA sequence.
ACCESSION     BU191090
VERSION       BU191090.1
KEYWORDS      GI:22705074
SOURCE        EST.
ORGANISM      Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     NIH-MGC http://mgi.nci.nih.gov/.
1 (bases 1 to 887)
AUTHORS       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished
COMMENT       Contact: Robert Strausberg, Ph.D.
Email: sgabs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM2320 row: f column: 19
High quality sequence stop: 592.
Location/Qualifiers
1..887
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6086034"
/tissue_type="ductal carcinoma, cell line"
/lab_host="NIH MGC 110"
/notes="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
BASE COUNT    179 a      223 c      269 g      216 t
ORIGIN
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Query Match 25.8%; Score 668; DB 13; Length 887;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

849 CCCCTGCCCCGAGAGGAGGAGCTTTGGCATGAGCCCGCCAGCCGGCTTCTGACCTCATC 908
 1 CCCCTGCCCCGAGAGGAGGAGCTTTGGCATGAGCCCGCCAGCCGGCTTCTGACCTCATC 60

909 ACCTGGAGAGCTAGAGCTGATGAGAGCTTTGAGAGCTTGGCTTGTGCGAGTGGCTCTTC 968
 61 ACCTGGAGAGCTAGAGCTGATGAGAGCTTTGAGAGCTTGGCTTGTGCGAGTGGCTCTTC 120

969 TGCAGAGCCACAGCCAGCCAGCTGTATGTATGTGAGAGCCGACTTGTGAGGAGAGCCCT 1028
 121 TGCAGAGCCACAGCCAGCCAGCTGTATGTATGTGAGAGCCGACTTGTGAGGAGAGCCCT 180

1029 GACCAAGATGAGAGAGATCTGCTGCTGCCAGAGAGGATCCCGATGATGATGAGTTGGCAGC 1088
 181 GACCAAGATGAGAGAGATCTGCTGCTGCCAGAGAGGATCCCGATGATGATGAGTTGGCAGC 240

1089 TTCAATGAGAGAGAGAGAGCCAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1148
 241 TTCAATGAG 300

1149 GCGCTGATC 1208
 301 GCGCTGATC 360

1209 TGAG 1268
 361 TGAG 420

1269 CTTAG 1328
 421 CTTAG 480

1329 GCGCTGATC 1388
 481 GCGCTGATC 540

1389 CACAGTCTGAG 1448
 541 CACAGTCTGAG 600

1449 TGTCAGATTAATGAG 1508
 601 TGTCAGATTAATGAG 660

1509 GCTTGAATTAATGAG 1567
 661 GCTTGAATTAATGAG 719

RESULT 35
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 LOCUS BUI49760
 DEFINITION AGENCOURT 8074878 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6086248
 5' mRNA sequence.
 ACCESSION BUI49760
 VERSION BUI49760.1 GI:22663292
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 921)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.lnl.gov
 Plate: LNCM2320 row: 0 column: 17
 High quality sequence stop: 647.

FEATURES
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 1. 921
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6086248"
 /tissue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOT7; Site_1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using RP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC library."

BASE COUNT 183 a 231 c 278 g 229 t

ORIGIN

Query Match 25.8%; Score 668; DB 13; Length 921;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

849 CCCCTGCCCCGAGAGGAGGAGCTTTGCCATGAGCCCGCCAGCCGGCTTCTGACCTCATC 908
 1 CCCCTGCCCCGAGAGGAGGAGCTTTGCCATGAGCCCGCCAGCCGGCTTCTGACCTCATC 60

909 ACCTGGAGAGCTAGAGCTGATGAGAGCTTTGAGAGCTTGGCTTGTGCGAGTGGCTCTTC 968
 61 ACCTGGAGAGCTAGAGCTGATGAGAGCTTTGAGAGCTTGGCTTGTGCGAGTGGCTCTTC 120

969 TGCAGAGCCACAGCCAGCCAGCTGTATGTATGTGAGAGCCGACTTGTGAGGAGAGCCCT 1028
 121 TGCAGAGCCACAGCCAGCCAGCTGTATGTATGTGAGAGCCGACTTGTGAGGAGAGCCCT 180

1029 GACCAAGATGAGAGAGATCTGCTGCTGCCAGAGAGGATCCCGATGATGATGAGTTGGCAGC 1088
 181 GACCAAGATGAGAGAGATCTGCTGCTGCCAGAGAGGATCCCGATGATGATGAGTTGGCAGC 240

1089 TTCAATGAGAGAGAGAGAGCCAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1148
 241 TTCAATGAGAGAGAGAGAGCCAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300

1149 GCGCTGATC 1208
 301 GCGCTGATC 360

1209 TGAG 1268
 361 TGAG 420

1269 CTTAG 1328
 421 CTTAG 480

1329 GCGCTGATC 1388
 481 GCGCTGATC 540

1389 CACAGTCTGAG 1448
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1449 TGTCAGATTAATGAG 1508

Db 601 TGTCCAGATTAATGCTGCTTTCCTCTACAGCTTGAGCAGACAGCGTTGTTACATG 660
QY 1509 GCTTTGATTAATGTTTGGAGGAGAGAGATGGAACAATGTGGAGTCCCTCTGATGG 1567
Db 661 GCTTTGATTAATGTTTGGAGGAGAGATGGAACAATGTGGAGTCCCTCTGATGG 719

RESULT 36
BO689566 996 bp mRNA linear EST 15-JUL-2002
LOCUS BO689566
DEFINITION: AGENCOURT_8341957 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6248912
5', mRNA sequence.
ACCESSION BO689566
VERSION BO689566.1 GI:21814882
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/
1 (bases 1 to 996)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM2389 row: 1 column: 09
High quality sequence stop: 610.
Location/Qualifiers
1. 996
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6248912"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 110"
/note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."

BASE COUNT 196 a 256 c 292 g 252 t
ORIGIN
Query Match 25.8%; Score 668; DB 13; Length 996;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 849 CCCCTGCGCGTGGAGGCGAGCTTGGCATGACCCCGCAGCGGCTTGTGACCTTC 908
Db 1 CCCCTGCGCGTGGAGGCGAGCTTGGCATGACCCCGCAGCGGCTTGTGACCTTC 60
QY 909 ACTCTGAGAGCTAGAGCTTGTAGAGCTTGGACCGATGCTTGTGCACTGCTTC 968
Db 61 ACTCTGAGAGCTAGAGCTTGTAGAGCTTGGACCGATGCTTGTGCACTGCTTC 120
QY 969 TGCACGCCCCCAGACCAAGCTGTATGTATGTGCAAGCCGACTTCTGTGGAGACCGT 1028
Db 121 TGCACGCCCCCAGACCAAGCTGTATGTATGTGCAAGCCGACTTCTGTGGAGACCGT 180
QY 1029 GACCAAGATGGGAGATCTGCTGCCCCAGAGAGGTCCCCGATGATGAAGTTGGACG 1088

Db 181 GACCAAGATGGGAGATCTGCTGCCCCAGAGAGGTCCCCGATGATGAAGTTGGACG 240
QY 1089 TTACTGAGAGAGGTGGCCCAAGAGCTGAGAGACCTGAGAGAGACCTGATGAAGATG 1148
Db 241 TTACTGAGAGAGGTGGCCCAAGAGCTGAGAGACCTGAGAGAGACCTGATGAAGATG 300
QY 1149 GCGCTGAGGAGACCTGCGGCTGCGCCCGCTGCACTGCTGGAGAGGAGATTTGATC 1208
Db 301 GCGCTGAGGAGACCTGCGGCTGCGCCCGCTGCACTGCTGGAGAGGAGATTTGATC 360
QY 1209 TGAACACAGCTGTGGGATGATGCAATAGATTAATTTATTTCCCAAGTGTG 1268
Db 361 TGAACACAGCTGTGGGATGATGCAATAGATTAATTTATTTCCCAAGTGTG 420
QY 1269 CTTTAGGCGTGGGCTGACCAAGCTTCTTCTTACATCTTCTCCAGTAAGTTCCCTCT 1328
Db 421 CTTTAGGCGTGGGCTGACCAAGCTTCTTCTTACATCTTCTCCAGTAAGTTCCCTCT 480
QY 1329 GGCTTGACAGATGAGATGTTGTGCATTTGTTCAGCTCCCAAGGCTGTCTCCAGCTT 1388
Db 481 GGCTTGACAGATGAGATGTTGTGCATTTGTTCAGCTCCCAAGGCTGTCTCCAGCTT 540
QY 1389 CACAGTGTGCTGCTGGAGAGTCAAGCAGGTTAACTGCAAGACGATTTGCCACCCC 1448
Db 541 CACAGTGTGCTGCTGGAGAGTCAAGCAGGTTAACTGCAAGACGATTTGCCACCCC 600
QY 1449 TGTCCAGATTAATGAGCTTGTGCTTCTTCTTACAGTTGGCAGACGCTTGTCTACATG 1508
Db 601 TGTCCAGATTAATGAGCTTGTGCTTCTTCTTACAGTTGGCAGACGCTTGTCTACATG 660
QY 1509 GCTTTGATTAATGTTTGGAGGAGAGATGGAACAATGTGGAGTCCCTCTGATGG 1567
Db 661 GCTTTGATTAATGTTTGGAGGAGAGATGGAACAATGTGGAGTCCCTCTGATGG 719

RESULT 37
BO689791 858 bp mRNA linear EST 15-JUL-2002
LOCUS BO689791
DEFINITION: AGENCOURT_8046319 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6209170
5', mRNA sequence.
ACCESSION BO689791.1 GI:21815107
VERSION BO689791
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/
1 (bases 1 to 858)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM2368 row: a column: 11
High quality sequence stop: 584.
Location/Qualifiers
1. 858
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6209170"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 110"
/note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming."

Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library.

BASE COUNT 170 a 212 c 263 g 212 t 1 others
ORIGIN

Query Match 25.8%; Score 667; DB 13; Length 858;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 767; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 849 CCCCTGCCCTGGAGGGCGAGCTTGGCATGACCCCGCAGCCGGCTTGTGACCTCAGC 908
Db 1 CCCCTGCCCTGGAGGGCGAGCTTGGCATGACCCCGCAGCCGGCTTGTGACCTCAGC 60
QY 909 ACCTGGAGCTAGAGCCTGTGATGAGACCTTGACCGATGACCTTGTGACAGTGGCTCTC 968
Db 61 ACCTGGAGCTAGAGCCTGTGATGAGACCTTGACCGATGACCTTGTGACAGTGGCTCTC 120
QY 969 TGGCAGCCCCCAAGCCCAAGCTTGGTATGATGTGCAAGCCCACTTCCGTGGGAGACCGT 1028
Db 121 TGGCAGCCCCCAAGCCCAAGCTTGGTATGATGTGCAAGCCCACTTCCGTGGGAGACCGT 180
QY 1029 GACCAAGATGGGAGATCTGCTGCCAGAGAGTCCCGCATGATGATGAATGGAGCAGC 1088
Db 181 GACCAAGATGGGAGATCTGCTGCCAGAGAGTCCCGCATGATGATGAATGGAGCAGC 240
QY 1089 TTCATGAGAGAGTGGCCGCAAGAGCTGAGAGACCTGAGAGAGAGCTGACTGAAGAGATG 1148
Db 241 TTCATGAGAGAGTGGCCGCAAGAGCTGAGAGACCTGAGAGAGAGCTGACTGAAGAGATG 300
QY 1149 GCGCTGGGGAGAGCTGCGCTGCGCGCGCTGCACTGTGGAGAGGGAGAGATTTAGATC 1208
Db 301 GCGCTGGGGAGAGCTGCGCTGCGCGCGCTGCACTGTGGAGAGGGAGAGATTTAGATC 360
QY 1209 TGGACCAAGCTGTGGGTGATGATGCAATAGAAATAGCTAATTTATTTCCCAAGTGTG 1268
Db 361 TGGACCAAGCTGTGGGTGATGATGCAATAGAAATAGCTAATTTATTTCCCAAGTGTG 420
QY 1269 CTTTGAAGCGTGGGTGAGCCAGAGCTTCTTCAATCTTCTCCCAATAGTTCCCTCT 1328
Db 421 CTTTGAAGCGTGGGTGAGCCAGAGCTTCTTCAATCTTCTCCCAATAGTTCCCTCT 480
QY 1329 GAGCTTGACAGATGAGGTGTGTGCAATTTGTCAAGTCCCGAGGCTGTTCACAGCTT 1388
Db 481 GAGCTTGACAGATGAGGTGTGTGCAATTTGTCAAGTCCCGAGGCTGTTCACAGCTT 540
QY 1389 CACAGTGTGCTGTGGAGAGTCAAGCAGGTTAAATGCAAGAGAGAGTTCACACCCC 1448
Db 541 CACAGTGTGCTGTGGAGAGTCAAGCAGGTTAAATGCAAGAGAGAGTTCACACCCC 600
QY 1449 TGTCACATATTTAGGCTGCTTGTGCTCAACAGTTGGCAGACAGCGTTTGTCTACATG 1508
Db 601 TGTCACATATTTAGGCTGCTTGTGCTCAACAGTTGGCAGACAGCGTTTGTCTACATG 660
QY 1509 GCTTTGATTAATTTGTGAGAGAGAGATGAAACAAATGTGAGTCTCCCTCTGATTTG 1568
Db 661 GCTTTGATTAATTTGTGAGAGAGAGATGAAACAAATGTGAGTCTCCCTCTGATTTG 720
QY 1569 TTTGGGAGAAATGGAGAGAGAGTCCCTGCTTTGCAAAACATCAACCTGG 1617
Db 721 TTTGGGAGAAATGGAGAGAGAGTCCCTGCTTTGCAAAACATCAACCTGG 769
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RESULT 38
B0688783 940 bp mRNA linear EST 15-JUL-2002
LOCUS B0688783
DEFINITION AGENCOURT 8344454 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:5251276
5' mRNA sequence.
ACCESSION B0688783
VERSION B0688783.1 GI:21814099

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 940)
REFERENCE NIH-MGC <http://mgc.ncl.nih.gov/>
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapds-remail.nih.gov
Tissue Procurement: ARCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LNCM2395 row: k column: 21
High quality sequence stop: 684.

FEATURES
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/organism="Homo sapiens"
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/tissue_type="ductal carcinoma, cell line"
/lab_host="RD10B (phage-resistant)"
/clone_lib="NIH_MGC_110"
/note="Organ: pancreas; Vector: pOT7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 188 a 235 c 276 g 239 t 2 others
ORIGIN

Query Match 25.8%; Score 667; DB 13; Length 940;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 767; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 849 CCCCTGCCCTGGAGGGCGAGCTTGGCATGACCCCGCAGCCGGCTTGTGACCTCAGC 908
Db 1 CCCCTGCCCTGGAGGGCGAGCTTGGCATGACCCCGCAGCCGGCTTGTGACCTCAGC 60
QY 909 ACCTGGAGCTAGAGCCTGTGATGAGACCTTGACCGATGACCTTGTGACAGTGGCTCTC 968
Db 61 ACCTGGAGCTAGAGCCTGTGATGAGACCTTGACCGATGACCTTGTGACAGTGGCTCTC 120
QY 969 TGGCAGCCCCCAAGCCCAAGCTTGGTATGATGTGCAAGCCCACTTCCGTGGGAGACCGT 1028
Db 121 TGGCAGCCCCCAAGCCCAAGCTTGGTATGATGTGCAAGCCCACTTCCGTGGGAGACCGT 180
QY 1029 GACCAAGATGGGAGATCTGCTGCCAGAGAGTCCCGCATGATGATGAATGGAGCAGC 1088
Db 181 GACCAAGATGGGAGATCTGCTGCCAGAGAGTCCCGCATGATGATGAATGGAGCAGC 240
QY 1089 TTCATGAGAGAGTGGCCGCAAGAGCTGAGAGACCTGAGAGAGAGCTGACTGAAGAGATG 1148
Db 241 TTCATGAGAGAGTGGCCGCAAGAGCTGAGAGACCTGAGAGAGAGCTGACTGAAGAGATG 300
QY 1149 GCGCTGGGGAGAGCTGCGCTGCGCGCGCTGCACTGTGGAGAGGGAGAGATTTAGATC 1208
Db 301 GCGCTGGGGAGAGCTGCGCTGCGCGCGCTGCACTGTGGAGAGGGAGAGATTTAGATC 360
QY 1209 TGGACCAAGCTGTGGGTGATGATGCAATAGAAATAGCTAATTTATTTCCCAAGTGTG 1268
Db 361 TGGACCAAGCTGTGGGTGATGATGCAATAGAAATAGCTAATTTATTTCCCAAGTGTG 420
QY 1269 CTTTGAAGCGTGGGTGAGCCAGAGCTTCTTCAATCTTCTCCCAATAGTTCCCTCT 1328
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Db 421 CTTTAGCGCTGGGCTACCAAGGCTTCTTCTCTACATCTTCTTCCCAAGTTTCCCTCT 480
QY 1329 GGGTTGACAGCATGAGGTGTGTGATTTGTTCACTCCCAAGCTGTCTTCCAGGCTT 1388
Db 481 GGGTTGACAGCATGAGGTGTGTGATTTGTTCACTCCCAAGCTGTCTTCCAGGCTT 540
QY 1389 CACAGTCTGTGTGGGAGAGTCAGGAGGTTAACTGAGGAGCAATTTGGCAACCC 1448
Db 541 CACAGTCTGTGTGGGAGAGTCAGGAGGTTAACTGAGGAGCAATTTGGCAACCC 600
QY 1449 TGTCCAGATTATTTGCTGCTTTGCTCTTACCAAGTTGGAGACAGCCGTTTCTACATG 1508
Db 601 TGTCCAGATTATTTGCTGCTTTGCTCTTACCAAGTTGGAGACAGCCGTTTCTACATG 660
QY 1509 GCTTTGATTAATTTGTTGAGGGGAGAGATGAAACAATGTGAGTCTCCCTGATTTGAT 1568
Db 661 GCTTTGATTAATTTGTTGAGGGGAGAGATGAAACAATGTGAGTCTCCCTGATTTGAT 720
QY 1569 TTGGGGAATGTGAGAAAGTGCCTCTTTCACCAATCAACCTG 1617
Db 721 TTGGGGAATGTGAGAAAGTGCCTCTTTCACCAATCAACCTG 769
RESULT 39
BU191108 871 bp mRNA linear EST 04-SEP-2002
LOCUS AGENCOURT 7975077 NIH_MGC_110 Homo sapiens CDNA clone IMAGE:6081790
DEFINITION 5', mRNA sequence.
ACCESSION BU191108
VERSION BU191108.1 GI:22705092
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC http://mgs.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM2309 row: e column: 23
High quality sequence stop: 502.
Location/Qualifiers
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1..871
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6081790"
/issue_type="dctal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_110"
/notes="Organ: pancreas; Vector: pOTB7, Site_1: XhoI;
Site_2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."
BASE COUNT 177 a 218 c 260 g 216 t
Query Match 25.7%; Score 665; DB 13; Length 871;
Best Local Similarity 99.9%; Pred. No. 0;

Matches 715; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 849 CCCTGCCCCGTGAGAGGCGAGCTTTGCAATGACCCCGCAGCCGGCTTCTGACCTCATC 908
Db 1 CCCCCTGCCGTGAGAGGCGAGCTTTGCAATGACCCCGCAGCCGGCTTCTGACCTCATC 60
QY 909 ACTGGAGAGCTAGAGCTGTATGAGAGCTTGGACCGATGCCCTTGTGCAATGAGCTCTC 968
Db 61 ACTGGAGAGCTAGAGCTGTATGAGAGCTTGGACCGATGCCCTTGTGCAATGAGCTCTC 120
QY 969 TGCAGCCCCCAAGCCAGCCAGCTGTGTATGTGTGCAAGCCGACCTTGTGGAGCCGT 1028
Db 121 TGCAGCCCCCAAGCCAGCCAGCTGTGTATGTGTGCAAGCCGACCTTGTGGAGCCGT 180
QY 1029 GACCAAGTGGGAGATCCTGTGCCAGAGAGTCCCGATGATGATGAATGAGTGGCAGC 1088
Db 181 GACCAAGTGGGAGATCCTGTGCCAGAGAGTCCCGATGATGATGAATGAGTGGCAGC 240
QY 1089 TTCATGAGAGAGTGCAGAGCTGTGAGAGCTGTGAGAGAGCTGACTGAAGAGATG 1148
Db 241 TTCATGAGAGAGTGCAGAGCTGTGAGAGCTGTGAGAGAGCTGACTGAAGAGATG 300
QY 1149 GCGCTGGGGAGCCTGTGGGCTGTGCGCCGCTGCACTGTGGGAGGGAGAGATTGATC 1208
Db 301 GCGCTGGGGAGCCTGTGGGCTGTGCGCCGCTGCACTGTGGGAGGGAGAGATTGATC 360
QY 1209 TGACACAGGCTGTGGGTAGATGTGCATATAGAAATAGCTAATTTATTTCCACAGGTGTG 1268
Db 361 TGACACAGGCTGTGGGTAGATGTGCATATAGAAATAGCTAATTTATTTCCACAGGTGTG 420
QY 1268 CTTTAAAGCGTGGGTGACCAAGCTTCTTCTACATCTTCTCCAGTAATTTCCCTCT 1328
Db 421 CTTTAAAGCGTGGGTGACCAAGCTTCTTCTACATCTTCTCCAGTAATTTCCCTCT 480
QY 1329 GCGTTGACAGATAGAGTGTGTGATTTGTTCAGCTCCCGCAGGCTGTCTCAGGCTT 1388
Db 481 GCGTTGACAGATAGAGTGTGTGATTTGTTCAGCTCCCGCAGGCTGTCTCAGGCTT 540
QY 1389 CACAGTCTGTGTGTGGAGAGTGCAGGAGGTTAACTGACAGAGAGTTTCCACCC 1448
Db 541 CACAGTCTGTGTGTGGAGAGTGCAGGAGGTTAACTGACAGAGAGTTTCCACCC 600
QY 1449 TGTCCAGATTATTTGCTGCTTTGCTCTTACCAAGTTGGAGACAGCCGTTTCTACATG 1508
Db 601 TGTCCAGATTATTTGCTGCTTTGCTCTTACCAAGTTGGAGACAGCCGTTTCTACATG 660
QY 1509 GCTTTGATTAATTTGTTGAGGGGAGAGATGAAACAATGTGAGTCTCCCTGATTTGAT 1564
Db 661 GCTTTGATTAATTTGTTGAGGGGAGAGATGAAACAATGTGAGTCTCCCTGATTTGAT 716
RESULT 40
BO876718 923 bp mRNA linear EST 16-AUG-2002
LOCUS AGENCOURT 8415247 Lupski_sympatricc_ltrunk Homo sapiens CDNA clone
DEFINITION IMAGE:6192192 5', mRNA sequence.
ACCESSION BO876718
VERSION BO876718.1 GI:22268726
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC http://mgs.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1M13593 row: n column: 01

High quality sequence stop: 568.

Location/Qualifiers

1..923

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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6192192"

/sex="male"

/tissue_type="sympathetic trunk"

/dev_stage="adult, 16 yr"

/lab_host="DH10B"

/clone_lib="dupski_sympathetic trunk"

/note="Vector: pCMV-SPORT6 (Life Technologies); Site 1: NotI; Site 2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCGCGTCCG-3' and 5'-GACTAGTTCTAGATCGGAGCGGCGGCGCTT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Dupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."

BASE COUNT 195 a 304 c 299 g 125 t

Query Match 25.4%; Score 656; DB 13; Length 923;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 656; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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2 GCCGCGCTCCCGACCCGCGCGCGCGCGCGCGCTCCGATCTGCACCCGAGCC 61

62 CGGCGGCTCCCGCGCGCGCGCGCGCGCGCGCTCCGATCTGCACCCGAGCC 121

61 CGGCGGCTCCCGCGCGCGCGCGCGCGCGCGCTCCGATCTGCACCCGAGCC 120

122 TCGGCGCGCGCGCTCCCGCGCGCGCGCGCGCGCTCCGATCTGCACCCGAGCC 181

121 TCGGCGCGCGCGCTCCCGCGCGCGCGCGCGCGCTCCGATCTGCACCCGAGCC 180

182 CTGCTGCTGCGCGCGCGCGCGCGCGCGCGCTCCGATCTGCACCCGAGCC 241

181 CTGCTGCTGCGCGCGCGCGCGCGCGCGCGCTCCGATCTGCACCCGAGCC 240

242 TCCAGTCAACCCGCGCGCGCTCCGATCTGCACCCGAGCGAGGAGGAGCCCTCAATGAGT 301

241 TCCAGTCAACCCGCGCGCGCTCCGATCTGCACCCGAGGAGGAGGAGCCCTCAATGAGT 300

302 GTTCCGCGAGTTGAGGAACTGATGAGAGCAGCGACCAAAATTGCGAGCGCGTGA 361

301 GTTCCGCGAGTTGAGGAACTGATGAGAGCAGCGACCAAAATTGCGAGCGCGTGA 360

362 AGAGATGAGAGCGAGAGAGCTGCTGTAAGCATATGAGAGTAACTTGGCAACTT 421

361 AGAGATGAGAGCGAGAGAGCTGCTGTAAGCATATGAGAGTAACTTGGCAACTT 420

422 ACCTCCAGCTATCAATGAGAGCAACAGACAGAGGTTGAAATATATACATCA 481

421 ACCTCCAGCTATCAATGAGAGCAACAGACAGAGGTTGAAATATATACATCA 480

482 TGTGACCGGAAATTCAGAAATTAACCAACAGCTGAGCAAAATGCTTTTCA 541

481 TGTGACCGGAAATTCAGAAATTAACCAACAGCTGAGCAAAATGCTTTTCA 540

542 GACAGTTATACATCTGTGGAGAGCAGAGAGCAGAGAGGAGCAAGATGATCA 601

541 GACAGTTATACATCTGTGTGGAGAGCAGAGAGGAGCAAGATGATCA 600

QY 602 CGAGAGCTGTGGCGCCGACAGTACTGCGAGTTGGCAGCTTCCAGTACACTGCC 657

DB 601 CGAGAGCTGTGGCGCCGACAGTACTGCGAGTTGGCAGCTTCCAGTACACTGCC 656

RESULT 41

BU185743

LOCUS

DEFINITION

AGENCY

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished

Contact: Robert Strassberg, Ph.D.

Email: cga@ds-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1CM2320 row: p column: 13

High quality sequence stop: 640.

Location/Qualifiers

1..905

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6086268"

/tissue_type="ductal carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC 110"

/note="Organ: pancreas; Vector: pOT7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library."

BASE COUNT 179 a 229 c 272 g 225 t

Query Match 25.3%; Score 653; DB 13; Length 905;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 703; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

849 CCCCTGCGCGTGGAGGCGAGCTTGCATGACCCGCGAGCGGCTTGGACCTATC 908

1 CCCCTGCGCGTGGAGGCGAGCTTGCATGACCCGCGAGCGGCTTGGACCTATC 907

909 ACTTGGAGCTAGAGCTGATGAGACCTTGGACCGATGCCCTTGTGCAGTGGCTCTC 968

908 ACTTGGAGCTAGAGCTGATGAGACCTTGGACCGATGCCCTTGTGCAGTGGCTCTC 967

61 ACTTGGAGCTAGAGCTGATGAGACCTTGGACCGATGCCCTTGTGCAGTGGCTCTC 120

969 TGCAGCGCCGACAGCGACGCTGATGATGAGAGCGAGCTTGTGGAGGAGCGCT 1028

121 TGCAGCGCCGACAGCGACGCTGATGATGAGAGCGAGCTTGTGGAGGAGCGCT 1027

1029 GACCAAGATGGAGAGATCTCTGCCAGAGAGGTGCCGATGAGATGAGATTGGCAGC 1088

181 GACCAAGATGGAGAGATCTCTGCCAGAGAGGTGCCGATGAGATGAGATTGGCAGC 240

1089 TTCAATGAGAGAGTGGCGCAGAGAGCTGAGAGCCTGAGAGAGAGCTGAGAGAGATG 1148

[illegible]

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FEATURES
  source
    Location/Qualifiers
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        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:6189394"
        /sex="male"
        /tissue_type="sympathetic trunk"
        /dev_stage="adult, 16 yr"
        /lab_host="DH10B"
        /clone_lib="lupski_symphathetic_trunk"
        /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1
NotCl; site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:

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5'-TGACCCACACGCTCCG-3' and
5'-GACATTCTAGATACGACGCGCCG(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by D.
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine); available through Life
Technologies. "

BASE COUNT 196 a 217 c 235 g 240 t 2 others
ORIGIN

Query Match 25.2% Score 652; DB 13; Length 890;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 652; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

	BASE COUNT	196 a 217 c 235 g 240 t 2 others
ORIGIN		
Query Match	25.2%; Score 652; DB 13; Length 890;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 652; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
OY	1156 GGGAGCCTGCGGCCTGCCCGCCGTCACTGCTGGAGGGGAAGAATTAGATCTGACCA	1215
Dd	14 GGAGAGCTTGGCGCTGCCCGCCGCTCACTGCTGGAGGGGAAGAATTAGATCTGACCA	73
OY	1216 GCGTGCGGTAGATGTGCATAAGAAATAGTAATTTATTTCCCCAGGTGTGCTTAGS	1275
Dd	74 GCGTGCGGTAGATGTGCATAAGAAATAGTAATTTATTTCCCCAGGTGTGCTTAGS	133
OY	1276 CGTGGCGGTAGACAAGGCTTCCTCCAATCTCTCCAGTAAGTTCCCCTGAGCTTGA	1335
Dd	134 CGTGGCGGTAGACAAGGCTTCCTCCAATCTCTCCAGTAAGTTCCCCTGAGCTTGA	193
OY	1336 CAGCATGAGGTGTGTGCATTGTTGACTGCCCTCCCGAGCTGTTTCCAGGCTTCAAGTC	1395
Dd	194 CAGCATGAGGTGTGTGCATTGTTGACTGCCCTCCCGAGCTGTTTCCAGGCTTCAAGTC	253
OY	1396 TGTGCTTGGAGAGTCAAGCACAGGCTTAACTGAGAGAGCAAGTTGGCACCCCTGTCCAG	1455
Dd	254 TGTGCTTGGAGAGTCAAGCACAGGCTTAACTGAGAGAGCAAGTTGGCACCCCTGTCCAG	313
OY	1456 ATTAATGGCTGCTTGGCTCTTACCAGTGTGGCAGACAGCCGTTTTCTTCAATGAGCTTGA	1515
Dd	314 ATTAATGGCTGCTTGGCTCTTACCAGTGTGGCAGACAGCCGTTTTCTTCAATGAGCTTGA	373
OY	1516 TAATTTGTTGAGGGAGAGATGAAAACATGTGAGTCTCCCTCTGATTTGGTTTTGGGG	1575
Dd	374 TAATTTGTTGAGGGAGAGATGAAAACATGTGAGTCTCCCTCTGATTTGGTTTTGGGG	433
OY	1576 AAATGTGAGAAAGTAGTGCCTGCTTGGCAAATCATCACTGGCAAAAAATGCAACAAATGA	1635
Dd	434 AAATGTGAGAAAGTAGTGCCTGCTTGGCAAATCATCACTGGCAAAAAATGCAACAAATGA	493
OY	1636 AATTTCCACGAGTTCTTTCCATGGGAGATGATGATGCTGCTTCAAGCTGTGGCATG	1695
Dd	494 AATTTCCACGAGTTCTTTCCATGGGAGATGATGATGCTGCTTCAAGCTGTGGCATG	553
OY	1696 AAATGTCCTGTGTAACCCCTGCATTTAATGATGTATTATTCATCCAGCAGTGTGCTGACTCC	1755
Dd	554 AAATGTCCTGTGTAACCCCTGCATTTAATGATGTATTATTCATCCAGCAGTGTGCTGACTCC	613
OY	1756 TACCTCTGTGTCAGAGGACGATTTTTCATATTCAAAGATCAATTCCTCTCTCA	1807
Dd	614 TACCTCTGTGTCAGAGGACGATTTTTCATATTCAAAGATCAATTCCTCTCTCTCA	665
RESULT 43		
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	B0688234 B0688234.1 GI:21813550	
	EST.	
	Homo sapiens (human)	
	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
	(bases 1 to 883)	
	NIH-MGC http://mgi.nci.nih.gov/.	

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM2364 row: h column: 02
High quality sequence stop: 680.
Location/Qualifiers
1. 883
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:6207793"
/issue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 110"
/note="Organ: pancreas; Vector: pORF7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library." 1 others

BASE COUNT 175 a 223 c 263 g 221 t 1 others
ORIGIN

Query Match 25.2%; Score 651; DB 13; Length 883;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 751; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 849 CCCCTGCCCTGGAGGGCGAGCTTGGCATGACCCCGGACGGGCTTGGACCTCAGC 908
Db 1 CCCCTGCCCTGGAGGGCGAGCTTGGCATGACCCCGGACGGGCTTGGACCTCAGC 60

QY 909 ACCTGGAGCTAGAGCCTGTATGAGAGCCTTGGACCGATGCCCTTGTGCAAGTGGCCCTC 968
Db 61 ACCTGGAGCTAGAGCCTGTATGAGAGCCTTGGACCGATGCCCTTGTGCAAGTGGCCCTC 120

QY 969 TGGCAGCCCAACAGCCACACAGCTGTGTATGTGTGCAAGCCGACCTTCCGTGGGAGACCGCT 1028
Db 121 TGGCAGCCCAACAGCCACACAGCTGTGTATGTGTGCAAGCCGACCTTCCGTGGGAGACCGCT 180

QY 1029 GACCAAGATGGGAGATCCTGTGCTGCCAGAGAGATCCCGATGATGATGAATGGGACG 1088
Db 181 GACCAAGATGGGAGATCCTGTGCTGCCAGAGAGATCCCGATGATGATGAATGGGACG 240

QY 1089 TTCAATGAGAGAGTGGCCCAAGAGAGCTGGAGAGCCTGGAGAGAGCCTGACTGAAGAGATG 1148
Db 241 TTCAATGAGAGAGTGGCCCAAGAGAGCTGGAGAGCCTGGAGAGAGCCTGACTGAAGAGATG 300

QY 1149 GCGCTGGGAGAGCCTGTGGCTGCCGCGCGCTGCACTGTGTGGAGGGGAGAGATTAGATC 1208
Db 301 GCGCTGGGAGAGCCTGTGGCTGCCGCGCGCTGCACTGTGTGGAGGGGAGAGATTAGATC 360

QY 1209 TGGACCAAGGCTGTGGAGATGTGCATAGAAATAGCTAATTTATTTCCAGAGTGTG 1268
Db 361 TGGACCAAGGCTGTGGAGATGTGCATAGAAATAGCTAATTTATTTCCAGAGTGTG 420

QY 1269 CTTAGAGAGTGGAGTGAACAGAGCTTTCTTCAATCTTTTCCAGATGATTTCCCTCT 1328
Db 421 CTTAGAGAGTGGAGTGAACAGAGCTTTCTTCAATCTTTTCCAGATGATTTCCCTCT 480

QY 1329 GGGCTTGACAGATAGAGTGTGTGATTTGTTCAGCTCCCCAGGCTGTTCACAGCTT 1388
Db 481 GGGCTTGACAGATAGAGTGTGTGATTTGTTCAGCTCCCCAGGCTGTTCACAGCTT 540

QY 1389 CACAGTCTGGTCTTGGAGAGATGACGAGAGGTTAACTGACAGAGAGTTGGACCCC 1448
Db 541 CACAGTCTGGTCTTGGAGAGATGACGAGAGGTTAACTGACAGAGAGTTGGACCCC 600

QY 1449 TGTCCAGATTATTTGGCTGCTTTTGCTTTTACCAAGTTGGCAAGACCGCTTTGTTCAATG 1508
Db 601 TGTCCAGATTATTTGGCTGCTTTTGCTTTTACCAAGTTGGCAAGACCGCTTTGTTCAATG 660

QY 1509 GCTTGATTAATTTGTTGGAGGAGAGATGGAACATATGTGAGTCTCCCTGATTTGT 1568
Db 661 GCTTGATTAATTTGTTGGAGGAGAGATGGAACATATGTGAGTCTCCCTGATTTGT 720

QY 1569 TTTGGGGAATATGTGAGAGAGTGCCTGCTTT 1601
Db 721 TTTGGGGAATATGTGAGAGAGTGCCTGCTTT 753

RESULT 44
B0691372 916 bp mRNA linear EST 15-JUL-2002
LOCUS AGENCOURT_8340692 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6249265
DEFINITION 5', mRNA sequence.
B0691372
B0691372.1 GI:21816688
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 916)
NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM2390 row: h column: 02
High quality sequence stop: 704.
Location/Qualifiers
1. 916
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6249265"
/issue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 110"
/note="Organ: pancreas; Vector: pORF7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library." 1 others

BASE COUNT 193 a 224 c 275 g 224 t
ORIGIN

Query Match 25.2%; Score 651; DB 13; Length 916;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 701; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 849 CCCCTGCCCTGGAGGGCGAGCTTGGCATGACCCCGGACGGGCTTGGACCTCAGC 908
Db 1 CCCCTGCCCTGGAGGGCGAGCTTGGCATGACCCCGGACGGGCTTGGACCTCAGC 60

QY 909 ACCTGGAGCTAGAGCCTGTATGAGAGCCTTGGACCGATGCCCTTGTGCAAGTGGCCCTC 968

LOCUS BU157606 908 bp mRNA linear EST 04-SEP-2002
 DEFINITION AGENCOURT_8042460 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6085176
 5' mRNA sequence.
 ACCESSION BU157606
 VERSION BU157606.1 GI:22671138
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 908)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LNCM2318 row: c column: 01
 High quality sequence stop: 574.
 Location/Qualifiers

FEATURES
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6085176"
 /tissue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOTB7; Site: 1; XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

BASE COUNT 179 a 226 c 275 g 225 t 3 others
 ORIGIN

Query Match 25.1%; Score 648; DB 13; Length 908;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 698; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

849 CCCCTGCCCCGCTGAGAGGAGCTTGGCCATGAGCCCGCCAGCCGGCTTCTGAGACCTGATC 908
 1 CCCCTGCCCCGCTGAGAGGAGCTTGGCCATGAGCCCGCCAGCCGGCTTCTGAGACCTGATC 60
 909 ACCTGGAGCTTAGAGCTGATGAGAGCTTGGACCGATGCCCTTGTGCGAGTGGCTTC 968
 61 ACCTGGAGCTTAGAGCTGATGAGAGCTTGGACCGATGCCCTTGTGCGAGTGGCTTC 120
 969 TGGCAGCCCCCAGCAGCAGCCTGATGATGTCGCAAGCCGACCTTGTGGGAGCCGT 1028
 121 TGGCAGCCCCCAGCAGCAGCCTGATGATGTCGCAAGCCGACCTTGTGGGAGCCGT 180
 1029 GACCAAGTGGGAGAGTCTCTCTGCTCCAGAGAGTCCCGCATGATGATGAAGTTGGAGC 1088
 181 GACCAAGTGGGAGAGTCTCTCTGCTCCAGAGAGTCCCGCATGATGATGAAGTTGGAGC 240
 1089 TTCAATGAGAGAGTTCGCGCAGAGAGCTGAGAGAGCTGAGAGAGAGCTGATGAAGATG 1148
 241 TTCAATGAGAGAGTTCGCGCAGAGAGCTGAGAGAGCTGAGAGAGAGCTGATGAAGATG 300
 1149 GCGCTGGGAGAGCTTGGCGCTGCGCCGCTGCACTGCTGGAGGGGAGAGAGATTGAATC 1208
 301 GCGCTGGAGAGAGCTTGGCGCTGCGCCGCTGCACTGCTGGAGGGGAGAGAGATTGAATC 360

QY 1209 TGAACAGAGCTGTGGGTAGATGTGCATATAGAAATAGCTAATTTATTTCCCCAGGTGTG 1268
 DB 361 TGAACAGAGCTGTGGGTAGATGTGCATATAGAAATAGCTAATTTATTTCCCCAGGTGTG 420
 QY 1269 CTTTAGGCGGTGGGTGACACAGAGGCTTCTCTACATCTCTTCCCAAGTAATTTCCCTCT 1328
 DB 421 CTTTAGGCGGTGGGTGACACAGAGGCTTCTCTACATCTCTTCCCAAGTAATTTCCCTCT 480
 QY 1329 GGCCTGACAGATAGAGTGTGTGATTTGTCAGCTCTCCCAAGCTGTCTCCAGGCTT 1388
 DB 481 GGCCTGACAGATAGAGTGTGTGATTTGTCAGCTCTCCCAAGCTGTCTCCAGGCTT 540
 QY 1389 CACAGCTGTGCTTGGAGAGATGACAGGCTTAACCTGACAGAGAGCTTGGACCC 1448
 DB 541 CACAGCTGTGCTTGGAGAGATGACAGGCTTAACCTGACAGAGAGCTTGGACCC 600
 QY 1449 TGTCAGATTATTTGGCTGTCTTGTGCTTACACAGTTGACAGACAGCCGTTTCTACATG 1508
 DB 601 TGTCAGATTATTTGGCTGTCTTGTGCTTACACAGTTGACAGACAGCCGTTTCTACATG 660
 QY 1509 GCTTGTATATTTGTTGAGGGAGAGAGATGGAACATG 1547
 DB 661 GCTTGTATATTTGTTGAGGGAGAGAGATGGAACATG 699

RESULT 47
 BO686410 879 bp mRNA linear EST 15-JUL-2002
 LOCUS AGENCOURT_8046835 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6209080
 DEFINITION 5' mRNA sequence.
 ACCESSION BO686410
 VERSION BO686410.1 GI:21811726
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 879)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LNCM2367 row: m column: 17
 High quality sequence stop: 614.
 Location/Qualifiers

FEATURES
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1..879
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6209080"
 /tissue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOTB7; Site: 1; XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

BASE COUNT 174 a 219 c 262 g 223 t 1 others
 ORIGIN

Query Match 24.9%; Score 643; DB 13; Length 879;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 693; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 849 CCCCTGCCGTGGAGAGGCGAGCTTTTGCATGACCCCGCAGCCGGCTTTGAGACTC 908
Db 1 CCCCTGCCGTGGAGAGGCGAGCTTTTGCATGACCCCGCAGCCGGCTTTGAGACTC 60
QY 909 ACCCTGGAGGCTGAGAGCTTGATGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCT 968
Db 61 ACCCTGGAGGCTGAGAGCTTGATGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCT 120
QY 969 TCCAGAGGCTGAGAGCTTGATGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCT 1028
Db 121 TCCAGAGGCTGAGAGCTTGATGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCT 180
QY 1029 GACCAAGATGGAGAGCTTGATGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCT 1088
Db 181 GACCAAGATGGAGAGCTTGATGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCT 240
QY 1089 TTCATGAGAGAGTGGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCT 1148
Db 241 TTCATGAGAGAGTGGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCT 300
QY 1149 GCGCTGGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCT 1208
Db 301 GCGCTGGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCT 360
QY 1209 TGGACAGAGCTTGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCT 1268
Db 361 TGGACAGAGCTTGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCT 420
QY 1269 CTTTACGCTGGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCT 1328
Db 421 CTTTACGCTGGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCT 480
QY 1329 GCGCTGGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCT 1388
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QY 1389 CACAGTCTGGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCT 1448
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QY 1509 GCTTTGATTAATTTGTTGAGAGAGAGATGAAA 1542
Db 661 GCTTTGATTAATTTGTTGAGAGAGAGATGAAA 694

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RESULT 48
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LOCUS B0687171
DEFINITION AGENCOURT 8039967 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6210042
5', mRNA sequence.
ACCESSION B0687171
VERSION B0687171.1 GI:21812487
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: L1CM2370 row: e column: 19
High quality sequence stop: 567.
Location/Qualifiers

FEATURES

source

1. 883

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6210042"

/tissue_type="ductal carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: pancreas; Vector: pORF7, Site: 1; XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

BASE COUNT 178 a 222 c 263 g 219 t 1 others
ORIGIN

Query Match

Best Local Similarity 99.9%; Pred. No. 0;
Matches 693; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 909 ACCCTGGAGGCTGAGAGCTTGATGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCT 968
Db 61 ACCCTGGAGGCTGAGAGCTTGATGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCT 120
QY 969 TCCAGAGGCTGAGAGCTTGATGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCT 1028
Db 121 TCCAGAGGCTGAGAGCTTGATGAGAGCTTGAGAGCTTGAGAGCTTGAGAGCT 180
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 VERSION BQ878479.1 GI:22270487
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 1 (bases 1 to 871)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 REFERENCE Unpublished
 AUTHORS Contact: Robert Strausberg, Ph.D.
 TITLE Email: cgaabs-remail.nih.gov
 JOURNAL Tissue Procurement: ATCC
 COMMENT cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
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 /clone_lib="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

BASE COUNT 173 a 219 c 262 g 216 t 1 others
 ORIGIN

Query Match 24.7%; Score 640; DB 13; Length 871;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 690; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 969 TGGCAGCCCCCAGCCAGCAGCTGTGTATGTGTGCAAGCCGACCTTGTGAGGAGCCGT 1028
 DB 121 TGGCAGCCCCCAGCCAGCAGCTGTGTATGTGTGCAAGCCGACCTTGTGAGGAGCCGT 180

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 DB 181 GACCAAGATGGGGAGATCTGTGCGCAGAGAGGTCCCGCATGATGAAGTTGGCAGC 240

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QY 1149 GCGCTGAGGAGAGCGCTGCGGCTGCCCGCTGACCTGCTGGAGGGGAGAGATTAGATC 1208
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 DB 361 TGGACCGAGCTGTGGTAGATGTGCATATAGAAATAGCTAATTTTCCCGAGGTGTG 420

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QY 1329 GCGTTGACAGATAGAGTGTGTGATTTGTTTCCAGCTCCCGCAGGCTGTCCAGGCTT 1388
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QY 1389 CACAGCTGTGTGCTGGAGAGATGACGAGCGGTTAACTGACAGAGCAGTTGCCCCC 1448
 DB 541 CACAGCTGTGTGCTGGAGAGATGACGAGCGGTTAACTGACAGAGCAGTTGCCCCC 600

QY 1449 TGTCCAGATTATTTGCTGCTTCTTCTTACCACTTTGAGCAGACAGCCGTTGTCTACATG 1508
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QY 1509 GCTTGTATATTGTTTGAGGGAGAGATGG 1539
 DB 661 GCTTGTATATTGTTTGAGGGAGAGATGG 691

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 VERSION BQ689559.1 GI:21814875
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 926)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 REFERENCE Unpublished
 AUTHORS Contact: Robert Strausberg, Ph.D.
 TITLE Email: cgaabs-remail.nih.gov
 JOURNAL Tissue Procurement: ATCC
 COMMENT cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
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 High quality sequence stop: 584.
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 /clone_lib="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed by

Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH WGC Library."

BASE COUNT 181 a 232 c 272 g 237 t 4 others
ORIGIN

Query Match 24.7%; Score 640; DB 13; Length 926;
Best Local Similarity 99.9%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;
Matches 690; Conservative 0;

QY 849 CCCCTGCCCGTGGAGGCGCAGCTTTGCCATGACCCCGCCAGCCGCTTCTGACCTCATC 908
Db 1 CCCCTGCCCGTGGAGGCGCAGCTTTGCCATGACCCCGCCAGCCGCTTCTGACCTCATC 60
QY 909 ACCTGGAGACTAGAGCTTATGAGGCTTGGACCGATGCTTGTGCCATGAGCCCTCTC 968
Db 61 ACCTGGAGACTAGAGCTTATGAGGCTTGGACCGATGCTTGTGCCATGAGCCCTCTC 120
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QY 1029 GACCAAGATGGGGAGATCTCTGCTGCCAGAGAGTCCCGATGATGAAATTTGGCAGC 1088
Db 181 GACCAAGATGGGGAGATCTCTGCTGCCAGAGAGTCCCGATGATGAAATTTGGCAGC 240
QY 1089 TTCATGAGAGAGGTGGCCAGAGAGCTGAGAGACCTGAGAGAGAGCTGAGAGAGATG 1148
Db 241 TTCATGAGAGAGGTGGCCAGAGAGCTGAGAGAGCTGAGAGAGAGCTGAGAGAGATG 300
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QY 1509 GCTTTGATAATTTGTTGAGGGGAGAGATGG 1539
Db 661 GCTTTGATAATTTGTTGAGGGGAGAGATGG 691

Search completed: February 20, 2004, 05:50:44
Job time : 5389 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 20, 2004, 19:18:30 ; Search time 74 Seconds
(without alignments)
750.734 Million cell updates/sec

Title: US-10-063-671-8

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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 6

Total number of hits satisfying chosen parameters: 8391

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARYS

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1	350	100.0	350 19	AAAG2535 Homo sapiens cereb
2	350	100.0	350 21	AAAG2070 Human DKK-3. Homo
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4	350	100.0	350 22	AAAG62468 Human reduced expr
5	350	100.0	350 22	AAAB87528 Human PRO295. Hom
6	350	100.0	350 22	AAAB80252 Human PRO295. prote
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8	350	100.0	350 23	ABBS5447 Human angiogenesis
9	350	100.0	350 23	ABBS90735 Human Tumour Endoc

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29	14	4.0	14 22	AAU24777 Schizophrenia-asso
30	14	4.0	14 22	AAU15121 Schizophrenia-asso
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33	12	3.4	12 22	ABBS52342 Human APL-121 try
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97	2.3	302	17	AAE89202	Recombinant synerg	170	8	2.3	1212	20	AAE87503	Human N-methyl-D-a
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115	2.3	415	24	ABU54364	Human secreted/tra	188	8	2.0	9	24	ABE96465	HLA class I molecu
116	2.3	417	21	AAE94319	Murine Mnt-10A pro	189	8	2.0	9	24	ABE96466	HLA class I molecu
117	2.3	419	22	ABG22064	Novel human diageno	190	8	2.0	9	24	ABE96467	HLA class I molecu
118	2.3	427	22	ABE65442	Drosophila melanog	191	8	2.0	9	24	ABE96469	HLA class I molecu
119	2.3	449	22	ABE68879	Human RBCAP polype	192	8	2.0	9	24	ABE96470	HLA class I molecu
120	2.3	453	21	AAE94340	Human cell surface	193	8	2.0	9	24	ABE96473	HLA class I molecu
121	2.3	503	15	AAE5370	Human Actin regu	194	8	2.0	9	24	ABE96475	HLA class I molecu
122	2.3	503	19	AAE49909	Signal regulatory	195	8	2.0	9	24	ABE96479	HLA class I molecu
123	2.3	503	19	AAE40481	Human SH2 binding	196	8	2.0	10	19	AAE61561	HLA class I molecu
124	2.3	503	20	AAE33303	Human hAUK-5 clone	197	8	2.0	12	23	ABE68392	HIV envelope prote
125	2.3	503	21	AAE59452	Human Transforming	198	8	2.0	12	23	ABE57821	Peptide based on t
126	2.3	503	23	AAU79935	Human SHPS-1 (not	199	8	2.0	14	17	AAE02569	AKAP79 A37-50 muta
127	2.3	521	20	AAE30638	Partial human 7-tr	200	8	2.0	14	21	AAE14909	Mutant peptide AKA
128	2.3	537	22	ABE60713	Drosophila melanog	201	8	2.0	14	21	AAE14909	MGRLA putative si
129	2.3	540	15	AAE48667	Chitinase 1. Rhiz	202	8	2.0	17	24	ABE38873	Amino acid sequenc
130	2.3	551	21	AAE24049	Human ORFX ORF1813	203	8	2.0	20	22	ABE68494	Amino acid sequenc
131	2.3	576	21	AAE24234	Human vesicle asso	204	8	2.0	21	22	AAE68496	Amino acid sequenc
132	2.3	576	22	AAE95100	Human protein sequ	205	8	2.0	21	22	AAE67602	Human RIZ alternat
133	2.3	577	23	ABG70269	Human Epsin-like p	206	8	2.0	22	17	AAE92102	5' terminal of hum
134	2.3	593	23	AAE020499	Protein of App rel	207	8	2.0	22	23	AAE12111	Peptide sequence #
135	2.3	593	24	ABE26245	Aspergillus fumiga	208	8	2.0	22	23	AAU10792	Human Rb-interacti
136	2.3	611	23	AAE18647	Human G-protein co	209	8	2.0	22	23	AAE05790	HIV tat related am
137	2.3	638	22	ABE71320	Drosophila melanog	210	8	2.0	26	14	AAE41301	Peptide fragment F
138	2.3	645	23	AAE020500	Protein of App rel	211	8	2.0	30	14	AAE33088	Human cytochrome P
139	2.3	646	23	AAE020501	Protein of App rel	212	8	2.0	30	14	ABE59489	Human liver peptid
140	2.3	647	11	AAE06001	Insect receptor po	213	8	2.0	30	22	ABE44107	Peptide #11613 enco
141	2.3	651	24	ABG74687	Human CGSD protein	214	8	2.0	30	22	ABE26997	Protein #8996 enco
142	2.3	652	20	AAE30637	Human 7-epsilon mem	215	8	2.0	30	22	AAE65129	Human bone marrow
143	2.3	652	21	AAE59300	Human EGFR polype	216	8	2.0	30	22	AAE77835	Peptide #8173 enco
144	2.3	652	24	ABE75634	Human ERM-1-like G	217	8	2.0	30	22	AAE21739	Peptide #12091 enco
145	2.3	652	24	ABE81739	Human ERM3 protein	218	8	2.0	30	22	AAE38054	Human peptide enco
146	2.3	661	22	ABE03062	Human expressed po	219	8	2.0	30	22	ABE46867	Human cytochrome P
147	2.3	661	22	ABE10371	Human CDNA SEQ ID	220	8	2.0	32	17	AAE05632	L. acidophilus S 1
148	2.3	661	22	AAU18138	Novel human uterin	221	8	2.0	32	17	AAE06912	Arctic fish antifer
149	2.3	661	22	AAU18139	Human endocrine po	222	8	2.0	33	18	AAE27490	Human cytochrome P
150	2.3	661	22	AAU18138	Human novel secret	223	8	2.0	33	18	AAE33083	Human liver peptid
151	2.3	661	23	ABE68358	Human polypeptide	224	8	2.0	35	14	ABE56523	Human cytochrome P
152	2.3	661	23	ABE05765	Novel human protei	225	8	2.0	35	22	ABE41080	Peptide #8586 enco
153	2.3	696	22	ABE04995	Novel human diageno	226	8	2.0	35	22	ABE25142	Protein #7141 enco
154	2.3	757	22	ABE85017	Shrimp white spot	227	8	2.0	35	22	ABE25142	Human brain expres
155	2.3	800	23	AAE13609	Human mature EGF-1	228	8	2.0	35	22	AAE61938	

229	7	2.0	35	22	AAW74740	Human bone marrow	302	7	2.0	87	22	AAW5996	Peptide #10033 enc
230	7	2.0	35	22	AAW20398	Peptide #6832 enco	303	7	2.0	87	23	ABG65672	Oeisk 3 protein
231	7	2.0	35	22	AAW34856	Peptide #8932 enco	304	7	2.0	87	23	ABG45328	Human peptide enco
232	7	2.0	35	23	ABG44539	Human peptide enco	305	7	2.0	93	22	AAW06419	Human foetal prote
233	7	2.0	37	13	AAW26105	Antifreeze protein	306	7	2.0	95	22	ABW03487	Human musculoskele
234	7	2.0	37	20	AAW23879	Protein derived fr	307	7	2.0	95	24	ABU12781	Novel human muscul
235	7	2.0	37	20	AAW23880	Protein derived fr	308	7	2.0	96	22	AAU49577	Propionibacterium
236	7	2.0	37	20	AAW86157	P. americanus anti	309	7	2.0	97	20	AAW86160	P. americanus anti
237	7	2.0	37	20	AAW86158	P. americanus anti	310	7	2.0	97	20	AAW84334	Human reproductive
238	7	2.0	37	20	AAW86156	P. americanus anti	311	7	2.0	102	21	AAW32715	Zea mays protein f
239	7	2.0	37	21	AAW44713	Wntler floclunder 11	312	7	2.0	102	22	AAO10668	Human polypeptide
240	7	2.0	38	12	AAW14375	Wntling p. depress	313	7	2.0	104	19	AAW56088	Murine monocyte ch
241	7	2.0	38	20	AAW25427	P. americanus anti	314	7	2.0	104	19	AAW57322	Mouse monocyte che
242	7	2.0	39	18	AAW22874	P. americanus skin	315	7	2.0	105	21	AAW19719	Arabidopsis thalia
243	7	2.0	40	11	AAW08077	Synthetic antifree	316	7	2.0	105	21	AAW19719	Arabidopsis thalia
244	7	2.0	40	21	AAW20091	Arabidopsis thalia	317	7	2.0	106	22	ABG03609	Novel human diagno
245	7	2.0	41	11	AAW08080	Synthetic antifree	318	7	2.0	107	22	AAW08884	Propionibacterium
246	7	2.0	41	11	AAW08082	Synthetic antifree	319	7	2.0	110	22	ABG23072	Novel human diagno
247	7	2.0	41	11	AAW08086	Synthetic antifree	320	7	2.0	111	22	ABG54420	Human liver peptid
248	7	2.0	41	11	AAW08097	Synthetic antifree	321	7	2.0	111	22	ABW39430	Peptide #6936 enco
249	7	2.0	41	14	AAW33090	Human cytomagalovi	322	7	2.0	111	22	AAW24202	Protein #6201 enco
250	7	2.0	41	14	AAW33092	Human cytomagalovi	323	7	2.0	111	22	AAW60110	Human brain expres
251	7	2.0	43	20	AAW24058	Synthetic antifree	324	7	2.0	111	22	AAW72722	Human bone marrow
252	7	2.0	46	11	AAW08098	Synthetic antifree	325	7	2.0	111	22	AAW19703	Peptide #6137 enco
253	7	2.0	50	22	AAW63812	Propionibacterium	326	7	2.0	111	22	AAW32953	Peptide #6990 enco
254	7	2.0	51	11	AAW08078	Synthetic antifree	327	7	2.0	111	22	ABG42546	Human peptide enco
255	7	2.0	52	11	AAW08081	Synthetic antifree	328	7	2.0	112	23	ABW60402	Drosophila melanog
256	7	2.0	52	11	AAW08083	Synthetic antifree	329	7	2.0	112	23	ABG80431	Moraxella catarrha
257	7	2.0	52	22	ABG56552	Human liver peptid	330	7	2.0	112	24	ABW25291	Mouse BACE-interac
258	7	2.0	52	22	ABW41079	Peptide #8585 enco	331	7	2.0	114	20	AAW12363	Human 5' EST seque
259	7	2.0	52	22	ABW25141	Protein #7140 enco	332	7	2.0	114	20	AAO11765	Human polypeptide
260	7	2.0	52	22	ABW61937	Human brain expres	333	7	2.0	114	23	ABW88127	Human polypeptide
261	7	2.0	52	22	AAW74739	Human bone marrow	334	7	2.0	114	24	ABP76179	Human GENSRT prote
262	7	2.0	52	22	AAW20397	Peptide #6831 enco	335	7	2.0	114	24	ABP76179	Human GENSRT prote
263	7	2.0	52	22	AAW44855	Peptide #8892 enco	336	7	2.0	116	22	AAW67380	Propionibacterium
264	7	2.0	52	23	ABG44538	Human peptide enco	337	7	2.0	117	24	ABP78211	N. gonorrhoeae amf
265	7	2.0	54	18	AAW22875	P. americanus skin	338	7	2.0	119	22	AAW88653	Human immune/haem
266	7	2.0	54	21	AAW00160	Human secreted pro	339	7	2.0	120	22	ABW59393	Drosophila melanog
267	7	2.0	55	22	ABW14770	Human nervous syst	340	7	2.0	121	23	AAW98749	Chicken anemia vir
268	7	2.0	57	21	AAW19701	Arabidopsis thalia	341	7	2.0	122	21	AAW41997	Arabidopsis thalia
269	7	2.0	57	21	AAW61016	Propionibacterium	342	7	2.0	125	21	AAW57848	Zea mays protein f
270	7	2.0	57	22	AAW44856	Synthetic antifree	343	7	2.0	126	21	AAW35185	Zea mays protein f
271	7	2.0	62	11	AAW08079	Synthetic antifree	344	7	2.0	127	20	AAW12339	Human 5' EST seque
272	7	2.0	63	21	AAW08090	Arabidopsis thalia	345	7	2.0	131	20	AAW23876	Hypothetical hybr
273	7	2.0	66	11	AAW08087	Synthetic antifree	346	7	2.0	131	20	AAW95195	Arabidopsis thalia
274	7	2.0	68	22	ABW58436	Human liver peptid	347	7	2.0	131	21	AAW08967	Arabidopsis thalia
275	7	2.0	68	22	ABW43028	Peptide #10534 enc	348	7	2.0	131	21	AAW26759	Zea mays protein f
276	7	2.0	68	22	ABW26216	Protein #8215 enco	349	7	2.0	131	21	AAW46356	Arabidopsis thalia
277	7	2.0	68	22	AAW63933	Human bone marrow	350	7	2.0	132	21	AAW34164	Zea mays protein f
278	7	2.0	68	22	AAW67551	Human bone marrow	351	7	2.0	132	21	AAW92498	TMV AL3 mutant, m
279	7	2.0	68	22	AAW20992	Peptide #7426 enco	352	7	2.0	133	23	ABP43013	Human ovarian anti
280	7	2.0	68	22	AAW68858	Peptide #10895 enc	353	7	2.0	135	22	ABW67507	Drosophila melanog
281	7	2.0	68	23	ABW45929	Human peptide enco	354	7	2.0	135	22	ABW2058	Novel human diagno
282	7	2.0	69	19	AAW20990	Human glial fibril	355	7	2.0	135	22	ABW25332	Novel human diagno
283	7	2.0	70	23	ABW09457	L. helveticus exp	356	7	2.0	136	20	AAW88593	Secreted protein e
284	7	2.0	73	11	AAW08068	Synthetic antifree	357	7	2.0	136	22	ABW50517	Human secreted pro
285	7	2.0	73	16	AAW81407	Hepatitis GB virus	358	7	2.0	137	22	ABW49580	Human liver peptid
286	7	2.0	73	21	AAW42000	Hepatitis GB virus	359	7	2.0	137	22	ABW29575	Peptide #2226 enco
287	7	2.0	73	21	AAW08990	Arabidopsis thalia	360	7	2.0	137	22	ABW34752	Peptide #2258 enco
288	7	2.0	73	21	ABW18265	Hepatitis GB virus	361	7	2.0	137	22	ABW50360	Human secreted pro
289	7	2.0	75	22	ABW64202	Novel human diagno	362	7	2.0	137	22	ABW20167	Protein #2166 enco
290	7	2.0	76	13	AAW22354	Drosophila melanog	363	7	2.0	137	22	AAW55554	Human brain expres
291	7	2.0	82	20	AAW38777	Antigen tc-10a. E	364	7	2.0	137	22	AAW67938	Human bone marrow
292	7	2.0	82	23	AAW79431	Human transcrip	365	7	2.0	137	22	AAW15755	Peptide #2189 enco
293	7	2.0	86	21	AAW08968	Human transcrip	366	7	2.0	137	22	AAW28264	Peptide #2301 enco
294	7	2.0	86	21	AAW46357	Arabidopsis thalia	367	7	2.0	137	22	AAW03489	Peptide #2171 enco
295	7	2.0	86	21	ABW22535	Human transp	368	7	2.0	137	23	ABW37472	Human peptide enco
296	7	2.0	87	22	ABW37619	Human liver peptid	369	7	2.0	139	13	AAW22382	Human peptide enco
297	7	2.0	87	22	ABW42189	Peptide #9695 enco	370	7	2.0	139	20	AAW12341	Human 5' EST seque
298	7	2.0	87	22	ABW25739	Protein #7738 enco	371	7	2.0	139	22	ABW22196	Novel human diagno
299	7	2.0	87	22	AAW63074	Human brain expres	372	7	2.0	140	22	ABW10534	Human cDNA S9Q ID
300	7	2.0	87	22	AAW75885	Human bone marrow	373	7	2.0	140	22	AAU18150	Novel human uterin
301	7	2.0	87	22	AAW20728	Peptide #7162 enco	374	7	2.0	140	22	AAU18488	Human endocrine po

375	7	2.0	140	22	AAU17050	Human novel secret	448	7	2.0	195	22	AB370905	Drosophila melanog
376	7	2.0	140	23	ABP67121	Human polypeptide	449	7	2.0	197	20	AAW68467	Rice ferritin OsFe
377	7	2.0	140	23	ABJ05777	Novel human protei	450	7	2.0	198	22	AB367664	Drosophila melanog
378	7	2.0	143	22	AAW95440	Human reproductive	451	7	2.0	198	22	AB316672	Novel human diagno
379	7	2.0	143	22	AAW63868	Human prostate can	452	7	2.0	200	20	AAV01305	Human tropoelastin
380	7	2.0	143	22	AAW63870	Human prostate can	453	7	2.0	201	21	AAW64057	Human tropoelastin
381	7	2.0	147	20	AAV01304	Human tropoelastin	454	7	2.0	202	22	ABW10977	Drosophila thalia
382	7	2.0	148	21	AAW14960	Arabidopsis thalia	455	7	2.0	204	22	ABW10487	Human CPNA SEQ ID
383	7	2.0	149	21	AAW14959	Arabidopsis thalia	456	7	2.0	204	22	AAW89007	Human CPNA SEQ ID
384	7	2.0	149	21	AAW14959	Arabidopsis thalia	457	7	2.0	204	22	AAW89007	Human CPNA SEQ ID
385	7	2.0	150	21	AAW14959	Arabidopsis thalia	458	7	2.0	204	22	AAW89007	Human CPNA SEQ ID
386	7	2.0	152	21	AAW14959	Arabidopsis thalia	459	7	2.0	206	18	AAW14574	Human tropoelastin
387	7	2.0	152	21	AAW14959	Arabidopsis thalia	460	7	2.0	206	18	AAW14574	Human tropoelastin
388	7	2.0	153	21	AAW14959	Arabidopsis thalia	461	7	2.0	207	21	AAW14959	Arabidopsis thalia
389	7	2.0	154	21	AAW14959	Arabidopsis thalia	462	7	2.0	208	20	AAW14959	Arabidopsis thalia
390	7	2.0	154	21	AAW14959	Arabidopsis thalia	463	7	2.0	209	21	AAW14959	Arabidopsis thalia
391	7	2.0	155	21	AAW14959	Arabidopsis thalia	464	7	2.0	210	22	AAW14959	Arabidopsis thalia
392	7	2.0	156	21	AAW14959	Arabidopsis thalia	465	7	2.0	212	21	AAW14959	Arabidopsis thalia
393	7	2.0	158	21	AAW14959	Arabidopsis thalia	466	7	2.0	214	21	AAW14959	Arabidopsis thalia
394	7	2.0	158	21	AAW14959	Arabidopsis thalia	467	7	2.0	214	21	AAW14959	Arabidopsis thalia
395	7	2.0	158	21	AAW14959	Arabidopsis thalia	468	7	2.0	214	21	AAW14959	Arabidopsis thalia
396	7	2.0	159	22	AAW14959	Arabidopsis thalia	469	7	2.0	214	22	AAW14959	Arabidopsis thalia
397	7	2.0	161	22	AAW14959	Arabidopsis thalia	470	7	2.0	215	22	AAW14959	Arabidopsis thalia
398	7	2.0	161	22	AAW14959	Arabidopsis thalia	471	7	2.0	215	22	AAW14959	Arabidopsis thalia
399	7	2.0	161	22	AAW14959	Arabidopsis thalia	472	7	2.0	215	22	AAW14959	Arabidopsis thalia
400	7	2.0	161	22	AAW14959	Arabidopsis thalia	473	7	2.0	216	20	AAW14959	Arabidopsis thalia
401	7	2.0	161	22	AAW14959	Arabidopsis thalia	474	7	2.0	219	21	AAW14959	Arabidopsis thalia
402	7	2.0	161	22	AAW14959	Arabidopsis thalia	475	7	2.0	219	21	AAW14959	Arabidopsis thalia
403	7	2.0	161	22	AAW14959	Arabidopsis thalia	476	7	2.0	221	21	AAW14959	Arabidopsis thalia
404	7	2.0	161	22	AAW14959	Arabidopsis thalia	477	7	2.0	221	21	AAW14959	Arabidopsis thalia
405	7	2.0	162	23	AAW14959	Arabidopsis thalia	478	7	2.0	223	22	AAW14959	Arabidopsis thalia
406	7	2.0	162	23	AAW14959	Arabidopsis thalia	479	7	2.0	223	22	AAW14959	Arabidopsis thalia
407	7	2.0	162	23	AAW14959	Arabidopsis thalia	480	7	2.0	223	22	AAW14959	Arabidopsis thalia
408	7	2.0	163	20	AAW14959	Arabidopsis thalia	481	7	2.0	223	22	AAW14959	Arabidopsis thalia
409	7	2.0	163	20	AAW14959	Arabidopsis thalia	482	7	2.0	223	22	AAW14959	Arabidopsis thalia
410	7	2.0	163	20	AAW14959	Arabidopsis thalia	483	7	2.0	223	22	AAW14959	Arabidopsis thalia
411	7	2.0	164	21	AAW14959	Arabidopsis thalia	484	7	2.0	223	22	AAW14959	Arabidopsis thalia
412	7	2.0	164	21	AAW14959	Arabidopsis thalia	485	7	2.0	223	22	AAW14959	Arabidopsis thalia
413	7	2.0	164	21	AAW14959	Arabidopsis thalia	486	7	2.0	223	22	AAW14959	Arabidopsis thalia
414	7	2.0	165	21	AAW14959	Arabidopsis thalia	487	7	2.0	223	22	AAW14959	Arabidopsis thalia
415	7	2.0	165	21	AAW14959	Arabidopsis thalia	488	7	2.0	224	22	AAW14959	Arabidopsis thalia
416	7	2.0	166	18	AAW14959	Arabidopsis thalia	489	7	2.0	227	20	AAW14959	Arabidopsis thalia
417	7	2.0	166	18	AAW14959	Arabidopsis thalia	490	7	2.0	228	21	AAW14959	Arabidopsis thalia
418	7	2.0	167	18	AAW14959	Arabidopsis thalia	491	7	2.0	230	21	AAW14959	Arabidopsis thalia
419	7	2.0	167	18	AAW14959	Arabidopsis thalia	492	7	2.0	230	21	AAW14959	Arabidopsis thalia
420	7	2.0	167	22	AAW14959	Arabidopsis thalia	493	7	2.0	230	24	AAW14959	Arabidopsis thalia
421	7	2.0	167	22	AAW14959	Arabidopsis thalia	494	7	2.0	233	23	AAW14959	Arabidopsis thalia
422	7	2.0	171	21	AAW14959	Arabidopsis thalia	495	7	2.0	234	22	AAW14959	Arabidopsis thalia
423	7	2.0	171	21	AAW14959	Arabidopsis thalia	496	7	2.0	234	22	AAW14959	Arabidopsis thalia
424	7	2.0	172	21	AAW14959	Arabidopsis thalia	497	7	2.0	237	20	AAW14959	Arabidopsis thalia
425	7	2.0	172	21	AAW14959	Arabidopsis thalia	498	7	2.0	237	20	AAW14959	Arabidopsis thalia
426	7	2.0	172	21	AAW14959	Arabidopsis thalia	499	7	2.0	241	22	AAW14959	Arabidopsis thalia
427	7	2.0	172	21	AAW14959	Arabidopsis thalia	500	7	2.0	241	23	AAW14959	Arabidopsis thalia
428	7	2.0	172	21	AAW14959	Arabidopsis thalia							
429	7	2.0	174	22	AAW14959	Arabidopsis thalia							
430	7	2.0	176	23	AAW14959	Arabidopsis thalia							
431	7	2.0	178	22	AAW14959	Arabidopsis thalia							
432	7	2.0	180	13	AAW14959	Arabidopsis thalia							
433	7	2.0	180	13	AAW14959	Arabidopsis thalia							
434	7	2.0	180	21	AAW14959	Arabidopsis thalia							
435	7	2.0	180	22	AAW14959	Arabidopsis thalia							
436	7	2.0	182	22	AAW14959	Arabidopsis thalia							
437	7	2.0	182	22	AAW14959	Arabidopsis thalia							
438	7	2.0	183	18	AAW14959	Arabidopsis thalia							
439	7	2.0	183	20	AAW14959	Arabidopsis thalia							
440	7	2.0	183	20	AAW14959	Arabidopsis thalia							
441	7	2.0	186	22	AAW14959	Arabidopsis thalia							
442	7	2.0	187	23	AAW14959	Arabidopsis thalia							
443	7	2.0	188	23	AAW14959	Arabidopsis thalia							
444	7	2.0	190	21	AAW14959	Arabidopsis thalia							
445	7	2.0	190	24	AAW14959	Arabidopsis thalia							
446	7	2.0	191	22	AAW14959	Arabidopsis thalia							
447	7	2.0	194	13	AAW14959	Arabidopsis thalia							
448	7	2.0	194	23	AAW14959	Arabidopsis thalia							

ALIGNMENTS

RESULT 1
ID AA62595 standard; Protein; 350 AA.

XX AA62595;

XX AC 09-NOV-1998 (first entry)

XX DE Homo sapiens cerebellum and embryo specific protein.

XX CE: cerebellum and embryo specific protein; restenosis;

XX KW myocardial infarction; arrhythmia; heart disease;

XX KM atherosclerosis.

OS Homo sapiens.

XX	Key	Location/Qualifiers
XX	Peptide	1..21
XX		/note= "signal peptide"
XX	MO9827932-A2.	
XX	02-JUL-1998.	
XX	18-DEC-1997;	97WO-US23518.
XX	20-DEC-1996;	96US-0033870.
XX	(HUMA-) HUMAN GENOME SCI INC.	
XX	Ruben SM, Soppet DR;	
XX	WPI: 1998-377366/32.	
XX	N-PSDB; AAV38798.	
XX	New isolated cerebellum and embryo specific polypeptide - used to	
XX	develop products for treating e.g. coronary restenosis, myocardial	
XX	infarction, heart disease and artery or venous thrombosis	
XX	Claim 17; Fig 1; 77pp; English.	
XX	The sequence is that of cerebellum and embryo specific protein	
XX	(CESP). CESP is involved in: (i) the regulation of collateral	
XX	circulation (particularly in the heart), coronary artery restenosis	
XX	following a revascularisation procedure, apoptosis in myocytes; (ii) the	
XX	regulation of myocyte development in the developing heart; (iii) the	
XX	regulation of circulating blood volume, vascular tone, blood pressure and	
XX	cardiac output, diuresis, natriuresis; (iv) facilitation of transudation	
XX	of plasma water to the interstitium, and (v) inhibition of the release	
XX	or action of hormones such as aldosterone, angiotensin II, endothelins,	
XX	renin and vasopressin. The products can be used in the diagnosis and	
XX	treatment of CESP related disorders, e.g. coronary restenosis following	
XX	coronary revascularisation, coronary artery thrombus or occlusion,	
XX	myocardial infarction, atrial and/or ventricular arrhythmias, heart	
XX	block, hereditary medial necrosis of small coronary arteries,	
XX	cardiomyopathy, arrhythmogenic right ventricular dysplasia, athero-	
XX	sclerotic heart disease, venous thrombosis or Reynaud's syndrome.	
XX	Sequence 350 AA;	
XX	Query Match 100.0%; Score 350; DB 19; Length 350;	
XX	Best Local Similarity 100.0%; Pred. No. 0;	
XX	Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX	1 MORLGATLLCLLLAAAVPTAPAPATATSAVPKGPALSIPOEATLNMFRVEELMED 60	
XX	1 MORLGATLLCLLLAAAVPTAPAPATATSAVPKGPALSIPOEATLNMFRVEELMED 60	
XX	61 TORKLSAIVEEMAEBAEAAKASSEVNLANLPSTYNETNTDTTVGNNTIHWREIHKTN 120	
XX	61 TORKLSAIVEEMAEBAEAAKASSEVNLANLPSTYNETNTDTTVGNNTIHWREIHKTN 120	
XX	121 NOTGQWVFSEVTVTSVDEGRSHSECIIDEDCGPSMYCOFASFOYTCQPCRGQMLCTR 180	
XX	121 NOTGQWVFSEVTVTSVDEGRSHSECIIDEDCGPSMYCOFASFOYTCQPCRGQMLCTR 180	
XX	121 NOTGQWVFSEVTVTSVDEGRSHSECIIDEDCGPSMYCOFASFOYTCQPCRGQMLCTR 180	
XX	181 DSECCGDQLCVWGCHCTKMATRGSGNTICDNQDQPGQLCCAFQRLGILFVCTPLPYEGEL 240	
XX	181 DSECCGDQLCVWGCHCTKMATRGSGNTICDNQDQPGQLCCAFQRLGILFVCTPLPYEGEL 240	
XX	241 CHDPASRLDLITWELPEPDGLRCPASGLTCQPSHSIVYVCKPTFGSRDQDEILL 300	
XX	241 CHDPASRLDLITWELPEPDGLRCPASGLTCQPSHSIVYVCKPTFGSRDQDEILL 300	
XX	301 PREVPDEYEGVSMEEVROLEDLERSLTERVALGSEPAALALLGGEEL 350	
XX	301 PREVPDEYEGVSMEEVROLEDLERSLTERVALGSEPAALALLGGEEL 350	

XX	Key	Location/Qualifiers
XX	Peptide	1..20
XX		/label= "signal_peptide"
XX		/note= "putative"
XX	Peptide	1..21
XX		/label= "signal peptide"
XX		/note= "putative"
XX	Cleavage-site	16..17
XX		/note= "putative endogenous processing site"
XX	Region	21..145
XX		/note= "alpha helical region and region of N-linked glycosylation"
XX	Cleavage-site	22..23
XX		/note= "putative endogenous processing site"
XX	Cleavage-site	32..33
XX		/note= "putative endogenous processing site"
XX	Cleavage-site	41..42
XX		/note= "putative endogenous processing site"
XX	Modified-site	96
XX		/note= "N-glycosylated"
XX	Modified-site	106
XX		/note= "N-glycosylated"
XX	Modified-site	121
XX		/note= "N-glycosylated"
XX	Modified-site	204
XX		/note= "N-glycosylated"
XX	Region	300..350
XX		/note= "alpha helical region"
XX	MO200018914-A2.	
XX	06-APR-2000.	
XX	17-SEP-1999;	99WO-US21647.
XX	25-SEP-1998;	98US-0161241.
XX	(AMGE-) AMGEN INC.	
XX	Base MB, Sullivan JK, Theill LE, Wang D;	
XX	WPI: 2000-293153/25.	
XX	N-PSDB; AAA08839.	
XX	New nucleic acid molecule encoding a biologically active DKR	
XX	polypeptide, useful in treatment of cancer, e.g. mammary tumors and	
XX	stem cell tumors	
XX	Claim 18; Page 126-127; 143pp; English.	
XX	AA92069-75 are novel mouse and human DKR polypeptides.	
XX	The human DKR-3 open reading frame has homology to human rig-like 7-1	
XX	mRNA and to chicken lens fiber protein cleft 4 gene. Human DKR-3	
XX	appears to be secreted, with a signal peptide cleavage site after either	
XX	amino acid 20 or 21.	
XX	DKR-1 is a human ortholog of dkk-1 (dickkopf-1), a novel gene identified	

CC in Xenopus and mouse, purportedly an antagonist of wnt-8 signaling.
 CC DKK-2, -3 and -4 are each related to DKK-1 by their cysteine pattern.
 CC DKK-1 is also involved in morphogenesis in the developing embryo, and
 CC therefore a growth factor, by inference DKK polypeptides are also
 CC growth factors. The DKK polypeptides are useful for treating cancer,
 CC e.g. mammary tumors, stem cell tumors, or other cancers in which the wnt
 CC and/or sonic hedgehog (shh) signal transduction pathways are activated.
 CC They can also be used to enhance tissue differentiation, such as bone
 CC formation and hematopoietic cell formation.

XX Sequence 350 AA;

Query Match 100.0%; Score 350; DB 21; Length 350;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORIGATILLCILAAVPTAPAPATATSAVKGPAALSYPOEATLNEMFREVEELMED 60
 DB 1 MORIGATILLCILAAVPTAPAPATATSAVKGPAALSYPOEATLNEMFREVEELMED 60
 QY 61 TOHKLRSVAEEMAEEMAAKASSEVNLANLPSYHNETNTDTVGNNTIHHREIHKITN 120
 DB 61 TOHKLRSVAEEMAEEMAAKASSEVNLANLPSYHNETNTDTVGNNTIHHREIHKITN 120
 QY 121 NOTGQWVSEFVITVSDDEGRSHSCIIDEDCGPSMYCQFASFOYTQPCRGQRLCTR 180
 DB 121 NOTGQWVSEFVITVSDDEGRSHSCIIDEDCGPSMYCQFASFOYTQPCRGQRLCTR 180
 QY 181 DSECCGQQLCWGHCTMTATRGSGNGTICDNORCCQPGLCAPFGRLFPVCTPLPVEGEL 240
 DB 181 DSECCGQQLCWGHCTMTATRGSGNGTICDNORCCQPGLCAPFGRLFPVCTPLPVEGEL 240
 QY 241 CHDPASRLDLITWLEPDPDALRCPASGLLQPHSHSLVYVCKPTFVSSRDQDEILL 300
 DB 241 CHDPASRLDLITWLEPDPDALRCPASGLLQPHSHSLVYVCKPTFVSSRDQDEILL 300
 QY 301 PREVPDEYEVGSFMEYRQLEDLERSLTEMALGSPAAAAALLGGEEL 350
 DB 301 PREVPDEYEVGSFMEYRQLEDLERSLTEMALGSPAAAAALLGGEEL 350

RESULT 3

AAG80271
 ID AAG80271 standard; Protein; 350 AA.

XX AAG80271;
 XX 11-FEB-2002 (first entry)
 XX DT Human DKK-3 protein.
 XX DE
 XX KW DKK-3; detection; schizophrenia; neuroleptic; vaccine; gene therapy;
 XX KM neuralgic defect; neuropsychiatric disorder; human.
 XX OS Homo sapiens.
 XX PN WO200163295-A2.
 XX PD 30-AUG-2001.
 XX PF 26-FEB-2001; 2001WO-IB00259.
 XX PR 24-FEB-2000; 2000GB-0004412.
 XX PR 15-MAR-2000; 2000GB-0004415.
 XX PR 24-NOV-2000; 2000GB-0006285.
 XX PR 28-NOV-2000; 2000GB-0028734.
 XX PR 08-DEC-2000; 2000GB-0030050.
 XX PR 12-DEC-2000; 2000US-0254830.
 XX PR 28-DEC-2000; 2000US-0750395.

(OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Herath HMA, Parekh RB, Ronliff C, Patel TP;
 XX WPI; 2001-570652/64.
 DR N-PSDB; AAI69309.

PT Diagnosing and monitoring Schizophrenia by detecting the presence of
 PT Schizophrenia Associated Features and Schizophrenia Associated Protein
 PT Isoforms in samples of cerebrospinal fluid -
 XX
 XX
 PS Claim 1a; Fig 1; 91pp; English.

CC This invention describes a novel method for detecting the presence of
 CC schizophrenia associated features (SFs) and schizophrenia associated
 CC protein isoforms (SPIs) in samples, e.g. by electrophoresis, immunoassay
 CC or hybridisation assay, for diagnosing and monitoring schizophrenia,
 CC studying the effectiveness of treatments and for identifying potential
 CC therapeutic agents. The products of the invention have neuroleptic
 CC activity and can be used in vaccines or for gene therapy. The method (I)
 CC is used: (i) for screening or diagnosis of schizophrenia and the relative
 CC abundance of at least 1 chosen feature correlates with the presence or
 CC absence of schizophrenia and for monitoring the effect of therapy
 CC administered to a subject with schizophrenia and the relative abundance
 CC of at least 1 chosen feature which correlates with the severity of
 CC schizophrenia. The expression and activity of the SFs, SPIs and related
 CC molecules (e.g. secondary messengers) are studied to diagnose
 CC schizophrenia, monitor the progress of the disorder and the effectiveness
 CC of treatment and as targets to identify and produce potential therapeutic
 CC agents for the treatment of schizophrenia. The paucity of detectable
 CC neuralgic defects distinguishes neuropsychiatric disorders such as
 CC schizophrenia from neurological disorders, where manifestations of
 CC anatomical and biochemical changes have been identified in many cases.
 CC Consequently the identification and characterisation of cellular and/or
 CC molecular causative defects and neuropathies are necessary for improved
 CC treatment of neuropsychiatric disorders. This sequence represents the
 CC human DKK-3 protein described in the method of the invention.

XX Sequence 350 AA;

Query Match 100.0%; Score 350; DB 22; Length 350;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORIGATILLCILAAVPTAPAPATATSAVKGPAALSYPOEATLNEMFREVEELMED 60
 DB 1 MORIGATILLCILAAVPTAPAPATATSAVKGPAALSYPOEATLNEMFREVEELMED 60
 QY 61 TOHKLRSVAEEMAEEMAAKASSEVNLANLPSYHNETNTDTVGNNTIHHREIHKITN 120
 DB 61 TOHKLRSVAEEMAEEMAAKASSEVNLANLPSYHNETNTDTVGNNTIHHREIHKITN 120
 QY 121 NOTGQWVSEFVITVSDDEGRSHSCIIDEDCGPSMYCQFASFOYTQPCRGQRLCTR 180
 DB 121 NOTGQWVSEFVITVSDDEGRSHSCIIDEDCGPSMYCQFASFOYTQPCRGQRLCTR 180
 QY 181 DSECCGQQLCWGHCTMTATRGSGNGTICDNORCCQPGLCAPFGRLFPVCTPLPVEGEL 240
 DB 181 DSECCGQQLCWGHCTMTATRGSGNGTICDNORCCQPGLCAPFGRLFPVCTPLPVEGEL 240
 QY 241 CHDPASRLDLITWLEPDPDALRCPASGLLQPHSHSLVYVCKPTFVSSRDQDEILL 300
 DB 241 CHDPASRLDLITWLEPDPDALRCPASGLLQPHSHSLVYVCKPTFVSSRDQDEILL 300
 QY 301 PREVPDEYEVGSFMEYRQLEDLERSLTEMALGSPAAAAALLGGEEL 350
 DB 301 PREVPDEYEVGSFMEYRQLEDLERSLTEMALGSPAAAAALLGGEEL 350

RESULT 4

AAG62468
 ID AAG62468 standard; Protein; 350 AA.

XX AAG62468;
 XX

DT 10-SEP-2001 (first entry)
 XX Human reduced expression in immortalised cells protein.
 DE
 XX REIC; reduced expression in immortalised cells; cancer; tumour;
 KM proliferation inhibitor; viral infection; human.
 XX
 OS Homo sapiens.
 XX
 PN MO200138528-A1.
 XX
 PD 31-MAY-2001.
 XX
 PF 30-AUG-2000; 2000MO-JP05879.
 XX
 PR 19-NOV-1999; 99JP-0330604.
 XX
 PA (HISM) HISAMITSU PHARM CO LTD.
 XX
 PI Namba M, Tsuji T;
 XX
 WP1; 2001-367688/38.
 DR N-PSDB; AAH45489, AAH45490, AAH45491.
 XX
 PT Cell proliferation inhibiting protein REIC and polynucleotide encoding
 XX it for diagnosis and therapy of cancer and as an antiviral agent
 PS Claim 2; Page 56-57; 66pp; Japanese.
 CC This invention relates to a protein designated REIC (reduced expression
 CC in immortalised cells) which inhibits proliferation. REIC shows reduced
 CC or suppressed expression in immortalised cells such as cancer cells. The
 CC invention includes DNA and protein sequences for REIC. The protein is
 CC useful for the treatment and diagnosis of a wide range of benign and
 CC malignant tumours and of viral infections (including HIV, influenza,
 CC hepatitis and Epstein-Barr virus). The present sequence represents REIC.
 XX
 SQ Sequence 350 AA;
 Query Match 100.0%; Score 350; DB 22; Length 350;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MORIGATILCLLLAAAVPTAPAPATATSAVVKRGPAISYQBEATINEMFREVEELMED 60
 DB 1 MORIGATILCLLLAAAVPTAPAPATATSAVVKRGPAISYQBEATINEMFREVEELMED 60
 QY 61 TOHKLRAVEMEEMEAATAKASSEVNLANLPSSYHNENTDTKYGNNTIIVHREIHKITN 120
 DB 61 TOHKLRAVEMEEMEAATAKASSEVNLANLPSSYHNENTDTKYGNNTIIVHREIHKITN 120
 QY 121 NOTGQWVSEVITVSVGDEGRSHCEIIDDCGSPMYCQFASFOYTCQPCRGQMLCTR 180
 DB 121 NOTGQWVSEVITVSVGDEGRSHCEIIDDCGSPMYCQFASFOYTCQPCRGQMLCTR 180
 QY 181 DSECCGQQLCWGHCCTKMATRGNSNGTICDNQDQCPGLCAFORGLLPVCTPLPVEGEL 240
 DB 181 DSECCGQQLCWGHCCTKMATRGNSNGTICDNQDQCPGLCAFORGLLPVCTPLPVEGEL 240
 QY 241 CHDPASLLDLITWELPPDGLDRCPCASGLLCOPSHSLVYVCKPTFVGSRRQDEIILL 300
 DB 241 CHDPASLLDLITWELPPDGLDRCPCASGLLCOPSHSLVYVCKPTFVGSRRQDEIILL 300
 QY 301 PREVPDSEYGVSEMEVROELEDLERSLTERVALGEPAAAAALLGGEET 350
 DB 301 PREVPDSEYGVSEMEVROELEDLERSLTERVALGEPAAAAALLGGEET 350
 RESULT 5
 ID AAB87529 standard; Protein; 350 AA.
 XX AAB87529;
 AC

XX 15-MAY-2001 (first entry)
 DT
 XX Human PRO295.
 DE
 XX Human; PRO protein; mapping.
 KM
 XX
 OS Homo sapiens.
 XX
 PN MO200116318-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 24-AUG-2000; 2000MO-US23328.
 XX
 PR 01-SEP-1999; 99MO-US20111.
 XX
 PR 15-SEP-1999; 99MO-US21090.
 PR 07-DEC-1999; 99US-0169495.
 PR 09-DEC-1999; 99US-0170262.
 PR 11-JUN-2000; 2000US-0175481.
 PR 18-FEB-2000; 2000MO-US04341.
 PR 22-FEB-2000; 2000MO-US04342.
 PR 01-MAR-2000; 2000MO-US05601.
 PR 03-MAR-2000; 2000US-0187202.
 PR 25-APR-2000; 2000US-0199397.
 PR 22-MAY-2000; 2000MO-US14042.
 PR 05-JUN-2000; 2000US-0209832.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Eaton DL, Flivarov E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WJ;
 XX
 DR WP1; 2001-183260/18.
 DR N-PSDB; AAF92061.
 XX
 PT Eighty four nucleic acids encoding PRO polypeptides, useful in
 PT molecular biology, including use as hybridization probes, and in
 PT chromosome and gene mapping.
 XX
 PS Claim 12; Fig 8; 27bp; English.
 CC The present sequence is a human PRO polypeptide (secreted and
 CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
 CC anti-PRO antibodies are useful for preparation of a medicament useful in
 CC the treatment of a condition which is responsive to the PRO protein,
 CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
 CC employed as molecular weight markers for protein electrophoresis. The PRO
 CC coding sequence has applications in molecular biology, including use as
 CC hybridisation probes, and in chromosome and gene mapping.
 XX
 SQ Sequence 350 AA;
 Query Match 100.0%; Score 350; DB 22; Length 350;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MORIGATILCLLLAAAVPTAPAPATATSAVVKRGPAISYQBEATINEMFREVEELMED 60
 DB 1 MORIGATILCLLLAAAVPTAPAPATATSAVVKRGPAISYQBEATINEMFREVEELMED 60
 QY 61 TOHKLRAVEMEEMEAATAKASSEVNLANLPSSYHNENTDTKYGNNTIIVHREIHKITN 120
 DB 61 TOHKLRAVEMEEMEAATAKASSEVNLANLPSSYHNENTDTKYGNNTIIVHREIHKITN 120
 QY 121 NOTGQWVSEVITVSVGDEGRSHCEIIDDCGSPMYCQFASFOYTCQPCRGQMLCTR 180
 DB 121 NOTGQWVSEVITVSVGDEGRSHCEIIDDCGSPMYCQFASFOYTCQPCRGQMLCTR 180
 QY 181 DSECCGQQLCWGHCCTKMATRGNSNGTICDNQDQCPGLCAFORGLLPVCTPLPVEGEL 240
 DB 181 DSECCGQQLCWGHCCTKMATRGNSNGTICDNQDQCPGLCAFORGLLPVCTPLPVEGEL 240

QY 241 CHDPASRLDLITWLEPDGALDRCPGASGLTQPHSHSLVYVCKPTFGSRDQDGEILL 300
 DB 241 CHDPASRLDLITWLEPDGALDRCPGASGLTQPHSHSLVYVCKPTFGSRDQDGEILL 300
 QY 301 PREVPDEYVGSFMEVROELEDLERSLTERMALGEPAAAAALLGGEI 350
 DB 301 PREVPDEYVGSFMEVROELEDLERSLTERMALGEPAAAAALLGGEI 350

RESULT 6
 AAB80252
 ID AAB80252 standard; Protein: 350 AA.
 XX

AC AAB80252;
 XX

DT 24-APR-2001 (first entry)
 XX

DE Human PRO295 protein.
 XX

KW Human; PRO; dermatological; antipruritic; cytostatic; antiinflammatory;
 KW antiParkinsonian neurotropic; neuroprotective; vulnerary; cardiant;
 KW antiangiogenic; vasotropic; antiaesthetic; antineumatic; cancer;
 KW antidiabetic; antihypertensive; antidiabetic; antiviral; diabetes;
 KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
 KW ischaemia; inflammation.
 XX

OS Homo sapiens.
 XX

PN WC200104311-A1.
 XX

PD 18-JAN-2001.
 XX

PF 22-FEB-2000; 2000WC-US04414.
 XX

XX 07-JUL-1999; 99US-0143048.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146222.
 PR 08-SEP-1999; 99WC-US20594.
 PR 13-SEP-1999; 99WC-US20944.
 PR 15-SEP-1999; 99WC-US21090.
 PR 15-SEP-1999; 99WC-US21547.
 PR 05-OCT-1999; 99WC-US23089.
 PR 29-NOV-1999; 99WC-US28214.
 PR 30-NOV-1999; 99WC-US28313.
 PR 16-DEC-1999; 99WC-US30095.
 PR 20-DEC-1999; 99WC-US30911.
 PR 20-DEC-1999; 99WC-US30999.
 PR 05-JAN-2000; 99WC-US00219.
 XX

XX (GERTH) GENENTECH INC.
 XX

PI Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
 PI Fliviaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PM, Wood WI;
 XX

DR WPI, 2001-081051/09.
 DR N-PSDB; AAF72413.
 XX

XX Sixty one nucleic acids encoding PRO polypeptides which are useful in
 PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung
 PT squamous cell carcinoma) and neurodegenerative diseases (e.g.
 PT Alzheimer's disease) -
 PT

PS Claim 1; Fig 84; 393pp; English.
 XX

XX The present sequence is one of sixty one novel secreted and
 CC transmembrane PRO polypeptides. The PRO polypeptides are
 CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung
 CC squamous cell carcinoma), gastrointestinal disorders (e.g.
 CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,
 CC

CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.
 CC endometrial bleeding angiogenesis, ischaemias such as coronary
 CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,
 CC rheumatoid arthritis, multiple sclerosis), infertility, AIDS and
 CC diabetes and retinal disorders such as retinitis pigmentosa.
 CC The PRO nucleic acids have applications in molecular biology, including
 CC use as hybridization probes, and in chromosome and gene mapping.
 XX

XX Sequence 350 AA;

Query Match 100.0%; Score 350; DB 22; Length 350;
 Best local similarity 100.0%; Pred. No. 0;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORGATLLCLLLAAVPTAPAPATSAVKKPAPALSYPOEBATINMEFVEEIMED 60
 DB 1 MORGATLLCLLLAAVPTAPAPATSAVKKPAPALSYPOEBATINMEFVEEIMED 60
 QY 61 TOHKLRSVEMEAEEAAKASSEVNLANLPSPYHNETNTDTKGNNTIHVREIHKITN 120
 DB 61 TOHKLRSVEMEAEEAAKASSEVNLANLPSPYHNETNTDTKGNNTIHVREIHKITN 120
 QY 121 NOTGQWSEFVITSVGDEGRSHCEIIDDCGSPMYCQFASFOYTCOPCRGRMLCTR 180
 DB 121 NOTGQWSEFVITSVGDEGRSHCEIIDDCGSPMYCQFASFOYTCOPCRGRMLCTR 180
 QY 121 NOTGQWSEFVITSVGDEGRSHCEIIDDCGSPMYCQFASFOYTCOPCRGRMLCTR 180
 DB 181 DSECCGDLQWGHCTKATRTGNSGTICDNORDCQPGICCAFQGRLLFPVCTPLPVGEEL 240
 DB 181 DSECCGDLQWGHCTKATRTGNSGTICDNORDCQPGICCAFQGRLLFPVCTPLPVGEEL 240
 QY 241 CHDPASRLDLITWLEPDGALDRCPGASGLTQPHSHSLVYVCKPTFGSRDQDGEILL 300
 DB 241 CHDPASRLDLITWLEPDGALDRCPGASGLTQPHSHSLVYVCKPTFGSRDQDGEILL 300
 QY 301 PREVPDEYVGSFMEVROELEDLERSLTERMALGEPAAAAALLGGEI 350
 DB 301 PREVPDEYVGSFMEVROELEDLERSLTERMALGEPAAAAALLGGEI 350

RESULT 7

ID AAB95854 standard; Protein: 350 AA.
 XX

AC AAB95854;
 XX

DT 10-DEC-2002 (first entry)
 XX

DE Human secreted/transmembrane protein PRO295.
 XX

KW Human; secreted protein; transmembrane protein; antineumatic;
 KW antiarthritic; osteopathic; sports-related joint problem;
 KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
 XX

OS Homo sapiens.
 XX

PN US2002119130-A1.
 XX

PD 29-AUG-2002.
 XX

PF 06-DEC-2001; 2001US-0006867.
 XX

XX 29-OCT-1997; 97US-063435P.
 PR 29-OCT-1997; 97US-064215P.
 PR 22-APR-1998; 98US-082797P.
 PR 29-APR-1998; 98US-083495P.
 PR 15-MAY-1998; 98US-085579P.
 PR 10-JUN-1998; 98US-088811P.
 PR 10-JUN-1998; 98US-088824P.
 PR 10-JUN-1998; 98US-088825P.
 PR 11-JUN-1998; 98US-088863P.
 PR 12-JUN-1998; 98US-089105P.
 PR 16-JUN-1998; 98US-089514P.
 PR 16-SEP-1998; 98WC-US19350.
 XX

PR 08-NOV-2000; 2000MO-US30952.
 PR 10-NOV-2000; 2000MO-US30873.
 PR 01-DEC-2000; 2000MO-US32678.
 PR 20-DEC-2000; 2000MO-US74259.
 PR 20-DEC-2000; 2000MO-US34969.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-076498.
 PR 28-FEB-2001; 2001MO-US06520.
 PR 01-MAR-2001; 2001MO-US06666.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828356.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001MO-US66034.
 PR 25-MAY-2001; 2001MO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001MO-US17443.
 PR 01-JUN-2001; 2001MO-US17800.
 PR 20-JUN-2001; 2001MO-US19692.
 PR 28-JUN-2001; 2001MO-US00000.

XX (GETH) GENENTECH INC.
 PA (BAKE/) BAKER K P.
 PA (FERR/) FERRARA N.
 PA (GERB/) GERBER H.
 PA (GERB/) GERBERTSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANU/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.

PI Baker KP, Ferrera N, Gerber H, Gerritsen ME, Goddard A,
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Paoni NF,
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,
 XX WPI; 2002-171999/22.
 DR N-PSDB; ABL95585.

PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -
 XX
 PS Claim 11; Fig 50; 567pp; English.

XX The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumor
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a PRO protein of the invention.

XX Sequence 350 AA;

Query Match 100.0%; Score 350; DB 23; Length 350;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORIGATLCLLLAAAVTAPAPAPTATSAVKGAPALSYPOEATLNMFEVLELMD 60
 Db 1 MORIGATLCLLLAAAVTAPAPAPTATSAVKGAPALSYPOEATLNMFEVLELMD 60

QY 61 TQHKLSAVEEMEAFAAKASSEVNLANLPSSYHNETNDTKYGNNTIHYREIHKITN 120
 Db 61 TQHKLSAVEEMEAFAAKASSEVNLANLPSSYHNETNDTKYGNNTIHYREIHKITN 120
 QY 121 NOTGMVSEETVITSVGDEGRSRSHCECTIDDCGPPSYCOPASFOYTCOPRGPMCTR 180
 Db 121 NOTGMVSEETVITSVGDEGRSRSHCECTIDDCGPPSYCOPASFOYTCOPRGPMCTR 180
 QY 181 DSECCGDLCTWGHCTKATGNSGTICDNORDCPGCGCFORGLLFPVCTP.PVGEEL 240
 Db 181 DSECCGDLCTWGHCTKATGNSGTICDNORDCPGCGCFORGLLFPVCTP.PVGEEL 240
 QY 241 CHDPASRLDILITWLEPFDGALDRCPASGLLCPHSHSLVYCKPTFVGSRDDGELTL 300
 Db 241 CHDPASRLDILITWLEPFDGALDRCPASGLLCPHSHSLVYCKPTFVGSRDDGELTL 300
 QY 301 PREVPDEYVGSFMEYVQGEJEDLERSLTFEEMALGEPAAAAALLGGEI 350
 Db 301 PREVPDEYVGSFMEYVQGEJEDLERSLTFEEMALGEPAAAAALLGGEI 350

RESULT 9
 ABB90735
 ID ABB90735 standard; Protein; 350 AA.

XX ABB90735;

DT 30-MAY-2002 (first entry)

DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 202.

KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
 KW normal endothelial marker; pan-endothelial marker; immunostimulant;
 KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
 KW psoriasis.

OS Homo sapiens.

PN WO200210217-A2.

XX 07-FEB-2002.

PF 01-AUG-2001; 2001MO-US24031.

PR 02-AUG-2000; 2000US-222599P.

PR 11-AUG-2000; 2000US-224360P.

PR 11-APR-2001; 2001US-282850P.

PA (UTVO) UNIV JOHNS HOPKINS.

PI St Croix B, Kinzler KW, Vogelstein B;

DR WPI; 2002-291656/33.

DR N-PSDB; ABL92089.

PT An isolated molecule comprising an antibody variable region which
 PT specifically binds to an extracellular domain of a tumor endothelial
 PT marker (TEM) protein, useful for inhibiting tumor growth -
 XX
 PS Claim 54; Page 156-157; 331pp; English.

XX The invention relates to an isolated molecule comprising an antibody
 CC variable region which specifically binds to an extracellular domain of a
 CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
 CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
 CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
 CC They are useful for inhibiting tumour growth, neoangiogenesis in
 CC subjects bearing a vascularised tumour, polycystic kidney disease,
 CC diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse
 CC and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and
 CC ABB90721-ABB90789) are disclosed, as are marker oligonucleotide
 CC sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and

CC ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074;
 CC and pan-endothelial markers (PEM) ABL91903-ABL91995.
 XX Sequence 350 AA;
 Query Match 100.0%; Score 350; DB 23; Length 350;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MORLGATLLCLLAAVPTAPAPATATSAVPKGPALSTPOEATLNMFEVEEIMED 60
 Db 1 MORLGATLLCLLAAVPTAPAPATATSAVPKGPALSTPOEATLNMFEVEEIMED 60
 QY 61 TQHKLSAVEMEAEBAKASSEVNLANLPSTYHNETNTDTKGNNTIHYHREIHKITN 120
 Db 61 TQHKLSAVEMEAEBAKASSEVNLANLPSTYHNETNTDTKGNNTIHYHREIHKITN 120
 QY 121 NOTGQWVFSEVITVSVDDEGRSHCEIIDEDCGPSMYCQFASFOYTCQPCRGQRLCTR 180
 Db 121 NOTGQWVFSEVITVSVDDEGRSHCEIIDEDCGPSMYCQFASFOYTCQPCRGQRLCTR 180
 QY 181 DSECCGQDLCTWGHCTKMATRGSGNTICDNQDCQPGLCARFQGLLPVCTPLPYEGEL 240
 Db 181 DSECCGQDLCTWGHCTKMATRGSGNTICDNQDCQPGLCARFQGLLPVCTPLPYEGEL 240
 QY 241 CHDPASRLDLITWELBPQALDRPCASGLLCQPHSHSLVYVCKPTFVGSRDQGEILL 300
 Db 241 CHDPASRLDLITWELBPQALDRPCASGLLCQPHSHSLVYVCKPTFVGSRDQGEILL 300
 QY 301 PREVPDEYEVGSFMEVRQELDLERSLTLEMAJGPAAAAALLGGEI 350
 Db 301 PREVPDEYEVGSFMEVRQELDLERSLTLEMAJGPAAAAALLGGEI 350
 RESULT 10
 ABB84841
 ID ABB84841 standard; Protein; 350 AA.
 AC ABB84841;
 XX DT 16-MAY-2002 (first entry)
 XX DE Human PRO295 protein sequence SEQ ID NO:50.
 XX KW Human; angiogenesis; cardiast; cytoslastic; antiangiogenic; hypotensive;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping.
 XX OS Homo sapiens.
 XX PN W0200200690-A2.
 XX PD 03-JAN-2002.
 XX PF 20-JUN-2001; 2001MO-US19692.
 XX PR 23-JUN-2000; 2000US-213637P.
 PR 26-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 28-JUL-2000; 2000MO-US20710.
 PR 02-AUG-2000; 2000US-222695P.
 PR 17-AUG-2000; 2000MO-US43657.
 PR 23-AUG-2000; 2000MO-US23522.
 PR 24-AUG-2000; 2000MO-US23328.
 PR 07-SEP-2000; 2000US-230978P.
 PR 18-SEP-2000; 2000US-0664610.
 PR 18-SEP-2000; 2000US-0665350.

PR 24-OCT-2000; 2000US-242922P.
 PR 08-NOV-2000; 2000US-0709238.
 PR 08-NOV-2000; 2000MO-US30952.
 PR 10-NOV-2000; 2000MO-US30873.
 PR 01-DEC-2000; 2000MO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000MO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 01-MAR-2001; 2001MO-US06666.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828368.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001MO-US17092.
 PR 30-MAY-2001; 2001MO-US17443.
 PR 01-JUN-2001; 2001MO-US17800.
 PA (GETH) GENENTECH INC.
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
 PI Godowski PJ, Gurney AL, Hillan KJ, Masters SA, Pan D, Paoni NF,
 PI Stephan OF, Watanabe CK, Williams FM, Wood WI, Ye W;
 DR WPI; 2002-090516/12.
 DR N-PSDB; ABL88096.
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -
 XX "PS
 XX Claim 11; Fig 50; 565pp; English.
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytoslastic,
 CC antiangiogenic, hypotensive, vulnery and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
 CC carcinoma) and wound healing. The PRO polynucleotides have applications
 CC in molecular biology, including use as hybridisation probes, and in
 CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
 CC probes used in the exemplification of the present invention.
 XX Sequence 350 AA;
 Query Match 100.0%; Score 350; DB 23; Length 350;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MORLGATLLCLLAAVPTAPAPATATSAVPKGPALSTPOEATLNMFEVEEIMED 60
 Db 1 MORLGATLLCLLAAVPTAPAPATATSAVPKGPALSTPOEATLNMFEVEEIMED 60
 QY 61 TQHKLSAVEMEAEBAKASSEVNLANLPSTYHNETNTDTKGNNTIHYHREIHKITN 120
 Db 61 TQHKLSAVEMEAEBAKASSEVNLANLPSTYHNETNTDTKGNNTIHYHREIHKITN 120
 QY 121 NOTGQWVFSEVITVSVDDEGRSHCEIIDEDCGPSMYCQFASFOYTCQPCRGQRLCTR 180
 Db 121 NOTGQWVFSEVITVSVDDEGRSHCEIIDEDCGPSMYCQFASFOYTCQPCRGQRLCTR 180
 QY 181 DSECCGQDLCTWGHCTKMATRGSGNTICDNQDCQPGLCARFQGLLPVCTPLPYEGEL 240

DB 181 DECCGDCQVGHGCHTKATRSNGTICNQRDCPGACAFRGILPVCTPLVEGEL 240
QY 241 CHDPASRLDLITWELPEPGALDRCPGASGLLCOPHSILVYVCKPTFGSRDQGEILL 300
DB 241 CHDPASRLDLITWELPEPGALDRCPGASGLLCOPHSILVYVCKPTFGSRDQGEILL 300
QY 301 PREVPDEYVGSFMEVRQELDLERSLTENALGEPAAAAALLGGEEL 350
DB 301 PREVPDEYVGSFMEVRQELDLERSLTENALGEPAAAAALLGGEEL 350
RESULT 11
ABU69662
ID ABU69662 standard; Protein; 350 AA.
AC ABU69662;
XX
XX 05-JUN-2003 (first entry)
DT
XX
XX Novel human secreted and transmembrane protein PROC95.
XX
XX Human; secreted and transmembrane protein; gene therapy; psoriasis;
XX enterocolitis; gastrointestinal ulceration; skin disease;
XX keratinocyte differentiation; epithelial cancer; Alzheimer's disease;
XX squamous cell carcinoma; Parkinson's disease; inflammatory disease;
XX amyotrophic lateral sclerosis; rheumatoid arthritis; asthma;
XX multiple sclerosis; organ failure; atherosclerosis; cardiac injury;
XX infertility; birth defect; premature aging; AIDS; cancer;
XX diabetic complication; wound repair; tissue re-growth.
XX Homo sapiens.
XX OS
XX PN US2003017463-A1.
XX
XX 23-JAN-2003.
XX
XX
XX 11-JUL-2001; 2001US-0903640.
XX
XX 10-SEP-1998; 98WO-US18624.
XX 14-SEP-1998; 98WO-US19177.
XX 16-SEP-1998; 98WO-US19330.
XX 17-SEP-1998; 98WO-US19437.
XX 01-DEC-1998; 98WO-US25108.
XX 08-SEP-1999; 99WO-US20594.
XX 13-SEP-1999; 99WO-US20944.
XX 15-SEP-1999; 99WO-US21090.
XX 15-SEP-1999; 99WO-US21547.
XX 05-OCT-1999; 99WO-US23089.
XX 29-NOV-1999; 99WO-US28214.
XX 30-NOV-1999; 99WO-US28313.
XX 01-DEC-1999; 99WO-US28301.
XX 02-DEC-1999; 99WO-US28564.
XX 02-DEC-1999; 99WO-US28565.
XX 16-DEC-1999; 99WO-US30095.
XX 20-DEC-1999; 99WO-US30811.
XX 20-DEC-1999; 99WO-US30999.
XX 05-JAN-2000; 2000WO-US00219.
XX 11-FEB-2000; 2000WO-US03565.
XX 22-FEB-2000; 2000WO-US04414.
XX 24-FEB-2000; 2000WO-US05004.
XX 02-MAR-2000; 2000WO-US05841.
XX 20-MAR-2000; 2000WO-US07377.
XX 30-MAR-2000; 2000WO-US08439.
XX 22-MAY-2000; 2000WO-US14042.
XX 02-JUN-2000; 2000WO-US15264.
XX 28-JUL-2000; 2000WO-US20710.
XX 24-AUG-2000; 2000WO-US23328.
XX 17-SEP-1997; 97US-059113P.
XX 17-SEP-1997; 97US-059115P.
XX 17-SEP-1997; 97US-059117P.
XX 17-SEP-1997; 97US-059119P.
XX 17-SEP-1997; 97US-059121P.

PR 17-SEP-1997; 97US-059122P.
PR 17-SEP-1997; 97US-059184P.
PR 18-SEP-1997; 97US-059263P.
PR 18-SEP-1997; 97US-059266P.
PR 15-OCT-1997; 97US-062125P.
PR 17-OCT-1997; 97US-062285P.
PR 17-OCT-1997; 97US-062287P.
PR 21-OCT-1997; 97US-063486P.
PR 24-OCT-1997; 97US-062814P.
PR 24-OCT-1997; 97US-062816P.
PR 24-OCT-1997; 97US-063045P.
PR 24-OCT-1997; 97US-063120P.
PR 24-OCT-1997; 97US-063120P.
PR 24-OCT-1997; 97US-063121P.
PR 24-OCT-1997; 97US-063127P.
PR 24-OCT-1997; 97US-063128P.
PR 27-OCT-1997; 97US-063327P.
PR 27-OCT-1997; 97US-063329P.
PR 28-OCT-1997; 97US-063541P.
PR 28-OCT-1997; 97US-063542P.
PR 28-OCT-1997; 97US-063544P.
PR 28-OCT-1997; 97US-063549P.
PR 28-OCT-1997; 97US-063550P.
PR 28-OCT-1997; 97US-063564P.
PR 29-OCT-1997; 97US-063435P.
PR 29-OCT-1997; 97US-063704P.
PR 29-OCT-1997; 97US-063732P.
PR 29-OCT-1997; 97US-063734P.
PR 29-OCT-1997; 97US-063735P.
PR 29-OCT-1997; 97US-063738P.
PR 29-OCT-1997; 97US-064215P.
PR 31-OCT-1997; 97US-063870P.
PR 31-OCT-1997; 97US-064103P.
PR 03-NOV-1997; 97US-064248P.
PR 07-NOV-1997; 97US-064809P.
PR 12-NOV-1997; 97US-065186P.
PR 17-NOV-1997; 97US-065846P.
PR 18-NOV-1997; 97US-065693P.
PR 21-NOV-1997; 97US-066120P.
PR 21-NOV-1997; 97US-066364P.
PR 24-NOV-1997; 97US-066453P.
PR 24-NOV-1997; 97US-066466P.
PR 24-NOV-1997; 97US-066511P.
PR 24-NOV-1997; 97US-066770P.
PR 24-NOV-1997; 97US-066772P.
PR 25-NOV-1997; 97US-066840P.
PR 12-DEC-1997; 97US-069425P.
PR 04-JUN-1998; 98US-088026P.
PR 10-SEP-1998; 98US-089803P.
PR 14-SEP-1998; 98US-100262P.
PR 17-SEP-1998; 98US-100858P.
PR 13-OCT-1998; 98US-104080P.
PR 20-NOV-1998; 98US-109304P.
PR 22-DEC-1998; 98US-113296P.
PR 07-JUL-1999; 99US-143048P.
PR 26-JUL-1999; 99US-145698P.
PR 28-JUL-1999; 99US-146222P.
PR 18-SEP-2000; 2000US-0665350.
PA (GETH) GENENTECH INC.
XX
XX Ashkenazi A, Botstein D, Desnovers L, Baton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Garber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather UP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams FM, Wood WI;
XX
XX WPI; 2003-341586/32.
DR N-PSDB; ACAS5002.
XX
XX New PRO polypeptides and nucleic acid molecules, useful in diagnosing
PT or treating inflammatory diseases, organ failure, atherosclerosis,
PT cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or
PT Parkinson's disease -

Claim 12, Fig 84: English.

The invention describes sixty one nucleic acids encoding PRO polypeptides (secreted and transmembrane). The PRO polypeptides and nucleic acids are useful in diagnosing or treating enterocolitis, gastrointestinal ulceration, skin diseases associated with abnormal keratinocyte differentiation, e.g., psoriasis or epithelial cancers such as squamous cell carcinoma, Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, inflammatory diseases, e.g. rheumatoid arthritis, asthma or multiple sclerosis, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, diabetic complications, or mutations in general. The polypeptides are also useful for wound repair and associated therapies concerned with re-growth of tissue. The PRO polypeptides and nucleic acid molecules are also useful in gene therapy, and as molecular weight markers for protein electrophoresis purposes. The anti-PRO antibodies may be used in diagnostic assays for PRO, or for the affinity purification of PRO from recombinant cell culture or natural sources. This is the amino acid sequence of a novel human PRO polypeptide.

SQ Sequence 350 AA;

Query Match	100.0%	Score 350;	DB 24;	Length 350;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 350; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

QY	1	MORLAATLTCLLIAA	PTAPAPATAPATASAVKRGPALSYOEBA	TLNEMFPEE	ME	60
Db	1	MORLAATLTCLLIAA	AVPTAPAPATASAVKRGPALSYOEBA	TLNEMFPEE	ME	60
QY	61	TOHKLRSAVEEMEA	EAALAKASSEYNLANLP	PSYHNETNTD	KVGNNT	120
Db	61	TOHKLRSAVEEMEA	EAALAKASSEYNLANLP	PSYHNETNTD	KVGNNT	120
QY	121	NOTGQWVSEVYIT	SVGDEBGRSHSECI	IIDDCGFSWY	CGPASFQY	180
Db	121	NOTGQWVSEVYIT	SVGDEBGRSHSECI	IIDDCGFSWY	CGPASFQY	180
QY	181	DSECCGGDOL	CWGHCTKAA	TRGSNGT	ICDNORD	240
Db	181	DSECCGGDOL	CWGHCTKAA	TRGSNGT	ICDNORD	240
QY	241	CHDPASRLDLIT	TWLEBPDGAL	DRCP	CA	300
Db	241	CHDPASRLDLIT	TWLEBPDGAL	DRCP	CA	300
QY	301	PREVDEDEVG	FSFMEVYQ	CELDLERS	LT	360
Db	301	PREVDEDEVG	FSFMEVYQ	CELDLERS	LT	360
QY	361	PREVDEDEVG	FSFMEVYQ	CELDLERS	LT	420
Db	361	PREVDEDEVG	FSFMEVYQ	CELDLERS	LT	420

RESULT 12	
ABU71485	
ID	ABU71485 standard; Protein; 350 AA

AC	ABU71485;
XX	
ND	10-JUN-2003 (first entry)
DE	
XX	
XX	Human PRO polypeptide #41.
XX	
XX	Human; secreted and transmembrane protein; PRO polypeptide; cancer;
KW	Alzheimer's disease; ischaemia; cytostatic; nootropic; vasotropic;
KW	neuroprotective.
XX	
XX	
OS	Homo sapiens.
XX	
PN	US2002192659-A1.
XX	
XX	
PD	19-DEC-2002.
XX	
XX	
FF	10-JUN-2001; 2001US-0902853.

XX	10-SEP-1998;	98WC-US18824.
XX	14-SEP-1998;	98WC-US19177.
PR	15-SEP-1998;	98WC-US19330.
PR	17-SEP-1998;	98WC-US19437.
PR	01-DEC-1998;	98WC-US25108.
PR	08-SEP-1999;	99WC-US20594.
PR	13-SEP-1999;	99WC-US20944.
PR	15-SEP-1999;	99WC-US21090.
PR	15-SEP-1999;	99WC-US21547.
PR	05-OCT-1999;	99WC-US23089.
PR	01-DEC-1999;	99WC-US28301.
PR	02-DEC-1999;	99WC-US28564.
PR	02-DEC-1999;	99WC-US28565.
PR	16-DEC-1999;	99WC-US30095.
PR	20-DEC-1999;	99WC-US30911.
PR	20-DEC-1999;	99WC-US30999.
PR	05-JAN-2000;	2000WC-US00219.
PR	11-FEB-2000;	2000WC-US03565.
PR	22-FEB-2000;	2000WC-US04414.
PR	28-JUL-2000;	2000WC-US20710.
PR	24-AUG-2000;	2000WC-US23328.
PR	17-SEP-1997;	97US-059113B.
PR	17-SEP-1997;	97US-059115B.
PR	17-SEP-1997;	97US-059117P.
PR	18-SEP-1997;	97US-059266P.
PR	15-OCT-1997;	97US-062125P.
PR	17-OCT-1997;	97US-062285P.
PR	17-OCT-1997;	97US-062287P.
PR	21-OCT-1997;	97US-063486P.
PR	24-OCT-1997;	97US-062814P.
PR	24-OCT-1997;	97US-062816P.

(GETH) GENENTECH INC.

PI Abkhentzi A, Borstein D, Desnoyers L, Eaton DL, Ferrara N, Filyavroff E, Fong S, Gao W, Geber H, Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gunney AL, Hillan KJ, Kijavlin IJ, Mather JP, Pan U, Paoni NF, Roy MA, Stewart TA, Williams PM, Wood WJ, Tumas D;

XX
WPI: 2003-361832/34.
DR
N-PSDB: ACA58487.

PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or
PT PRO1868, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy -

PS Claim 12; Fig 84; 474pp; English.

CC The present invention relates to the isolation of novel human secreted
CC and transmembrane proteins (PRO polypeptide), and the polynucleotide
CC sequences encoding them. The polynucleotide sequences are useful in
CC molecular biology, as hybridisation probes, in chromosome and gene
CC mapping, in generating antisense RNA and DNA, and in gene therapy. These
CC polynucleotide sequences may also be used in preparing PRO polypeptides
CC by recombinant techniques, and in generating either transgenic animals
CC or knock-out animals which, in turn, are useful in the development and
CC screening of therapeutically useful reagents. The PRO polypeptides or
CC their antibodies are useful in preparing a medicament for treating a
CC condition responsive to the polypeptide or antibody, such as cancer,
CC Alzheimer's disease or ischaemia, and in various diagnostic assays.
CC ABU71445-ABU71505 represent human PRO polypeptides of the invention.

Sequence 350 AA;

Query Match	100.0%;	Score 350;	DB 24;	Length 350;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 350;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy 1 MQRGATLLCLLAAAVPTAPAPAPATSAPVKPGPALSYQGEATLNEMFREVELMED 60
|||
Db 1 MQRGATLLCLLAAAVPTAPAPAPATSAPVKPGPALSYQGEATLNEMFREVELMED 60

QY	6	TOHKRSAAVEENDEAEAAKASSEYVLANLP	PSYHNENNTDTKXGNTIHHREIKITN	120
Db	61	TOHKRSAAVEENDEAEAAKASSEYVLANLP	PSYHNENNTDTKXGNTIHHREIKITN	120
QY	121	NOTGVMVFSEFVITVSGDEEGRSH	ECIIIDECGSMYCOFASFQYTCPCRGRML	CTR 160
Db	121	NOTGVMVFSEFVITVSGDEEGRSH	ECIIIDECGSMYCOFASFQYTCPCRGRML	CTR 160
QY	181	DSRCGGDOLCVMGHCKYKMATRGSNGTICD	QNPQDQPGICAFQFGILLFPVCTPLPVYGE	L 240
Db	181	DSRCGGDOLCVMGHCKYKMATRGSNGTICD	QNPQDQPGICAFQFGILLFPVCTPLPVYGE	L 240
QY	241	CHDPASRLDLITWELEPDGALDRCP	CAAGLLCQPHSHSLVYVKETPTFVSGR	DDGEIILL 300
Db	241	CHDPASRLDLITWELEPDGALDRCP	CAAGLLCQPHSHSLVYVKETPTFVSGR	DDGEIILL 300
QY	301	PRFVPEYEVGSMFEVROLEDLERSLT	EEVMALEGPAAAAALLGGEI	350
Db	301	PRFVPEYEVGSMFEVROLEDLERSLT	EEVMALEGPAAAAALLGGEI	350

ID ABU71931 standard; Protein; 350 AA.
 XX AC ABU71931;
 XX DT 12-JUN-2003 (first entry)
 DE Human secreted/transmembrane protein PRO295.
 XX KM Human; secreted protein; transmembrane protein; PRO.
 XX gene therapy; chromosome identification; chromosome marker.
 XX OS Homo sapiens.
 XX UN US2003003530-A1.
 PD 02-JAN-2003.
 XX 11-JUL-2001; 2001US-0904011.
 XX 10-SEP-1998; 98MO-US18824.
 PR 14-SEP-1998; 98MO-US19177.
 PR 16-SEP-1998; 98MO-US19330.
 PR 17-SEP-1998; 98MO-US19337.
 PR 01-DEC-1998; 98MO-US25108.
 PR 08-SEP-1999; 99MO-US20594.
 PR 13-SEP-1999; 99MO-US20944.
 PR 15-SEP-1999; 99MO-US21090.
 PR 05-OCT-1999; 99MO-US21547.
 PR 29-NOV-1999; 99MO-US28214.
 PR 30-NOV-1999; 99MO-US28313.
 PR 01-DEC-1999; 99MO-US28301.
 PR 02-DEC-1999; 99MO-US28564.
 PR 02-DEC-1999; 99MO-US28565.
 PR 16-DEC-1999; 99MO-US30095.
 PR 20-DEC-1999; 99MO-US30911.
 PR 20-DEC-1999; 99MO-US30999.
 PR 05-JAN-2000; 2000MO-US00219.
 PR 11-FEB-2000; 2000MO-US03565.
 PR 22-FEB-2000; 2000MO-US04414.
 PR 24-FEB-2000; 2000MO-US05004.
 PR 02-MAR-2000; 2000MO-US05841.
 PR 20-MAR-2000; 2000MO-US07377.
 PR 30-MAR-2000; 2000MO-US08439.
 PR 22-MAY-2000; 2000MO-US14042.
 PR 28-JUL-2000; 2000MO-US15264.
 PR 28-AUG-2000; 2000MO-US23328.
 PR 17-SEP-1997; 97US-059113P.
 PR 17-SEP-1997; 97US-059115P.
 PR 17-SEP-1997; 97US-059117P.
 PR 17-SEP-1997; 97US-059119P.
 PR 17-SEP-1997; 97US-059121P.
 PR 17-SEP-1997; 97US-059122P.
 PR 18-SEP-1997; 97US-059263P.
 PR 18-SEP-1997; 97US-059266P.
 PR 15-OCT-1997; 97US-062125P.
 PR 17-OCT-1997; 97US-062285P.
 PR 17-OCT-1997; 97US-062287P.
 PR 21-OCT-1997; 97US-063486P.
 PR 24-OCT-1997; 97US-062814P.
 PR 24-OCT-1997; 97US-062816P.
 PR 24-OCT-1997; 97US-063045P.
 PR 24-OCT-1997; 97US-063120P.
 PR 24-OCT-1997; 97US-063121P.
 PR 24-OCT-1997; 97US-063127P.
 PR 24-OCT-1997; 97US-063128P.
 PR 27-OCT-1997; 97US-063327P.
 PR 27-OCT-1997; 97US-063329P.
 PR 28-OCT-1997; 97US-063541P.
 PR 28-OCT-1997; 97US-063542P.
 PR 28-OCT-1997; 97US-063544P.

PR 28-OCT-1997; 97US-063549P.
 PR 28-OCT-1997; 97US-063550P.
 PR 28-OCT-1997; 97US-063564P.
 PR 29-OCT-1997; 97US-063435P.
 PR 29-OCT-1997; 97US-063704P.
 PR 29-OCT-1997; 97US-063732P.
 PR 29-OCT-1997; 97US-063734P.
 PR 29-OCT-1997; 97US-063735P.
 PR 29-OCT-1997; 97US-063738P.
 PR 29-OCT-1997; 97US-064215P.
 PR 31-OCT-1997; 97US-063870P.
 PR 31-OCT-1997; 97US-064103P.
 PR 03-NOV-1997; 97US-064240P.
 PR 07-NOV-1997; 97US-064809P.
 PR 12-NOV-1997; 97US-065186P.
 PR 17-NOV-1997; 97US-065846P.
 PR 18-NOV-1997; 97US-065693P.
 PR 21-NOV-1997; 97US-066120P.
 PR 21-NOV-1997; 97US-066364P.
 PR 24-NOV-1997; 97US-066453P.
 PR 24-NOV-1997; 97US-066466P.
 PR 24-NOV-1997; 97US-066511P.
 PR 24-NOV-1997; 97US-066770P.
 PR 24-NOV-1997; 97US-066772P.
 PR 18-SEP-2000; 2000US-0665350.
 XX (GETH) GENENTECH INC.
 XX PA Ashkenazi A, Botstein D, Deansoyers L, Baton DU, Ferrara N;
 XX PI Pong S, Gerber H, Gertsen ME, Goddard A;
 XX PI Godowski PJ, Grimaldi UC, Gurney AL, Hillan KJ, Kljavin IJ;
 XX PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 XX PI Williams PM, Wood WI;
 XX WIPI; 2003-329602/31.
 DR N-PSDB; ACA60194.
 XX
 PT New transmembrane polypeptides and nucleic acids encoding the
 PT polypeptides, useful in gene therapy, in chromosome identification, as
 PT chromosome markers, in generating probes and in tissue typing
 XX
 PS Claim 12; Fig 84; 484p; English.
 CC The invention relates to an isolated nucleic acid with at least 80%
 CC nucleic acid sequence identity to a nucleic acid sequence encoding one of
 CC 61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a
 CC PRO protein extracellular domain. Also included are a vector comprising
 CC the PRO nucleic acid, a host cell comprising the vector, producing a PRO
 CC polypeptide (by culturing the host cell for the expression of the PRO
 CC polypeptide, and recovering the PRO polypeptide from the cell culture),
 CC an isolated PRO polypeptide (having at least 80% sequence identity
 CC to: (a) an amino acid sequence selected from the 61 PRO proteins;
 CC (b) an amino acid sequence encoded by a nucleic acid molecule deposited
 CC with an ATCC number (detailed in the specification); or (c) an
 CC extracellular domain of a PRO polypeptide or to a PRO polypeptide lacking
 CC its associated signal peptide), a chimeric molecule comprising a PRO
 CC polypeptide of fused to a heterologous amino acid sequence, an anti-PRO
 CC antibody, detecting a PRO245 or PRO1868 in a sample suspected of
 CC containing the polypeptide, linking a bioactive molecule to a cell
 CC expressing a PRO245 or PRO1868 and modulating at least one biological
 CC activity of a cell expressing a PRO245 or PRO1868. Nucleic acids which
 CC encode PRO can be used to generate either transgenic animals or knock-out
 CC animals which may be used in the development and screening of
 CC therapeutically useful reagents. The nucleic acids may also be used in
 CC gene therapy, in chromosome identification, as chromosome markers, or in
 CC generating probes. The PRO polypeptides are useful as molecular markers
 CC for protein electrophoresis, and the isolated nucleic acids may be used
 CC for recombinantly expressing those markers. The PRO polypeptides and
 CC nucleic acids may also be used in tissue typing. Anti-PRO antibodies
 CC are useful in diagnostic assays for PRO, and in affinity purification
 CC of PRO from recombinant cell culture or natural sources. The
 XX present sequence represents a PRO protein.

XX DR MPI: 2003-331484/31.
XX N-PSDB; ACA63376.
PT Novel monoclonal antibody that binds to secreted and transmembrane
PT polypeptide, useful for detecting and purifying the polypeptide and
PT also for treating conditions responsive to the antibody
XX PS Disclosure; Fig 8; 408bp; English.
XX CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a
CC medicament useful in the treatment of a condition responsive to
CC anti-PRO antibody. Anti-PRO antibodies are useful in diagnostic
CC assays for PRO, by detecting its expression in specific cells,
CC tissues or serum, and for affinity purification of PRO from
CC recombinant cell culture or natural sources. AB072109-AB072192
CC represent the human PRO polypeptides of the invention.
XX SQ Sequence 350 AA;
Query Match 100.0%; Score 350; DB 24; Length 350;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQRIGATLLCLLAAVPTAPAPATAPAPVAPKPPALSYQEEATINEMFREVEELMED 60
1 MQRIGATLLCLLAAVPTAPAPATAPAPVAPKPPALSYQEEATINEMFREVEELMED 60
Db 61 TQHKLRSAVEEMEAEEAAKASSEVNLANPSPYHNETNDTVGNNTHVHEIKITN 120
61 TQHKLRSAVEEMEAEEAAKASSEVNLANPSPYHNETNDTVGNNTHVHEIKITN 120
QY 121 NOTGOWFSEVTITVSGDEGRSHCEIIDDCGSPMYCQFASFOYTCQPCRCQRMCTR 180
121 NOTGOWFSEVTITVSGDEGRSHCEIIDDCGSPMYCQFASFOYTCQPCRCQRMCTR 180
Db 181 DSECCGQOLCVWGHCTMTARGSNCTICDNRQCPQLCAFRGILLFPYCTPLPVEGEL 240
181 DSECCGQOLCVWGHCTMTARGSNCTICDNRQCPQLCAFRGILLFPYCTPLPVEGEL 240
QY 241 CHDPASRLDLITWELPDGALDRPCASGLICQPHSHSLVYVCKPTFVGSRRDQGEILL 300
241 CHDPASRLDLITWELPDGALDRPCASGLICQPHSHSLVYVCKPTFVGSRRDQGEILL 300
Db 301 PREVPDEYEVGSFMEYVRQLELIERSLTEMALGEPAAAAALLGGEET 350
301 PREVPDEYEVGSFMEYVRQLELIERSLTEMALGEPAAAAALLGGEET 350
RESULT 17
AB067385
ID AB067385 standard; Protein; 350 AA.
XX AC AB067385;
XX DT 29-MAY-2003 (first entry)
XX DE Human secreted protein PRO295.
XX KW Human; gene therapy; mucosal lesion; ulcer; enterocolitis; skin disease;
XX KW psoriasis; cancer; lung cancer; colon cancer; nerve cell disease;
XX KW Alzheimer's disease; Parkinson's disease; Usler syndrome; angiogenesis;
XX KW atropia areata; inflammatory disease; asthma; rheumatoid arthritis;
XX KW ischaemia.
XX OS Homo sapiens.
XX PN US2003023054-A1.
XX PD 30-JAN-2003.

XX PF 16-JUL-2001; 2001US-0906742.
XX XX
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 01-DEC-1998; 98WO-US25108.
PR 08-SEP-1999; 98WO-US20594.
PR 13-SEP-1999; 98WO-US21090.
PR 15-SEP-1999; 98WO-US21090.
PR 15-SEP-1999; 98WO-US21547.
PR 05-OCT-1999; 98WO-US22089.
PR 29-NOV-1999; 98WO-US28214.
PR 30-NOV-1999; 98WO-US28313.
PR 01-DEC-1999; 98WO-US28301.
PR 02-DEC-1999; 98WO-US28564.
PR 02-DEC-1999; 98WO-US28565.
PR 16-DEC-1999; 98WO-US30099.
PR 20-DEC-1999; 98WO-US30911.
PR 20-DEC-1999; 98WO-US30999.
PR 05-JAN-2000; 2000WO-US00219.
PR 11-FEB-2000; 2000WO-US03565.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 22-MAY-2000; 2000WO-US14042.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 17-SEP-1997; 97US-058113P.
PR 17-SEP-1997; 97US-059115P.
PR 17-SEP-1997; 97US-059117P.
PR 17-SEP-1997; 97US-059119P.
PR 17-SEP-1997; 97US-059121P.
PR 17-SEP-1997; 97US-059122P.
PR 17-SEP-1997; 97US-059184P.
PR 18-SEP-1997; 97US-059263P.
PR 18-SEP-1997; 97US-059266P.
PR 15-OCT-1997; 97US-062125P.
PR 17-OCT-1997; 97US-062285P.
PR 17-OCT-1997; 97US-062287P.
PR 21-OCT-1997; 97US-063486P.
PR 24-OCT-1997; 97US-063814P.
PR 24-OCT-1997; 97US-063816P.
PR 24-OCT-1997; 97US-063845P.
PR 24-OCT-1997; 97US-063120P.
PR 24-OCT-1997; 97US-063121P.
PR 24-OCT-1997; 97US-063127P.
PR 24-OCT-1997; 97US-063128P.
PR 27-OCT-1997; 97US-063327P.
PR 27-OCT-1997; 97US-063329P.
PR 28-OCT-1997; 97US-063341P.
PR 28-OCT-1997; 97US-063342P.
PR 28-OCT-1997; 97US-063544P.
PR 28-OCT-1997; 97US-063549P.
PR 28-OCT-1997; 97US-063550P.
PR 28-OCT-1997; 97US-063564P.
PR 29-OCT-1997; 97US-063435P.
PR 29-OCT-1997; 97US-063704P.
PR 29-OCT-1997; 97US-063732P.
PR 29-OCT-1997; 97US-063734P.
PR 29-OCT-1997; 97US-063735P.
PR 29-OCT-1997; 97US-063738P.
PR 29-OCT-1997; 97US-064215P.
PR 31-OCT-1997; 97US-063870P.
PR 31-OCT-1997; 97US-064103P.
PR 03-NOV-1997; 97US-064248P.
PR 07-NOV-1997; 97US-064809P.
PR 12-NOV-1997; 97US-065186P.
PR 17-NOV-1997; 97US-065846P.

PR 18-NOV-1997; 97US-065693P.
PR 21-NOV-1997; 97US-066120P.
PR 21-NOV-1997; 97US-066343P.
PR 24-NOV-1997; 97US-066453P.
PR 24-NOV-1997; 97US-066466P.
PR 24-NOV-1997; 97US-066511P.
PR 24-NOV-1997; 97US-066770P.
PR 25-NOV-1997; 97US-066772P.
PR 25-NOV-1997; 97US-066840P.
PR 12-DEC-1997; 97US-069425P.
PR 04-JUN-1998; 98US-088026P.
PR 10-SEP-1998; 98US-099803P.
PR 14-SEP-1998; 98US-100262P.
PR 17-SEP-1998; 98US-100858P.
PR 13-OCT-1998; 98US-104080P.
PR 20-NOV-1998; 98US-109304P.
PR 22-DEC-1998; 98US-113296P.
PR 07-JUL-1999; 99US-143048P.
PR 26-JUL-1999; 99US-145698P.
PR 28-JUL-1999; 99US-146222P.
PR 18-SEP-2000; 2000US-066530P.

(GETH) GENENTECH INC.

XX Ashkenazi A, Botstein D, Desnovers L, Eaton DL, Ferrara N,
PI Filvarotti E, Fong S, Gao W, Garber H, Gertsen ME, Goddard A,
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavich R,
PI Mather JP, Pan U, Peoni NF, Roy MA, Stewart TA, Thomas D,
PI Williams PM, Wood WI;
XX MPI; 2003-331485/31.
DR N-PSDB; ACA05532.

PT Sixty one isolated nucleic acids encoding a PRO polypeptide, e.g.
PT PRO245 or PRO168, useful in chromosome and gene mapping, in generating
PT antisense RNA and DNA, and in treating cancer and Alzheimer's disease -
XX Example 38; Fig 84; 481p; English.

XX The invention relates to sixty one nucleic acids encoding PRO
CC polypeptides (secreted and transmembrane). The polynucleotide is useful
CC in molecular biology, including uses as hybridization probes, in
CC chromosome and gene mapping, in generating antisense RNA and DNA, and in
CC gene therapy. The polynucleotide may also be used in preparing PRO
CC polypeptides by recombinant techniques, and in generating either
CC transgenic animals or knock-out animals which, in turn, are useful in the
CC development and screening of therapeutically useful reagents. The PRO
CC polypeptide or the antibody is used in preparing a medicament for
CC treating a condition responsive to the polypeptide or antibody, such as
CC mucosal lesions e.g. ulcers and enterocolitis, skin disease e.g.
CC psoriasis, cancer e.g. lung cancer and colon cancer, nerve cell disease
CC e.g. Alzheimer's disease and Parkinson's disease, Usher syndrome,
CC atrophica areata, angiogenesis, inflammatory disease e.g. asthma and
CC rheumatoid arthritis, ischaemia, and in various diagnostic assays. The
CC present sequence represents the amino acid sequence of a PRO polypeptide.

XX Sequence 350 AA;

Query Match 100.0%; Score 350; DB 24; Length 350;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLGATILCLIAAAPTAPAPATGAPKPGFALSYPOEATLNMFEVELEMD 60
DB 1 MRLGATILCLIAAAPTAPAPATGAPKPGFALSYPOEATLNMFEVELEMD 60
QY 61 TQHKLSAVEEMAEBAKASSEVNIAMLPSSYHNETTDPKVGNNTHVREIHKITN 120
DB 61 TQHKLSAVEEMAEBAKASSEVNIAMLPSSYHNETTDPKVGNNTHVREIHKITN 120
QY 121 NOTGQWVSEYITYSVDEBGRRSHECIIIDEGCFPMYQFASFOYTCPCGGMCLTR 180
DB 121 NOTGQWVSEYITYSVDEBGRRSHECIIIDEGCFPMYQFASFOYTCPCGGMCLTR 180

QY 181 DSECCGDLQVWGCHCTMATRGSGNGTICDNQDCQPGLCAGFORGLFPVCTPLPYEGEL 240
DB 181 DSECCGDLQVWGCHCTMATRGSGNGTICDNQDCQPGLCAGFORGLFPVCTPLPYEGEL 240
QY 241 CHDPASRLDLITWELPDPDALDRCPASGLLCQPHSHSLVYCKPTFVGSRRQDEILL 300
DB 241 CHDPASRLDLITWELPDPDALDRCPASGLLCQPHSHSLVYCKPTFVGSRRQDEILL 300
QY 301 PREVPDEYEVGSFMEYVQELDLERSLTREMAIGEPAAAAALLGGEI 350
DB 301 PREVPDEYEVGSFMEYVQELDLERSLTREMAIGEPAAAAALLGGEI 350

RESULT 18
ABU64539
ID ABU64539 standard; Protein; 350 AA.

XX ABU64539;

XX 13-MAY-2003 (first entry)

XX Human secreted/transmembrane protein, #43.

XX Human; PRO; secreted; transmembrane; pharmaceutical;
XX diagnostic; biosensor; bioreactor; therapeutic; hyperplasia;
XX endometriosis; cancer; tumour; ischaemia; coronary arterial disease;
XX polycystic kidney disease; renal failure; inflammatory response; asthma;
XX rheumatoid arthritis; psoriasis; multiple sclerosis; gene therapy;
XX cytoskeletal; gynecological; cardiac; nephrotropic; hepatotropic;
XX antiinflammatory.

XX Homo sapiens.

XX US2002160374-A1.

XX 31-OCT-2002.

XX 12-JUL-2001; 2001US-0905291.

XX 10-SEP-1998; 98MO-US18824.
XX 14-SEP-1998; 98MO-US19177.
XX 16-SEP-1998; 98MO-US19330.
XX 17-SEP-1998; 98MO-US19437.
XX 01-DEC-1998; 98MO-US25108.
XX 08-SEP-1999; 99MO-US20594.
XX 13-SEP-1999; 99MO-US20944.
XX 15-SEP-1999; 99MO-US21090.
XX 15-SEP-1999; 99MO-US21547.
XX 05-OCT-1999; 99MO-US23089.
XX 29-NOV-1999; 99MO-US28214.
XX 30-NOV-1999; 99MO-US28301.
XX 01-DEC-1999; 99MO-US28313.
XX 02-DEC-1999; 99MO-US28564.
XX 02-DEC-1999; 99MO-US28565.
XX 16-DEC-1999; 99MO-US30095.
XX 20-DEC-1999; 99MO-US30911.
XX 20-DEC-1999; 99MO-US30999.
XX 05-JAN-2000; 2000MO-US00219.
XX 11-FEB-2000; 2000MO-US03565.
XX 22-FEB-2000; 2000MO-US04414.
XX 24-FEB-2000; 2000MO-US05004.
XX 02-MAR-2000; 2000MO-US05841.
XX 20-MAR-2000; 2000MO-US07377.
XX 30-MAR-2000; 2000MO-US08439.
XX 22-MAY-2000; 2000MO-US14042.
XX 02-JUN-2000; 2000MO-US15264.
XX 28-JUL-2000; 2000MO-US20710.
XX 24-AUG-2000; 2000MO-US23328.
XX 17-SEP-1997; 97US-059113P.
XX 17-SEP-1997; 97US-059115P.
XX 17-SEP-1997; 97US-059117P.
XX 17-SEP-1997; 97US-059119P.

PR 17-SEP-1997; 97US-059121P.
 PR 17-SEP-1997; 97US-059122P.
 PR 17-SEP-1997; 97US-059123P.
 PR 18-SEP-1997; 97US-059263P.
 PR 18-SEP-1997; 97US-059264P.
 PR 15-OCT-1997; 97US-062125P.
 PR 17-OCT-1997; 97US-062285P.
 PR 17-OCT-1997; 97US-062287P.
 PR 21-OCT-1997; 97US-063486P.
 PR 24-OCT-1997; 97US-062814P.
 PR 24-OCT-1997; 97US-062816P.
 PR 24-OCT-1997; 97US-063045P.
 PR 24-OCT-1997; 97US-063120P.
 PR 24-OCT-1997; 97US-063121P.
 PR 24-OCT-1997; 97US-063127P.
 PR 24-OCT-1997; 97US-063128P.
 PR 27-OCT-1997; 97US-063327P.
 PR 27-OCT-1997; 97US-063329P.
 PR 28-OCT-1997; 97US-063541P.
 PR 28-OCT-1997; 97US-063542P.
 PR 28-OCT-1997; 97US-063544P.
 PR 28-OCT-1997; 97US-063549P.
 PR 28-OCT-1997; 97US-063550P.
 PR 28-OCT-1997; 97US-063564P.
 PR 29-OCT-1997; 97US-063435P.
 PR 29-OCT-1997; 97US-063704P.
 PR 29-OCT-1997; 97US-063732P.
 PR 29-OCT-1997; 97US-063734P.
 PR 29-OCT-1997; 97US-063735P.
 PR 29-OCT-1997; 97US-063738P.
 PR 29-OCT-1997; 97US-064215P.
 PR 31-OCT-1997; 97US-063870P.
 PR 31-OCT-1997; 97US-064103P.
 PR 03-NOV-1997; 97US-064248P.
 PR 07-NOV-1997; 97US-064809P.
 PR 12-NOV-1997; 97US-065186P.
 PR 17-NOV-1997; 97US-065846P.
 PR 18-NOV-1997; 97US-065933P.
 PR 21-NOV-1997; 97US-066120P.
 PR 21-NOV-1997; 97US-066364P.
 PR 24-NOV-1997; 97US-066453P.
 PR 24-NOV-1997; 97US-066466P.
 PR 24-NOV-1997; 97US-066511P.
 PR 24-NOV-1997; 97US-066770P.
 PR 24-NOV-1997; 97US-066772P.
 PR 18-SEP-2000; 2000US-0665350.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Ashkenazi A, Botstein D, Desnoyers L, Baton DL, Ferrara N,
 PI Filvaroff E, Fong S, Gao W, Gerritsen ME, Goddard A,
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ,
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D,
 PI Williams PM, Wood WI;
 XX WPI, 2003-288105/28.
 XX N-PSDB; ABX96211.
 XX
 PT New secreted and transmembrane PRO polypeptides (e.g. PRO533 or PRO245)
 PT and genes encoding them, useful for detecting or treating e.g.
 PT hyperplasia, endometriosis, cancers, ischemia, coronary arterial
 PT disease or inflammations -
 XX
 PS Claim 12; Fig 84; 477PP; English.
 XX
 CC The invention discloses isolated PRO secreted/transmembrane polypeptides
 CC and the nucleic acid encoding them. The polypeptides can be used to
 CC raise antibodies that specifically bind to the PRO polypeptide, for
 CC linking a bioactive molecule to a cell expressing a PRO protein and for
 CC modulating at least one biological activity of a cell. The PRO
 CC polypeptides or polynucleotides are also useful as pharmaceuticals,
 CC diagnostics, biosensors or bioreactors, for detecting or treating e.g.
 CC hyperplasia, endometriosis, cancers (e.g. those involving solid tumours),

CC ischaemia, coronary arterial disease, polycystic kidney disease, chronic
 CC or acute renal failure, or inflammatory responses (e.g. asthma,
 CC rheumatoid arthritis, psoriasis or multiple sclerosis) in mammals. The
 CC PRO genes may also be used in gene therapy, particularly for replacing a
 CC defective gene. The sequences presented in AB064499-AB064555 are the
 CC PRO polynucleotides of the invention.
 XX
 SQ Sequence 350 AA;
 Query Match 100.0%; Score 350; DB 24; Length 350;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQRIGATLCLILAAVPTAPAPATSAVPKPGPALSTPOEATINEMFREVEELMED 60
 DB 1 MQRIGATLCLILAAVPTAPAPATSAVPKPGPALSTPOEATINEMFREVEELMED 60
 QY 61 TQHLRSAVEEMEAEBAAXSSSEVNLANLPPSYHNETNTDTKXNNTHVHREIHKITN 120
 DB 61 TQHLRSAVEEMEAEBAAXSSSEVNLANLPPSYHNETNTDTKXNNTHVHREIHKITN 120
 QY 121 NQTSQWYFSETVITVSGDEBGRSHCEIIDDCGSPMYCQFASFOYTQPCRGRLMCTR 180
 DB 121 NQTSQWYFSETVITVSGDEBGRSHCEIIDDCGSPMYCQFASFOYTQPCRGRLMCTR 180
 QY 181 DSECCGQOLCWGHCCTKMAIRGSGNITCDNQRDQPGELCCAFQRGLLFPVCTPLPVGEL 240
 DB 181 DSECCGQOLCWGHCCTKMAIRGSGNITCDNQRDQPGELCCAFQRGLLFPVCTPLPVGEL 240
 QY 241 CHDPASRLDLITWELEPDPGALDRPCASGLLCPHSHSLVYVCKPTFVSGRDDGELL 300
 DB 241 CHDPASRLDLITWELEPDPGALDRPCASGLLCPHSHSLVYVCKPTFVSGRDDGELL 300
 QY 301 PREVPDEYEVGSFMEYVROSLIEDLRSLTBEMALGEPAAAAALLGGEI 350
 DB 301 PREVPDEYEVGSFMEYVROSLIEDLRSLTBEMALGEPAAAAALLGGEI 350
 RESULT 19
 ID AAE34069 standard; Protein: 350 AA.
 XX AAE34069;
 AC AAE34069;
 DT 02-MAY-2003 (first entry)
 XX
 DE DK 3 protein.
 XX
 KW Drug screening; toxicology assay; signalling pathway; DK 3.
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..94 /note= "Encoded by TAT"
 FT
 FN WO200290992-A2.
 XX
 PD 14-NOV-2002.
 XX
 PF 29-APR-2002; 2002WO-GB01946.
 XX
 PR 04-MAY-2001; 2001GB-0011004.
 XX
 PA (AXOR-) AXORDIA LTD.
 XX
 PI Andrews P, Draper J, Walsh J;
 XX
 DR WPI, 2003-120579/11.
 DR N-PSDB; AAB52567.
 XX
 PT Identifying biologically active agents comprises cloning transfected
 PT cells into a cell array, exposing the array to an agent to be tested,

PT and detecting signals generated by a reporter molecule as a result of
 PT exposure to the agent -
 XX Claim 16; Fig 90; 90pp; English.
 XX
 CC The present invention relates to a novel screening method which enables
 CC the identification of biologically active agents which mediate their
 CC effect through the activation of genes. The method involves providing a
 CC population of cells stably transfected with a nucleic acid encoding a
 CC reporter molecule, cloning the transfected cells into a cell array,
 CC exposing the array to at least one agent to be tested and detecting a
 CC signal generated by the reporter molecule as a result of exposure to
 CC the agent. The method is useful in identifying biologically active agents
 CC and the genes through which the agents act, in screening potential drugs
 CC for their ability to activate certain drug targets in a high-throughput
 CC assay, in identifying relationships between signalling pathways and
 CC specific signals that could be useful in eventually directing the
 CC differentiation of embryonic stem cells and in toxicology assays by
 CC testing for unwanted activation or inhibition of specific signalling
 CC pathways. The present sequence is DKK 3 protein used to illustrate the
 CC method of the invention.

XX Sequence 350 AA;
 XX
 SQ
 Query Match 100.0%; Score 350; DB 24; Length 350;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORLGATLTCLLAAAVPTAPAPATATSAVPKPGPALSYPOEATLNEMFEVEELMED 60
 DB 1 MORLGATLTCLLAAAVPTAPAPATATSAVPKPGPALSYPOEATLNEMFEVEELMED 60
 QY 61 TQHKRSAYEEMEAERAAKASSEVNLALPPSYHNETDTRKVGNTIHYRETHKTN 120
 DB 61 TQHKRSAYEEMEAERAAKASSEVNLALPPSYHNETDTRKVGNTIHYRETHKTN 120
 QY 121 NOTGQWVFSEVITVSGDEGRSHSCIIDEGSPMYCOPASFOYTCQPCGQMLCTR 180
 DB 121 NOTGQWVFSEVITVSGDEGRSHSCIIDEGSPMYCOPASFOYTCQPCGQMLCTR 180
 QY 121 NOTGQWVFSEVITVSGDEGRSHSCIIDEGSPMYCOPASFOYTCQPCGQMLCTR 180
 DB 121 NOTGQWVFSEVITVSGDEGRSHSCIIDEGSPMYCOPASFOYTCQPCGQMLCTR 180
 QY 181 DSCCGDCQCMWCHCTKMAITRGNCTICNORDCQGLCCARQGLIPVCTPLVVEGEL 240
 DB 181 DSCCGDCQCMWCHCTKMAITRGNCTICNORDCQGLCCARQGLIPVCTPLVVEGEL 240
 QY 241 CHDPASRLDLITWELPEPGALDRCPCASGLLCQPHSHLVVCKPTFGVSGSDQGEILL 300
 DB 241 CHDPASRLDLITWELPEPGALDRCPCASGLLCQPHSHLVVCKPTFGVSGSDQGEILL 300
 QY 301 PREVPDEYEVGSMERQLEBLSLTBEWALGEPAAAAALLGGEET 350
 DB 301 PREVPDEYEVGSMERQLEBLSLTBEWALGEPAAAAALLGGEET 350

RESULT 20
 ABUS5915
 ID ABUS5915 standard; Protein; 350 AA.

XX AC ABUS5915;
 XX DT 25-MAR-2003 (first entry)
 XX DE Human protein DKK3.
 XX Notch; Wnt; embryonic stem cell; embryogenesis; human;
 XX differentiation; ligand; Parkinson's disease; Huntington's disease;
 XX motor neuron disease; heart disease; diabetes; liver disease;
 XX cirrhosis; renal disease; AIDS; acquired immunodeficiency syndrome.
 XX Homo sapiens.
 XX OS
 XX MO200277204-A2.
 XX PD 03-OCT-2002.

XX 25-MAR-2002; 2002MO-GB01195.
 XX
 XX 23-MAR-2001; 2001GB-0007296.
 XX 23-MAR-2001; 2001GB-0007299.
 XX 17-APR-2001; 2001GB-0009346.
 XX (AXOR-) AXORDIA LTD.
 XX Andrews P, Walsh J, Gokhale P;
 XX WPI: 2003-092852/08.
 XX N-PSDB; ABX75342.
 XX
 XX Modulating the differentiation of embryonic stem cells by providing
 XX ligands which bind receptors in the Notch and Wnt pathways; useful for
 XX treating diseases such as Parkinson's, Huntington's, heart disease,
 XX diabetes and AIDS
 XX Disclosure; Fig 96; 121pp; English.

XX The invention relates to modulating the differentiation of an embryonic
 XX stem cell, comprising: (a) providing a culture of embryonic stem cells;
 XX (b) providing at least one ligand or its active binding fragment,
 XX capable of binding its cognate receptor polypeptide expressed by the
 XX embryonic stem cell; (c) forming a culture comprising embryonic stem
 XX cells and the ligand; and (d) growing the cell culture. Also included
 XX are: (1) Modulating the differentiation of embryonic stem cells,
 XX comprising: (a) providing a cell transfected with a nucleic acid molecule
 XX selected from: (i) any of 9 fully defined Wnt nucleic acid sequences;
 XX (ii) a nucleic acid molecule that hybridises to the nucleic acid in
 XX (i), and which encodes a ligand capable of modulating embryonic stem
 XX cell differentiation, or capable of binding a Wnt receptor; or
 XX (iii) nucleic acid molecules which are degenerate as a result of the
 XX genetic code to the sequences of (i) or (ii); (b) forming a culture
 XX comprising the cell identified in (a) with an embryonic stem cell; and
 XX (c) growing the culture for the maintenance and/or differentiation of
 XX the embryonic stem cell; (2) Inhibiting the differentiation of embryonic
 XX stem cells, comprising: (a) providing at least one polypeptide or its
 XX active fragment, that are inhibitors of the Wnt signalling pathway;
 XX (b) forming a culture comprising the cell identified in (a) with an
 XX embryonic stem cell; and (c) growing the culture for the maintenance of
 XX the embryonic stem cells in an undifferentiated state; or (3) Inhibiting the
 XX differentiation of embryonic stem cells, comprising: (a) providing a cell
 XX transfected with a nucleic acid molecule selected from: (i) a molecule
 XX encoding a Wnt inhibitory polypeptide; (ii) a molecule which hybridises
 XX to the molecule of (i) and encodes a polypeptide capable of inhibiting
 XX Wnt signalling; and (iii) nucleic acid molecules which are degenerate as
 XX a result of the genetic code to the sequences of (i) or (ii); (b) forming
 XX a culture comprising the cell identified in (a) with an embryonic stem
 XX cell; and (c) growing the culture for the maintenance of embryonic stem
 XX cells in an undifferentiated state; and (4) A cell, therapeutic cell or
 XX cell culture obtainable by any of the methods cited above.
 XX The therapeutic cell of the present invention is useful in the
 XX treatment of an animal, preferably a human, comprising administering a
 XX cell composition comprising embryonic stem cells which have been
 XX induced to differentiate into at least one cell-type. The cell is also
 XX useful for the manufacture of a composition for use in treatment of
 XX diseases such as Parkinson's disease, Huntington's disease, motor
 XX neuron disease, heart disease, diabetes, liver disease (e.g.
 XX cirrhosis), renal disease and AIDS (acquired immunodeficiency syndrome).
 XX The present sequence is represents a Wnt or Notch pathway protein
 XX (i.e. a ligand for the method of the invention).

XX Sequence 350 AA;
 XX
 SQ
 Query Match 100.0%; Score 350; DB 24; Length 350;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORLGATLTCLLAAAVPTAPAPATATSAVPKPGPALSYPOEATLNEMFEVEELMED 60
 DB 1 MORLGATLTCLLAAAVPTAPAPATATSAVPKPGPALSYPOEATLNEMFEVEELMED 60

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QY 61 TOHLRSVEMEAEEAAKASSEVNLANLPSPYHNETNTDTKGNNTIHVREIKITN 120
Db 61 TOHLRSVEMEAEEAAKASSEVNLANLPSPYHNETNTDTKGNNTIHVREIKITN 120
QY 121 NOTGQWVFSESTVITTSVGDEEGRSRSHCEIIDDCGSPMYCQFASFOYTCQPCRGQRLCTR 180
Db 121 NOTGQWVFSESTVITTSVGDEEGRSRSHCEIIDDCGSPMYCQFASFOYTCQPCRGQRLCTR 180
QY 181 DSECCGQOLCVMGCHCTMATRGNGTICDNQRCQGLCCAFGRGLLPVCTPLPVEGSL 240
Db 181 DSECCGQOLCVMGCHCTMATRGNGTICDNQRCQGLCCAFGRGLLPVCTPLPVEGSL 240
QY 241 CHDPASRLDLITWELPEPDGALDRCPASGLLCQPHSHSVVYCKPTFVGSRDQGEILL 300
Db 241 CHDPASRLDLITWELPEPDGALDRCPASGLLCQPHSHSVVYCKPTFVGSRDQGEILL 300
QY 301 PREVPDEYEGSFMEYRQLEDELSLTFEVALGSPAAAAALLGGEI 350
Db 301 PREVPDEYEGSFMEYRQLEDELSLTFEVALGSPAAAAALLGGEI 350
RESULT 21
ABUS4387
ID ABUS4387 standard; Protein; 350 AA.
AC ABUS4387;
XX 10-MAR-2003 (first entry)
DE Human secreted/transmembrane protein PRO295.
XX
XX Human; PRO, secreted protein, transmembrane protein, enterocolitis,
XX gastrointestinal ulceration; skin disease;
XX abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
XX squamous cell carcinoma; Alzheimer's disease; Parkinson's disease;
XX amyotrophic lateral sclerosis; inflammatory disease;
XX rheumatoid arthritis; asthma; multiple sclerosis; organ failure;
XX atherosclerosis; cardiac injury; infertility; birth defect; cancer;
XX premature aging; AIDS; acquired immunodeficiency syndrome; cancer;
XX diabetic complication; wound repair.
XX
XX Homo sapiens.
XX
XX US2002132240-A1.
XX
XX 19-SEP-2002.
XX
XX 18-JUL-2001; 2001US-0909320.
XX
XX 10-SEP-1998; 98MO-US18824.
XX 14-SEP-1998; 98MO-US19177.
XX 16-SEP-1998; 98MO-US19330.
XX 17-SEP-1998; 98MO-US19437.
XX 08-SEP-1999; 99MO-US20594.
XX 13-SEP-1999; 99MO-US20944.
XX 15-SEP-1999; 99MO-US21090.
XX 15-SEP-1999; 99MO-US21547.
XX 05-OCT-1999; 99MO-US23069.
XX 01-DEC-1999; 99MO-US28301.
XX 02-DEC-1999; 99MO-US28564.
XX 02-DEC-1999; 99MO-US28565.
XX 16-DEC-1999; 99MO-US30095.
XX 20-DEC-1999; 99MO-US30911.
XX 20-DEC-1999; 99MO-US30999.
XX 06-JAN-2000; 2000MO-US00219.
XX 11-FEB-2000; 2000MO-US03565.
XX 22-FEB-2000; 2000MO-US04414.
XX 28-JUL-2000; 2000MO-US20710.
XX 24-AUG-2000; 2000MO-US23328.
XX 17-SEP-1997; 97US-059113P.
XX 17-SEP-1997; 97US-059115P.

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PR 17-SEP-1997; 97US-059117P.
PR 15-OCT-1997; 97US-062125P.
PR 17-OCT-1997; 97US-062285P.
PR 17-OCT-1997; 97US-062287P.
PR 21-OCT-1997; 97US-063486P.
PR 24-OCT-1997; 97US-062814P.
PR 24-OCT-1997; 97US-062816P.
PA (GENTH ) GENENTECH INC.
XX
XX Ashkenazi A, Botstein D, Deenoyers L, Eaton DL, Ferrara N,
XX Filvarsoff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
XX Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijaviriv J,
XX Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D,
XX Williams PM, Wood WI,
XX
XX MPI, 2003-147434/14.
XX N-PEDB; ABX71642.
XX
XX New PRO polypeptides and nucleic acid molecules, useful in diagnosing
XX or treating inflammatory diseases, organ failure, atherosclerosis,
XX cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or
XX Parkinson's disease -
XX
XX Claim 12; Fig 84; 473pp; English.
XX
XX The invention relates to an isolated PRO polypeptide having at least 80%
XX amino acid sequence identity to: (a) any one of 61 fully defined amino
XX acid sequences given in the specification (appearing as ABUS4387-
XX ABUS4407); (b) an amino acid sequence encoded by the nucleotide sequence
XX deposited under American Type Culture Collection (accession numbers
XX listed in the specification); (c) any one of the PRO sequences which
XX lacks its associated signal peptide; (d) an extracellular domain of the
XX PRO polypeptide with its associated signal peptide; or (e) an
XX extracellular domain of the PRO polypeptide which lacks its associated
XX signal peptide. Also include are the nucleic acids encoding the PRO
XX polypeptides, vectors, host cells and anti-PRO antibodies.
XX
XX The PRO polypeptides and nucleic acids are useful in diagnosing
XX or treating enterocolitis, gastrointestinal ulceration, skin diseases
XX associated with abnormal keratinocyte differentiation, e.g. psoriasis
XX or epithelial cancers such as squamous cell carcinoma, Alzheimer's
XX disease, Parkinson's disease, amyotrophic lateral sclerosis,
XX inflammatory diseases, e.g. rheumatoid arthritis, asthma or multiple
XX sclerosis, organ failure, atherosclerosis, cardiac injury, infertility,
XX birth defects, premature aging, AIDS, cancer, diabetic complications,
XX or mutations in general. The polypeptides are also useful for wound
XX repair and associated therapies concerned with re-growth of tissue. The
XX nucleotide sequences may be used as hybridisation probes in chromosome
XX and gene mapping, or in generating antisense RNA and DNA. PRO nucleic
XX acids are also useful in preparing PRO polypeptides, in assays to
XX identify other proteins or molecules involved in binding reaction, to
XX generate transgenic animals or knockout animals, which in turn are
XX useful in the development and screening of therapeutically useful
XX reagents, for chromosome identification, and tissue typing. The PRO
XX polypeptides and nucleic acid molecules are also useful in gene
XX therapy, and as molecular weight markers for protein electrophoresis
XX purposes. The anti-PRO antibodies may be used in diagnostic assays for
XX PRO, or for the affinity purification of PRO from recombinant cell
XX culture or natural sources. The present sequence represents a PRO
XX polypeptide.
XX
XX Sequence 350 AA;
XX
XX Query Match 100.0%; Score 350; DB 24; Length 350;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MORGATLILCLILAAAPPTAPAPPTATSPVVRGAPLSPQERATINEMFRVREIEMD 60
Db 1 MORGATLILCLILAAAPPTAPAPPTATSPVVRGAPLSPQERATINEMFRVREIEMD 60
QY 61 TOHLRSVEMEAEEAAKASSEVNLANLPSPYHNETNTDTKGNNTIHVREIKITN 120

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D6	61	TOHKJSAVEENEAEBAKASSEVNLALPSSYNENINTDTKQGNNTIHYHSIRKITN	120
QY	121	NOHGQWVEBETVYTSVGDEGGRSHCCIIDECGSSWYQCFASFYCTQPCRGRMCTR	168
D6	121	NOTGQWVFESTVYTSVGDEGGRSHCCIIDECGSSWYQCFASFYCTQPCRGRMCTR	180
QY	181	DSECCDOLCVMGHCTKMAITRGSNGTICDNQRCQPGICCAFORGLLFPVCTPLPVEGEL	240
D6	181	DSECCGDTLCVMGHCTKMAITRGSNGTICDNQRCQPGICCAFORGLLFPVCTPLPVEGEL	240
QY	241	CHPFAARLLDLTWELBPDGALDRCPASGLICQSHSLVYVCKPTFVSGRDDGELL	300
D6	241	CHPFAARLLDLTWELBPDGALDRCPASGLICQSHSLVYVCKPTFVSGRDDGELL	300
QY	301	PREVPPEYEVGSMEEVROELDLDRSLTEEMALDEPAAAAAALLGGEI	350
D6	301	PREVPPEYEVGSMEEVROELDLDRSLTEEMALDEPAAAAAALLGGEI	350

XX PR 24-OCT-1997; 97US-0062814.
PR 24-OCT-1997; 97US-0062816.
PR 24-OCT-1997; 97US-0063045.
PR 24-OCT-1997; 97US-0063120.
PR 24-OCT-1997; 97US-0063121.
PR 24-OCT-1997; 97US-0063127.
PR 24-OCT-1997; 97US-0063128.
PR 27-OCT-1997; 97US-0063329.
PR 27-OCT-1997; 97US-0063327.
PR 28-OCT-1997; 97US-0063541.
PR 28-OCT-1997; 97US-0063542.
PR 28-OCT-1997; 97US-0063544.
PR 28-OCT-1997; 97US-0063549.
PR 28-OCT-1997; 97US-0063550.
PR 28-OCT-1997; 97US-0063564.
PR 29-OCT-1997; 97US-0063435.
PR 29-OCT-1997; 97US-0063704.
PR 29-OCT-1997; 97US-0063732.
PR 29-OCT-1997; 97US-0063738.
PR 29-OCT-1997; 97US-0063734.
PR 29-OCT-1997; 97US-0064215.
PR 29-OCT-1997; 97US-0063735.
PR 31-OCT-1997; 97US-0063870.
PR 31-OCT-1997; 97US-0064103.
PR 03-NOV-1997; 97US-0064248.
PR 07-NOV-1997; 97US-0064809.
PR 12-NOV-1997; 97US-0065186.
PR 17-NOV-1997; 97US-0065846.
PR 18-NOV-1997; 97US-0065693.
PR 21-NOV-1997; 97US-0066120.
PR 21-NOV-1997; 97US-0066364.
PR 24-NOV-1997; 97US-0066772.
PR 24-NOV-1997; 97US-0066466.
PR 24-NOV-1997; 97US-0066770.
PR 24-NOV-1997; 97US-0066511.
PR 24-NOV-1997; 97US-0066453.

XX PA (GETH) GENENTECH INC.
XX PI Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;
XX WPI: 1999-229533/19.
DR N-PDB: AAX52255.

XX PT New isolated human genes and polypeptides used in, e.g. treatment of
XX gastrointestinal ulceration

XX PS Claim 12; Fig 84; 320pp; English.

XX CC AAY13344-403 represent secreted and transmembrane human proteins.
CC The cDNA sequences are obtained from cDNA libraries, prepared from
CC fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.
CC The encoded polypeptides have specific uses based on their homology to
CC known polypeptides, e.g. PRO11 and PRO217 can be used for disorders
CC associated with the repair of acute and chronic mucosal lesions
CC mucosa and the repair of acute and chronic mucosal lesions
CC uleation and congenital microvillus atrophy), skin diseases associated
CC (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal
CC with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial
CC cancers such as lung squamous cell carcinoma of the vulva and gliomas),
CC potent effects on cell growth and development, diseases related to
CC growth or survival of nerve cells including Parkinson's disease,
CC Alzheimer's disease, AIDS, neuropathies or cancer. PRO265 can be used as
CC for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used
CC as a target for anti-tumor drugs. PRO533 may be used in the treatment
CC of Usher Syndrome or Atrophia areata; PRO269 can be used as an
CC anti-thrombotic agent; PRO287 polypeptides and portions may have
CC therapeutic applications in wound healing and tissue repair; PRO317 can
CC be used for treating problems of the kidney, uterus, endometrium, blood
CC vessels, or related tissue, e.g. in the heart of genital tract.

XX Sequence 350 AA;

Query Match	79.7%	Score 279	DB 20	Length 350
Best Local Similarity	100.0%	Pred. No. 4,5e-263		
Matches 279	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	MORLGATLILCLILAAAVPTAPAPAPATATSAVYKFGPLSLPQSEATLNMKPFVRELMED	60	
Db	1	MORLGATLILCLILAAAVPTAPAPAPATATSAVYKFGPLSLPQSEATLNMKPFVRELMED	60	
Qy	61	TOHKLSAAVEEMAEAEAAKASSEVNTLANTPPSYHNETNTDVTGNNTHVHREIHKITN	120	
Db	61	TOHKLSAAVEEMAEAEAAKASSEVNTLANTPPSYHNETNTDVTGNNTHVHREIHKITN	120	
Qy	121	NQNGWVSEETVYTSVGEDEGRHSHECIIDDCPSMYCQFASFOYTCQPCRCQRLCTR	180	
Db	121	NQNGWVSEETVYTSVGEDEGRHSHECIIDDCPSMYCQFASFOYTCQPCRCQRLCTR	180	
Qy	181	DSECCDQDLCVNGHCTKATGSGNGTICDNORDCQPGALCAFORGLIFVCTPLPYEGEL	240	
Db	181	DSECCDQDLCVNGHCTKATGSGNGTICDNORDCQPGALCAFORGLIFVCTPLPYEGEL	240	
Qy	241	CHDPASRLDLLTWLELPDQALDRPCASGLLCCPHSHS	279	
Db	241	CHDPASRLDLLTWLELPDQALDRPCASGLLCCPHSHS	279	

ID	AAW73016	standard; Protein; 350 AA.
XX	AAW73016;	
XX	18-JAN-1999	(first entry)
XX	Human cysteine-rich secreted protein CRSP-1.	
XX	CRSP-1; cysteine-rich secreted protein 1; tumour; cancer; leukaemia;	
XX	tissue repair; wound healing; infection; Parkinson's disease;	
XX	Alzheimer's disease; Huntington's chorea; multiple sclerosis;	
XX	myotonic lateral sclerosis; pontine myelinolysis;	
XX	human immunodeficiency associated myelopathy; bulbar palsy;	
XX	spinal muscular atrophy; primary lateral sclerosis; poliomyelitis;	
XX	Fazio-Londe syndrome; Charcot-Marie-Tooth disease; therapy;	
XX	diagnosis; drug screening; human; CRISP-1; TANGO 59;	
XX	signal transduction; cell differentiation; cell proliferation.	
XX	Homo sapiens.	
XX	Key	Location/Qualifiers
XX	Peptide	1..23
XX	/label= Sig.peptide	
XX	/note= "putative signal peptide spans amino acids	
XX	1-19, 1-21 or 1-23"	
XX	Protein	24..350
XX	/label= Mat_protein	
XX	/note= "putative mature protein spans amino acids	
XX	20-350, 22-350 or 24-350"	
XX	Domain	147..195
XX	/note= "cysteine-rich domain"	
XX	Peptide	156..200
XX	/note= "spacer"	
XX	Domain	201..284
XX	/note= "cysteine-rich domain"	
XX	WC9846755-A1.	
XX	16-APR-1998;	98WC-US07894.
XX	22-OCT-1998.	
XX	16-APR-1998;	98US-US09802.
XX	20-JAN-1998;	97US-US43704.
XX	16-APR-1997;	97US-US42898.
XX	17-APR-1997;	98US-US07589.
XX	15-JAN-1998;	

CC epilepsy, amnesia), inflammation, skeletal muscle disorders, pulmonary
 CC disorders (Goodpasture's syndrome), cardiovascular disorders, and
 CC hyperproliferative disorders (cancer). The Dk proteins and nucleic
 CC acids may also be used for research purposes, such as for chromosome
 CC mapping, tissue typing and in screening assays to identify modulators.

XX Sequence 350 AA;

Query Match 66.6%; Score 233; DB 21; Length 350;
 Best Local Similarity 99.7%; Pred. No. 2,9e-218;
 Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MORLGATLLCLLAAAVPTAPAPATSAVPKPGPALSYPOEATLNEMFREVEELMED 60
 DB 1 MQLRLGATLLCLLAAAVPTAPAPATSAVPKPGPALSYPOEATLNEMFREVEELMED 60
 QY 61 TQHKLRSAVEMEAEEAAVAASEVNIANLPSPYHNETNTDTKVGNNTHVREIHKITN 120
 DB 61 TQHKLRSAVEMEAEEAAVAASEVNIANLPSPYHNETNTDTKVGNNTHVREIHKITN 120
 QY 121 NOTGQWVSESTVITVSGDEGRSHCEIIDDCGSPMTQFASFOYTCOPCRGQRLCTR 180
 DB 121 NOTGQWVSESTVITVSGDEGRSHCEIIDDCGSPMTQFASFOYTCOPCRGQRLCTR 180
 QY 181 DSECCGPDLCWGHCTMATRGNGTICDNQDCQDGLCCAFQGLLPVCTPLPYEGEL 240
 DB 181 DSECCGPDLCWGHCTMATRGNGTICDNQDCQDGLCCAFQGLLPVCTPLPYEGEL 240
 QY 241 CHNPASILLLLIWELEFPDGLDRCPASGLLCQPSHSIYVYCKTFPGSRQDEIILL 300
 DB 241 CHNPASILLLLIWELEFPDGLDRCPASGLLCQPSHSIYVYCKTFPGSRQDEIILL 300
 QY 301 PREVPDEYEVGSFMEYRQLELDERSLTEEMAL 334
 DB 301 PREVPDEYEVGSFMEYRQLELDERSLTEEMAL 334

RESULT 26
 AAM73021
 ID AAM73021 standard; Protein; 349 AA.
 AC AAM73021;
 DT 18-JAN-1999 (first entry)
 DE Mouse cysteine-rich secreted protein-1.
 KW CRSP-1; cysteine-rich secreted protein 1; tumour; cancer;
 KW signal transduction; cell differentiation; cell proliferation;
 KW mouse.
 XX Mus sp.
 OS Mus sp.
 XX Key Location/Qualifiers
 FT Domain 147..195
 FT Domain /note="cysteine-rich domain"
 FT Region 196..207
 FT Domain /note="spacer"
 FT Domain 208..284
 FT /note="cystine-rich domain"
 XX MO9846755-A1.
 XX 22-OCT-1998.
 PD 22-OCT-1998.
 XX 16-APR-1998; 98MO-US07894.
 PF 16-APR-1998; 98US-0009802.
 PR 16-APR-1997; 97US-0843704.
 PR 17-APR-1997; 97US-0842898.
 PR 15-JAN-1998; 98US-0071589.
 XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX McCarthy SA;
 XX WPI; 1998-568730/48.
 DR N-PSDB; AAV07911.
 XX New isolated cysteine-rich secreted proteins - used to develop
 PT products for treating, e.g. hyperproliferative disorders, cancers,
 PT wounds, infectious lesions, degenerative lesions or demyelating
 PT diseases
 PS Disclosure; Page 114-115; 142pp; English.

XX This is the amino acid sequence of novel mouse cysteine-rich
 CC secreted protein 1 (CRSP-1), as deduced from an isolated cDNA clone
 CC (see AAV07911). The invention relates to novel human CRSP-1, -2, -3
 CC and -4 nucleic acid sequences (see AAV07905-09) and polypeptides (see
 CC AAM73016-19) that are suggested to be involved in signal transduction
 CC and cellular differentiation. These can be used in diagnostic,
 CC screening and therapeutic methods of the invention e.g. for treating
 CC hyperproliferative disorders, cancers, wounds, infectious or
 CC degenerative lesions and demyelating diseases, and in drug
 CC screening.

SQ Sequence 349 AA;
 Query Match 11.7%; Score 41; DB 19; Length 349;
 Best Local Similarity 100.0%; Pred. No. 3e-31;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 YPOEATLNEMFREVEELMEDTQHKLRSAVEMEAEEAAAK 80
 DB 40 YPOEATLNEMFREVEELMEDTQHKLRSAVEMEAEEAAAK 80

RESULT 27
 AAB08879
 ID AAB08879 standard; Protein; 349 AA.
 AC AAB08879;
 DT 15-JAN-2001 (first entry)
 DE A murine Dickkopf (Dkk)-3 protein.
 KW Human; Dickkopf-3 protein; Dkk-3 protein; Soggy protein; optic disorder;
 KW cysteine-rich secreted protein; glaucoma; conjunctivitis; brain disorder;
 KW Alzheimer's disease; epilepsy; amnesia; inflammation; pulmonary disorder;
 KW skeletal muscle disorder; Goodpasture's syndrome;
 KW cardiovascular disorder; hyperproliferative disorder; cancer.
 XX Mus sp.
 OS Mus sp.
 XX WO200052047-A2.
 PN 08-SEP-2000.
 PD 03-MAR-2000; 2000MO-US05452.
 PF 03-MAR-2000; 2000MO-US05452.
 PR 05-MAR-1999; 99US-0263022.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX McCarthy S;
 PI WPI; 2000-579276/54.
 DR N-PSDB; AAA75137.
 XX Human Dickkopf (hDkk) and soggy nucleic acids and proteins, useful as
 PT modulating agents in regulating cellular processes and particularly for
 PT treating disorders characterized by aberrant expression or activity of
 PT Dkk, e.g. Alzheimer's,

PS Example 2; Fig 5A-B; 208bp; English.

CC The present sequence represents a murine Dickkopf (Dkk)-3 protein. The
 CC specification also describes Soggy (Dkk-related) sequences. Dkk is a
 CC cysteine-rich secreted protein. The Dkk nucleic acids and proteins are
 CC useful as modulating agents in regulating cellular processes. They are
 CC particularly useful in treating subjects having a disorder characterized
 CC by aberrant expression or activity of Dkk such as optic disorders
 CC (glaucoma, conjunctivitis), brain disorders (Alzheimer's disease,
 CC epilepsy, amnesia), inflammation, skeletal muscle disorders, pulmonary
 CC disorders (Goodpasture's syndrome), cardiovascular disorders, and
 CC hyperproliferative disorders (cancer). The Dkk proteins and nucleic
 CC acids may also be used for research purposes, such as for chromosome
 CC mapping, tissue typing and in screening assays to identify modulators.

XX Sequence 349 AA;

Query Match 11.7%; Score 41; DB 21; Length 349;
 Best Local Similarity 100.0%; Pred. No. 3e-31;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 YPGEATLNEMFREVEIMEDTQKLRSAVEEMAEBAAK 80
 DB 40 YPGEATLNEMFREVEIMEDTQKLRSAVEEMAEBAAK 80

RESULT 28
 AA92069
 ID AA92069 standard; Protein; 349 AA.

AC AA92069;
 DT 01-AUG-2000 (first entry)
 DE Murine DKK-3.
 XX DKK-3; human rfg-like 7-1 mRNA; chicken lens fiber protein; cleft 4;
 XX dkk-1; dickkopf-1; antagonist; wnt-8 signaling; morphogenesis;
 XX growth factor; cyostatic; sonic hedgehog; tissue differentiation.
 XX Mus sp.
 XX WO200018914-A2.
 XX 06-APR-2000.
 XX 17-SEP-1999; 99WO-US21647.
 XX 25-SEP-1998; 98US-0161241.
 XX (AMGE-) AMGEN INC.
 XX Baas MB, Sullivan JK, Theill LE, Wang D;
 XX WPI; 2000-293153/25.
 XX N-PSDB; AAA08838.
 XX New nucleic acid molecule encoding a biologically active DKK
 XX polypeptide, useful in treatment of cancer, e.g. mammary tumors and
 XX stem cell tumors
 XX Claim 18; Page 127-128; 143p; English.

PS AA92069-75 are novel mouse and human DKK polypeptides.
 CC The murine DKK-3 open reading frame has homology to human rfg-like 7-1
 CC mRNA and to chicken lens fiber protein cleft 4 gene.
 CC DKK-1 is a human ortholog of dkk-1 (dickkopf-1), a novel gene identified
 CC in Xenopus and mouse, purportedly an antagonist of wnt-8 signaling.
 CC DKK-2, -3 and -4 are each related to DKK-1 by their cysteine pattern.
 CC DKK-1 is also involved in morphogenesis in the developing embryo, and
 CC therefore a growth factor. By inference DKK polypeptides are also
 CC growth factors. The DKK polypeptides are useful for treating cancer,
 CC e.g. mammary tumors, stem cell tumors, or other cancers in which the wnt

CC and/or sonic hedgehog (shh) signal transduction pathways are activated.
 CC They can also be used to enhance tissue differentiation, such as bone
 CC formation and hematopoietic cell formation.

XX Sequence 349 AA;

Query Match 11.7%; Score 41; DB 21; Length 349;
 Best Local Similarity 100.0%; Pred. No. 3e-31;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 YPGEATLNEMFREVEIMEDTQKLRSAVEEMAEBAAK 80
 DB 40 YPGEATLNEMFREVEIMEDTQKLRSAVEEMAEBAAK 80

RESULT 29
 AA024777
 ID AA024777 standard; Peptide; 14 AA.

AC AA024777;
 DT 18-DEC-2001 (first entry)
 DE Schizophrenia-Associated Protein Isoform (SPI) peptide #6.
 XX Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;
 XX neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.
 XX Homo sapiens.
 XX WO200162785-A2.
 XX 30-AUG-2001.
 XX 23-FEB-2001; 2001WO-GB00792.
 XX 24-FEB-2000; 2000GB-0004415.
 XX 28-NOV-2000; 2000US-0750395.
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX Herath HMC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;
 XX WPI; 2001-570624/64.
 XX The sequence represents a schizophrenia-associated protein isoform (SPI).
 XX These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable
 XX in cerebrospinal fluid, serum or plasma and are useful markers of
 XX schizophrenia. The sequences can be used for treatment and diagnosis of
 XX schizophrenia, screening, prognosis, monitoring the results of therapy,
 XX identifying patients most likely to respond to a particular therapy and
 XX identification of new targets for drug treatment. SPI DNA is useful as a
 XX nucleic acid probe to detect the presence of nucleic acids or SPIs.

PS Sequence 14 AA;

Query Match 4.0%; Score 14; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.4e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SAVERMEAEBAAK 80
 DB 1 SAVERMEAEBAAK 14

RESULT 30

AAU15121
 ID AAU15121 standard; Peptide; 14 AA.
 AC AAU15121;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Schizophrenia-associated isoform peptide #6.
 XX
 KW Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;
 KM neurological disorder; neuropathy.
 XX
 OS Homo sapiens.
 XX
 PN WO200163293-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 23-FEB-2001; 2001WO-GB00783.
 XX
 PR 24-FEB-2000; 2000GB-0004415.
 XX
 PR 28-NOV-2000; 2000US-0750395.
 XX
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX
 PI Herath HMAc, Parekh RB, Rohlf C;
 XX
 DR WPI; 2001-502868/55.
 XX
 PT Diagnosing and monitoring Schizophrenia by detecting the presence of
 PT Schizophrenia Associated Features and Schizophrenia Associated Protein
 PT Isoforms in samples of cerebrospinal fluid -
 XX
 PS Claim 6; Page 29; 160pp; English.
 XX
 CC The invention relates to methods and compositions for screening,
 CC diagnosis and prognosis of Schizophrenia. The method involves detecting
 CC the presence of Schizophrenia (SCH) Associated Features (SFS) and SCH
 CC Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis,
 CC immunoblotting or hybridisation assay, for diagnosing and monitoring SCH,
 CC studying the effectiveness of treatments and for identifying potential
 CC therapeutic agents. The method is used for (1) screening or diagnosis of
 CC SCH and the relative abundance of at least 1 chosen feature correlates
 CC with the presence or absence of SCH; and (2) monitoring the effect of
 CC therapy administered to a subject with SCH and the relative abundance of
 CC at least 1 chosen feature which correlates with the severity of SCH.
 CC The expression and activity of the SFS, SPIs and related molecules
 CC (e.g. secondary messengers) are studied to diagnose SCH, monitor the
 CC progress of the disorder and the effectiveness of treatment and as
 CC targets to identify and produce potential therapeutic agents for the
 CC treatment of SCH. The paucity of detectable neuronal defects
 CC distinguishes neuropsychiatric disorders such as SCH from neurological
 CC disorders, where manifestations of anatomical and biochemical changes
 CC have been identified in many cases. Consequently the identification and
 CC characterisation of cellular and/or molecular causative defects and
 CC neuroprotective agents are necessary for improved treatment of neuropsychiatric
 CC disorders. AAU1514-AAU15762 represent the amino acid sequences of
 CC schizophrenia-associated isoforms used in the method of the invention.
 XX
 SQ Sequence 14 AA;
 Query Match 4.0%; Score 14; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.4e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 67 SAVEEMAEERAAK 80
 |||||
 DB 1 SAVEEMAEERAAK 14
 RESULT 31
 ABB56096
 ID ABB56096 standard; Peptide; 12 AA.

XX
 AC ABB56096;
 XX
 DT 15-FEB-2002 (first entry)
 XX
 DE Vascular dementia-associated protein isoform (VPI) 296.
 XX
 KW Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
 KM diagnosis; prognosis; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200169261-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 14-MAR-2001; 2001WO-GB01106.
 XX
 PR 15-MAR-2000; 2000GB-0006285.
 XX
 PR 24-NOV-2000; 2000GB-0028734.
 XX
 PR 28-NOV-2000; 2000US-0724391.
 XX
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX
 PI Herath HMAc, Parekh RB, Rohlf C;
 XX
 DR WPI; 2001-557937/62.
 XX
 PT Screening, diagnosis or prognosis of vascular dementia (VD), useful for
 PT determining stage of VD and monitoring the effect of VD therapy,
 PT comprises analysing body fluid by 2-dimensional electrophoresis for
 PT features correlated with VD -
 XX
 PS Claim 6; Page 36; 151pp; English.
 XX
 CC The invention relates to screening, diagnosis or prognosis of Vascular
 CC Dementia (VD) in a subject comprising analysing body fluid from the
 CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
 CC features containing at least one chosen feature whose relative abundance
 CC correlates with the presence, absence, stage or severity of VD or
 CC predicts the onset or course of VD, especially detecting in a sample of
 CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
 CC protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the
 CC specification. Detecting VD-associated features and VPI is useful for the
 CC screening, diagnosis or prognosis of VD, for determining the stage or
 CC severity of VD, for identifying a subject at risk of VD or for
 CC monitoring the effect of therapy administered to a subject having VD.
 CC Nucleic acids encoding a VPI or inhibiting the function of a VPI are
 CC useful for the treatment of VD and for gene therapy.
 XX
 SQ Sequence 12 AA;
 Query Match 3.4%; Score 12; DB 22; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00026;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 53 EYEBLMDTQHK 64
 |||||
 DB 1 EYEBLMDTQHK 12
 RESULT 32
 ABB56097
 ID ABB56097 standard; Peptide; 12 AA.
 XX
 AC ABB56097;
 XX
 DT 15-FEB-2002 (first entry)
 XX
 DE Vascular dementia-associated protein isoform (VPI) 297.
 XX
 KW Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
 KM diagnosis; prognosis; gene therapy.

XX OS Homo sapiens.
XX XX WO200169261-A2.
XX XX
XX PD 20-SEP-2001.
XX PF 14-MAR-2001; 2001WO-GB01106.
XX PR 15-MAR-2000; 2000GB-0006285.
XX PR 24-NOV-2000; 2000GB-0028734.
XX PR 28-NOV-2000; 2000US-0724391.
XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX PI Herath HMAc, Parekh RB, Rohlf C,
XX DR WPI; 2001-557937/62.
XX PT Screening, diagnosis or prognosis of vascular dementia (VD), useful for
XX PT determining stage of VD and monitoring the effect of VD therapy,
XX PT comprises analysing body fluid by 2-dimensional electrophoresis for
XX PT features correlated with VD -
XX PS Claim 6; Page 36; 15pp; English.
XX CC The invention relates to screening, diagnosis or prognosis of Vascular
XX CC Dementia (VD) in a subject comprising analysing body fluid from the
XX CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
XX CC features containing at least one chosen feature whose relative abundance
XX CC correlates with the presence, absence, stage or severity of VD or
XX CC predicts the onset or course of VD, especially detecting in a sample of
XX CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
XX CC protein isoforms (VPIs) (ABBS5601-ABBS6295) as fully defined in the
XX CC specification. Detecting VD-associated features and VPI is useful for the
XX CC screening, diagnosis or prognosis of VD, for determining the stage or
XX CC severity of VD, for identifying a subject at risk of VD or for
XX CC monitoring the effect of therapy administered to a subject having VD.
XX CC Nucleic acids encoding a VPI or inhibiting the function of a VPI are
XX CC useful for the treatment of VD and for gene therapy.
XX SQ Sequence 12 AA;
XX
XX Query Match 3.4%; Score 12; DB 22; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 0.00026;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 213 DCQPGILCCAFQR 224
XX DB 1 DCQPGILCCAFQR 12
XX
XX RESULT 33
XX ABB52342 ID ABB52342 standard; Peptide; 12 AA.
XX XX
XX AC ABB52342;
XX XX
XX DT 08-FEB-2002 (first entry)
XX XX
XX DE Human API-121 tryptic digest peptide #2.
XX KW Human; neuroprotective; noctropic; gene therapy; vaccine;
XX KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;
XX KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
XX KW Expression Reference Protein Isoform; ERPI; proteolysis.
XX OS Homo sapiens.
XX XS WO200175454-A2.
XX PN
XX PD 11-OCT-2001.
XX XX

XX PF 03-APR-2001; 2001WO-US10908.
XX XX
XX PR 03-APR-2000; 2000US-194504P.
XX PR 28-NOV-2000; 2000US-253647P.
XX XX
XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX PA (PFIZ) PFIZER INC.
XX XX
XX PI Durham KL, Friedman DL, Herath HMAc, Kimmel LH, Parekh RB;
XX PI Potter DM, Rohlf C, Silber BW, Stiger TR, Sunderland PT;
XX PI Townsend RR, White F, Williams SA;
XX DR WPI; 2001-639384/73.
XX XX
XX PT Screening for Alzheimer's disease in a mammal, by making
XX PT two-dimensional array of a feature whose relative abundance correlates
XX PT with disease, and comparing with abundance of the feature in samples of
XX PT healthy persons -
XX PS Example; Page 34; 162pp; English.
XX XX
XX CC The invention relates to method for the screening, diagnosis and
XX CC prognosis of Alzheimer's disease. The methods involve the detection
XX CC of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's
XX CC Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid,
XX CC serum or plasma. The abundance of the AFs and APIs is then
XX CC normalised to an Expression Reference Protein Isoform (ERPI) in
XX CC order to determine whether a patient is suffering from, or has
XX CC a predisposition to, Alzheimer's Disease. The relative abundance of
XX CC the AFs and APIs correlates with the severity of Alzheimer's Disease.
XX CC The present sequence is a peptide produced from an API by proteolysis.
XX SQ Sequence 12 AA;
XX
XX Query Match 3.4%; Score 12; DB 22; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 0.00026;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 213 DCQPGILCCAFQR 224
XX DB 1 DCQPGILCCAFQR 12
XX
XX RESULT 34
XX ABB56098 ID ABB56098 standard; Peptide; 10 AA.
XX XX
XX AC ABB56098;
XX XX
XX DT 15-FEB-2002 (first entry)
XX XX
XX DE Vascular dementia-associated protein isoform (VPI) 298.
XX KW Vascular Dementia; VD, VD-associated protein isoform; VPI; screening;
XX KW diagnosis; prognosis; gene therapy.
XX OS Homo sapiens.
XX XS WO200169261-A2.
XX PN
XX PD 20-SEP-2001.
XX XX
XX PF 14-MAR-2001; 2001WO-GB01106.
XX KW 15-MAR-2000; 2000GB-0006285.
XX PR 24-NOV-2000; 2000GB-0028734.
XX PR 28-NOV-2000; 2000US-0724391.
XX XX
XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX PA Herath HMAc, Parekh RB, Rohlf C,
XX PI WPI; 2001-557937/62.
XX DR

XX Screening, diagnosis or prognosis of vascular dementia (VD), useful for
PT determining stage of VD and monitoring the effect of VD therapy.
PT comprises analysing body fluid by 2-dimensional electrophoresis for
PT features correlated with VD -
PS Claim 6; Page 36; 151pp; English.
XX
CC The invention relates to screening, diagnosis or prognosis of Vascular
CC Dementia (VD) in a subject comprising analysing body fluid from the
CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
CC features containing at least one chosen feature whose relative abundance
CC correlates with the presence, absence, stage or severity of VD or
CC predicts the onset or course of VD, especially detecting in a sample of
CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
CC protein isoforms (VPIs) (AB55801-AB56295) as fully defined in the
CC specification. Detecting VD-associated features and VPI is useful for the
CC screening, diagnosis or prognosis of VD, for determining the stage or
CC severity of VD, for identifying a subject at risk of VD or for
CC monitoring the effect of therapy administered to a subject having VD.
CC Nucleic acids encoding a VPI or inhibiting the function of a VPI are
CC useful for the treatment of VD and for gene therapy.

QY Sequence 10 AA;
SQ
Query Match 2.9%; Score 10; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02; Mismatches 0;
Matches 10; Conservative 0; Indels 0; Gaps 0;

293 DDGGILLPR 302
1 DDGGILLPR 10

RESULT 35
AAG80272
ID AAG80272 standard; Protein; 10 AA.

AC AAG80272;

DT 11-FEB-2002 (first entry)

XX Human DKK-3 protein derived tryptic peptide.

KM DKK-3; detection; schizophrenia; neuroleptic; vaccine; gene therapy;
KM neurologic defect; neuropsychiatric disorder; human; tryptic peptide.

OS Homo sapiens.

XX WO200163295-A2.

XX 30-AUG-2001.

PF 26-FEB-2001; 2001WO-IB00259.

XX 24-FEB-2000; 2000GB-0004412.

PR 24-FEB-2000; 2000GB-0004415.

PR 15-MAR-2000; 2000GB-0006285.

PR 24-NOV-2000; 2000GB-0028734.

PR 28-NOV-2000; 2000US-0724391.

PR 08-DEC-2000; 2000GB-0030050.

PR 12-DEC-2000; 2000US-0254830.

PR 28-DEC-2000; 2000US-0750395.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Herach HMAc, Parekh RB, Rohlf C, Patel TP;

XX WPI; 2001-570652/64.

PT Diagnosing and monitoring Schizophrenia by detecting the presence of
PT Schizophrenia Associated Features and Schizophrenia Associated Protein
PT isoforms in samples of cerebrospinal fluid -

XX Example 2; Fig 3; 91pp; English.

CC This invention describes a novel method for detecting the presence of
CC schizophrenia associated features (SFS) and schizophrenia associated
CC protein isoforms (SPIs) in samples, e.g. by electrophoresis, immunoassay
CC or hybridisation assay, for diagnosing and monitoring schizophrenia,
CC studying the effectiveness of treatments and for identifying potential
CC therapeutic agents. The products of the invention have neuroleptic
CC activity and can be used in vaccines or for gene therapy. The method (I)
CC is used: (1) for screening or diagnosis of schizophrenia and the relative
CC abundance of at least 1 chosen feature correlates with the presence or
CC absence of schizophrenia and for monitoring the effect of therapy
CC administered to a subject with schizophrenia and the relative abundance
CC of at least 1 chosen feature which correlates with the severity of
CC schizophrenia. The expression and activity of the SFS, SPIs and related
CC molecules (e.g. secondary messengers) are studied to diagnose
CC schizophrenia, monitor the progress of the disorder and the effectiveness
CC of treatment and as targets to identify and produce potential therapeutic
CC agents for the treatment of schizophrenia. The paucity of detectable
CC neurologic defects distinguishes neuropsychiatric disorders such as
CC schizophrenia from neurological disorders, where manifestations of
CC anatomical and biochemical changes have been identified in many cases.
CC Consequently the identification and characterisation of cellular and/or
CC molecular causative defects and neuropathies are necessary for improved
CC treatment of neuropsychiatric disorders. This sequence represents a
CC human DKK-3 protein derived tryptic peptide described in the method of
CC the invention.

QY Sequence 10 AA;
SQ

Query Match 2.9%; Score 10; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02; Mismatches 0;
Matches 10; Conservative 0; Indels 0; Gaps 0;

293 DDGGILLPR 302
1 DDGGILLPR 10

RESULT 36
AB552202
ID AB552202 standard; Peptide; 10 AA.

AC AB552202;

DT 08-FEB-2002 (first entry)

XX Human API-153 tryptic digest peptide.

KM Human; neuroprotective; nootropic; gene therapy; vaccine;
KM Alzheimer's disease; Alzheimer's Disease-Associated Feature; API;
KM Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
KM Expression Reference Protein Isoform; ERPI; proteolysis.

XX Homo sapiens.

XX WO200175454-A2.

XX 11-OCT-2001.

XX 03-APR-2001; 2001WO-US10908.

PR 03-APR-2000; 2000US-194504P.

PR 28-NOV-2000; 2000US-253647P.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX (PRIZ) PRIZER INC.

XX Durham KU, Friedman DL, Herach HMAc, Kimmel LH, Parekh RB;

PI Potter DM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;

PI Townsend RR, White F, Williams SA;

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DR WPI; 2001-639384/73.
XX
PT Screening for Alzheimer's disease in a mammal, by making
PT two-dimensional array of a feature whose relative abundance correlates
PT with disease, and comparing with abundance of the feature in samples of
PT healthy persons
XX
PS Example; Page 30; 162pp; English.
XX
CC The invention relates to methods for the screening, diagnosis and
CC prognosis of Alzheimer's disease. The methods involve the detection
CC of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's
CC Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid,
CC serum or plasma. The abundance of the APs and APIs is then
CC normalised to an Expression Reference Protein Isoform (ERPI) in
CC order to determine whether a patient is suffering from, or has
CC a predisposition to, Alzheimer's Disease. The relative abundance of
CC the APs and APIs correlates with the severity of Alzheimer's Disease.
CC The present sequence is a peptide produced from an API by proteolysis.
XX
SQ Sequence 10 AA;
XX
Query Match 2.9%; Score 10; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 293 DODGEILLPR 302
Db 1 DODGEILLPR 10
RESULT 37
ABBS2341
ID ABBS2341 standard; Peptide; 10 AA.
XX
AC ABBS2341;
XX
DT 08-FEB-2002 (first entry)
XX
DE Human API-121 tryptic digest peptide #1.
XX
DS Human; neuroprotective; nootropic; gene therapy; vaccine;
KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;
KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
KW Expression Reference Protein Isoform; ERPI; proteolysis.
XX
OS Homo sapiens.
XX
PN WO200175454-A2.
XX
PD 11-OCT-2001.
XX
PF 03-APR-2001; 2001WO-US10908.
XX
PR 03-APR-2000; 2000US-194504P.
XX
PR 28-NOV-2000; 2000US-253647P.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PA (PRIZ ) PRIZER INC.
XX
PI Durham XL, Friedman DL, Herach HMAc, Kimmel LH, Parekh RB;
PI Potter DM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;
PI Townsend RR, White F, Williams SA;
XX
DR WPI; 2001-639384/73.
XX
PT Screening for Alzheimer's disease in a mammal, by making
PT two-dimensional array of a feature whose relative abundance correlates
PT with disease, and comparing with abundance of the feature in samples of
PT healthy persons
XX
PS Example; Page 34; 162pp; English.
XX

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CC The invention relates to methods for the screening, diagnosis and
CC prognosis of Alzheimer's disease. The methods involve the detection
CC of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's
CC Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid,
CC serum or plasma. The abundance of the AFs and APIs is then
CC normalised to an Expression Reference Protein Isoform (ERPI) in
CC order to determine whether a patient is suffering from, or has
CC a predisposition to, Alzheimer's Disease. The relative abundance of
CC the AFs and APIs correlates with the severity of Alzheimer's Disease.
CC The present sequence is a peptide produced from an API by proteolysis.
XX
SQ Sequence 10 AA;
XX
Query Match 2.9%; Score 10; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 293 DQGEIILPR 302
Db 1 DQGEIILPR 10
RESULT 38
ABBS2343
ID ABBS2343 standard; Peptide: 10 AA.
XX
XX ABBS2343;
XX
XX AC
XX
XX DT
XX DE 08-FEB-2002 (first entry)
XX
XX Human API-122 tryptic digest peptide.
XX
XX Human; neuroprotective; nootropic; gene therapy; vaccine;
XX Alzheimer's Disease; Alzheimer's Disease-Associated Feature; AF;
XX Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
XX Expression Reference Protein Isoform; ERPI; proteolysis.
XX
XX Homo sapiens.
XX
XX OS
XX FN WO200175454-A2.
XX
XX PD 11-OCT-2001.
XX
XX PF 03-APR-2001; 2001WO-US10908.
XX
XX PR 03-APR-2000; 2000US-194504P.
XX 28-NOV-2000; 2000US-253647B.
XX
XX (OXFO-) OXFORD GLYSCSCIENCES UK LTD.
XX (PFIz ) PFIZER INC.
XX
XX PI Durham KU, Friedman DL, Herath HMAG, Kimmel IH, Parekh RB;
XX PI Potter DM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;
XX PI Townsend RR, White F, Williams SA;
XX
XX WPI; 2001-639384/73.
XX
XX Screening for Alzheimer's disease in a mammal, by making
XX two-dimensional array of a feature whose relative abundance correlates
XX with disease, and comparing with abundance of the feature in samples of
XX healthy persons -
XX
XX Example; Page 34; 162p; English.
XX
XX The invention relates to methods for the screening, diagnosis and
XX prognosis of Alzheimer's disease. The methods involve the detection
XX of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's
XX Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid,
XX serum or plasma. The abundance of the AFs and APIs is then
XX normalised to an Expression Reference Protein Isoform (ERPI) in
XX order to determine whether a patient is suffering from, or has
XX a predisposition to, Alzheimer's Disease. The relative abundance of
XX the AFs and APIs correlates with the severity of Alzheimer's Disease.
XX

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CC The present sequence is a peptide produced from an API by proteolysis.
XX
SQ Sequence 10 AA;
Query Match 2.9%; Score 10; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 293 DDDGELLPR 302
DB 1 DDDGELLPR 10
RESULT 39
AAU28428
ID AAU28428 standard; Peptide; 10 AA.
XX
XX AAU28428;
XX
XX 03-JAN-2002 (first entry)
XX
XX DPI tryptic digest peptide #25.
XX
XX Human; depression associated protein isoform; tryptic digest peptide;
XX DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
XX neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
XX manic-depressive illness; schizoaffective disorder.
XX Homo sapiens.
XX MO200162787-A1.
XX
XX 30-AUG-2001.
XX
XX 23-FEB-2001; 2001MO-GB00786.
XX
XX 24-FEB-2000; 2000GB-0004412.
XX 08-DEC-2000; 2000GB-0030050.
XX 12-DEC-2000; 2000US-0254830.
XX
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
XX Herath HMAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;
XX WPI; 2001-570626/64.
XX
XX Novel nucleic acid encoding a protein associated with bipolar affective
XX disorder, which is used for diagnosis, prophylaxis and therapy of
XX neuropsychiatric disorders, such as bipolar affective disorder -
XX
XX Disclosure; Page 31; 153pp; English.
XX
XX The present invention relates to the identification of depression
XX associated protein isoforms (DPIs), particularly the tryptic digest
XX peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)
XX described are decreased in the cerebrospinal fluid (CSF) of BAD
XX (bipolar affective disorder) subjects, whilst other DPIs
XX (AAU28626-AAU28887) are increased in BAD subjects. Also described
XX are peptide sequences identified from DPI-45 and DPI-213 and the
XX nucleic acid sequence they are encoded by. The sequences of the
XX invention are useful for clinical screening, diagnosis, prognosis,
XX therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also
XX known as bipolar mood disorder, BP), manic-depressive illnesses,
XX attention deficit disorders, schizoaffective disorders, and unipolar
XX affective disorders. The present sequence represents one of the DPI
XX tryptic digest peptides of the present invention.
XX
XX Sequence 10 AA;
SQ
Query Match 2.9%; Score 10; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ID AAU28566 standard; Peptide; 10 AA.

QY 293 DDDGELLPR 302
DB 1 DDDGELLPR 10
RESULT 40
AAU28553
ID AAU28553 standard; Peptide; 10 AA.
XX
XX AAU28553;
XX
XX 03-JAN-2002 (first entry)
XX
XX DPI tryptic digest peptide #150.
XX
XX Human; depression associated protein isoform; tryptic digest peptide;
XX DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
XX neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
XX manic-depressive illness; schizoaffective disorder.
XX Homo sapiens.
XX MO200162787-A1.
XX
XX 30-AUG-2001.
XX
XX 23-FEB-2001; 2001MO-GB00786.
XX
XX 24-FEB-2000; 2000GB-0004412.
XX 08-DEC-2000; 2000GB-0030050.
XX 12-DEC-2000; 2000US-0254830.
XX
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
XX Herath HMAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;
XX WPI; 2001-570626/64.
XX
XX Novel nucleic acid encoding a protein associated with bipolar affective
XX disorder, which is used for diagnosis, prophylaxis and therapy of
XX neuropsychiatric disorders, such as bipolar affective disorder -
XX
XX Disclosure; Page 33; 153pp; English.
XX
XX The present invention relates to the identification of depression
XX associated protein isoforms (DPIs), particularly the tryptic digest
XX peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)
XX described are decreased in the cerebrospinal fluid (CSF) of BAD
XX (bipolar affective disorder) subjects, whilst other DPIs
XX (AAU28626-AAU28887) are increased in BAD subjects. Also described
XX are peptide sequences identified from DPI-45 and DPI-213 and the
XX nucleic acid sequence they are encoded by. The sequences of the
XX invention are useful for clinical screening, diagnosis, prognosis,
XX therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also
XX known as bipolar mood disorder, BP), manic-depressive illnesses,
XX attention deficit disorders, schizoaffective disorders, and unipolar
XX affective disorders. The present sequence represents one of the DPI
XX tryptic digest peptides of the present invention.
XX
XX Sequence 10 AA;
SQ
Query Match 2.9%; Score 10; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 293 DDDGELLPR 302
DB 1 DDDGELLPR 10
RESULT 41
AAU28566
ID AAU28566 standard; Peptide; 10 AA.

XX	AC	AAU28566;
XX	DT	03-JAN-2002 (first entry)
XX	DE	DPI tryptic digest peptide #163.
XX	KM	Human; depression associated protein isoform; tryptic digest peptide;
XX	KM	DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
XX	KM	neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
XX	KM	manic-depressive illness; schizoaffective disorder.
XX	OS	Homo sapiens.
XX	PN	W0200162787-A1.
XX	PD	30-AUG-2001.
XX	PF	23-FEB-2001; 2001WO-GB00786.
XX	PR	24-FEB-2000; 2000GB-0004412.
XX	PR	08-DEC-2000; 2000GB-0030050.
XX	PR	12-DEC-2000; 2000US-0254830.
XX	PA	(OXFO-) OXFORD GLYCOSCSCIENCES UK LTD.
XX	PI	Herath HMAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL,
XX	DR	WPI; 2001-570626/64.
XX	PT	Novel nucleic acid encoding a protein associated with bipolar affective
XX	PT	disorder, which is used for diagnosis, prophylaxis and therapy of
XX	PT	neuropsychiatric disorders, such as bipolar affective disorder -
XX	PS	Disclosure; Page 34; 153pp; English.
XX	CC	The present invention relates to the identification of depression
XX	CC	associated protein isoforms (DPIs), particularly the tryptic digest
XX	CC	peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)
XX	CC	described are decreased in the cerebrospinal fluid (CSF) of BAD
XX	CC	(bipolar affective disorder) subjects, whilst other DPIs
XX	CC	(AAU28626-AAU28887) are increased in BAD subjects. Also described
XX	CC	are peptide sequences identified from DPI-45 and DPI-213 and the
XX	CC	nucleic acid sequence they are encoded by. The sequences of the
XX	CC	invention are useful for clinical screening, diagnosis, prognosis,
XX	CC	therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also
XX	CC	known as bipolar mood disorder, BP), manic-depressive illnesses,
XX	CC	attention deficit disorders, schizoaffective disorders, and unipolar
XX	CC	affective disorders. The present sequence represents one of the DPI
XX	CC	tryptic digest peptides of the present invention.
XX	SC	Sequence 10 AA;
XX	QY	Query Match 2.9%; Score 10; DB 22; Length 10;
XX	Db	Best Local Similarity 100.0%; Freq. No. 0.02;
XX		Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
XX		293 DQDGERLLPR 302
XX		
XX		1 DDGGERLLPR 10
XX	ID	AAU24776 standard; Peptide; 10 AA.
XX	AC	AAU24776;
XX	DT	18-DEC-2001 (first entry)
XX	DE	Schizophrenia-associated Protein Isoform (SPI) peptide #5.
XX	DM	Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;

XX	neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.
OS	Homo sapiens.
XN	WO200162785-A2.
XP	30-AUG-2001.
XX	
XX	23-FEB-2001; 2001WO-GS00792.
XX	
PR	24-FEB-2000; 2000GB-0004415.
PR	28-NOV-2000; 2000US-0750395.
XX	
PA	(OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX	
PI	Herath HMAG, Parekh RB, Rohlf C, Terrett JA, Tyson KL;
DR	WPI; 2001-570624/64.
XX	
PT	New schizophrenia associated protein isoforms and encoding nucleic acid
PT	molecules; useful for treatment, diagnosis and prognosis of
PT	schizophrenia and screening for potential drugs for treatment and new
PT	drug targets -
XX	
PS	Disclosure; Page 29; 14pp; English.
CC	
CC	The sequence represents a schizophrenia-associated protein isoform (SPI).
CC	These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable
CC	in cerebrospinal fluid, serum or plasma and are useful markers of
CC	schizophrenia. The sequences can be used for treatment and diagnosis of
CC	schizophrenia, screening, prognosis, monitoring the results of therapy,
CC	identifying patients most likely to respond to a particular therapy and
CC	identification of new targets for drug treatment. SPI DNA is useful as a
CC	nucleic acid probe to detect the presence of nucleic acids or SPis.
XX	
SQ	Sequence 10 AA;
OY	Query Match 2.9%; Score 10; DB 22; Length 10;
	Best Local Similarity 100.0%; Pred. No. 0.02;
	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DQ	293 DODGEILPPR 302
DB	1 DODGEILPPR 10
RESULT 43	
ID	AAU25210 standard; Peptide; 10 AA.
XX	
AC	AAU25210;
XX	
DT	18-DEC-2001 (first entry)
DE	Schizophrenia-Associated Protein Isoform (SPI) peptide #439.
KM	Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;
KX	neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.
OS	Homo sapiens.
PB	WO200162785-A2.
PN	30-AUG-2001.
XX	
PF	23-FEB-2001; 2001WO-GB00792.
XX	
PR	24-FEB-2000; 2000GB-0004415.
PR	28-NOV-2000; 2000US-0750395.
XX	
PA	(OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX	
PI	Herath HMAG, Parekh RB, Rohlf C, Terrett JA, Tyson KL;

XX WPI; 2001-570624/64.
XX
PT New schizophrenia associated protein isoforms and encoding nucleic acid
PT molecules, useful for treatment, diagnosis and prognosis of
PT schizophrenia and screening for potential drugs for treatment and new
PT drug targets -
PS Disclosure; Page 37; 148pp; English.
XX
XX The sequence represents a schizophrenia-associated protein isoform (SPI).
CC These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable
CC in cerebrospinal fluid, serum or plasma and are useful markers of
CC schizophrenia. The sequences can be used for treatment and diagnosis of
CC schizophrenia, screening, prognosis, monitoring the results of therapy,
CC identifying patients most likely to respond to a particular therapy and
CC identification of new targets for drug treatment. SPI DNA is useful as a
CC nucleic acid probe to detect the presence of nucleic acids or SPIs.
XX
SQ Sequence 10 AA;
Query Match 2.9%; Score 10; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 293 DQDGEIILPR 302
DB 1 DQDGEIILPR 10
RESULT 44
AAU25377
ID AAU25377 standard; Peptide; 10 AA.
XX
AC AAU25377;
XX
DT 18-DEC-2001 (first entry)
XX
DE Schizophrenia-Associated Protein Isoform (SPI) peptide #606.
XX
KW Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;
KW neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.
XX
OS Homo sapiens.
XX
PN WO200162785-A2.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-GB00792.
XX
PR 24-FEB-2000; 2000GB-0004415.
PR 28-NOV-2000; 2000US-0750395.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAc, Parekh RB, Rohlf C, Terrett JA, Tyson KL;
XX
DR WPI; 2001-570624/64.
XX
PT New schizophrenia associated protein isoforms and encoding nucleic acid
PT molecules, useful for treatment, diagnosis and prognosis of
PT schizophrenia and screening for potential drugs for treatment and new
PT drug targets -
PS Disclosure; Page 41; 148pp; English.
XX
XX The sequence represents a schizophrenia-associated protein isoform (SPI).
CC These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable
CC in cerebrospinal fluid, serum or plasma and are useful markers of
CC schizophrenia. The sequences can be used for treatment and diagnosis of
CC schizophrenia, screening, prognosis, monitoring the results of therapy,
CC identifying patients most likely to respond to a particular therapy and

CC identification of new targets for drug treatment. SPI DNA is useful as a
CC nucleic acid probe to detect the presence of nucleic acids or SPIs.
XX
SQ Sequence 10 AA;
Query Match 2.9%; Score 10; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 293 DQDGEIILPR 302
DB 1 DQDGEIILPR 10
RESULT 45
AAU26074
ID AAU26074 standard; Peptide; 10 AA.
XX
AC AAU26074;
XX
DT 18-DEC-2001 (first entry)
XX
DE Depression-Associated Protein Isoform DPI-6 #1.
XX
KW Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;
KW DPI; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;
KW CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic;
KW attention deficient disorder; schizoaffective disorder;
KW unipolar affective disorder.
XX
OS Homo sapiens.
XX
PN WO200163294-A2.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-GB00791.
XX
PR 24-FEB-2000; 2000GB-0004412.
PR 08-DEC-2000; 2000GB-0030050.
PR 12-DEC-2000; 2000US-0254830.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAc, Parekh RB, Rohlf C;
XX
DR WPI; 2001-582081/65.
XX
PT Preparation for diagnosing or treating bipolar affected disorder (BAD)
PT or unipolar depression, or for screening for modulators, comprises a
PT BAD-associated protein isoform -
PS Claim 8; Page 31; 163pp; English.
XX
XX The invention relates to a preparation comprising an isolated Bipolar
CC Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are
CC used to screen, diagnose or prognose of BAD or unipolar depression,
CC determine the stage or severity of BAD or unipolar depression, identify a
CC subject at risk of developing BAD or unipolar depression, or monitor the
CC effect of therapy in a subject. They are also used to screen for or
CC identify agents that interact with a DPI. These agents, antibodies
CC against the DPIs, and nucleic acids encoding the DPIs are used to treat
CC or prevent BAD or unipolar depression. Diseases that can be treated are
CC attention deficient disorder, a schizoaffective disorder, a bipolar or a
CC unipolar affective disorder. The DPIs are used in proteomics. The
CC proteomic approach of using DPIs for screening, diagnosis or prognosis of
CC BAD or unipolar depression overcomes the problems of using gene
CC expression analysis, such as not being able to obtain central nervous
CC system (CNS) tissue from a living patient under normal circumstances.
CC The present sequence is a DIP decreased in the CSF (cerebro-spinal
CC fluid) of subjects having BAD.
SQ Sequence 10 AA;

Query Match 2.9%; Score 10; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 DQDGEILLPR 302
| | | | |
| | | | |
Db 1 DQDGEILLPR 10

RESULT 46
AAU26200
ID AAU26200 standard; Peptide; 10 AA.
XX
XX AAU26200;
XX
DT 18-DEC-2001 (first entry)
XX
XX Depression-Associated Protein Isoform DPI-186.
XX
XX Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;
KM DF; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;
KM CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic;
KM attention deficient disorder; schizoaffective disorder;
KM unipolar affective disorder.
XX
XX Homo sapiens.
XX
XX WO200163294-A2.
XX
XX 30-AUG-2001.
XX
XX 23-FEB-2001; 2001WO-GB00791.
XX
XX 24-FEB-2000; 2000GB-0004412.
PR 08-DEC-2000; 2000GB-0030050.
PR 12-DEC-2000; 2000US-0254830.
XX
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
XX Herath HMAC, Parekh RB, Rohlf C;
PI WPI; 2001-582081/65.
XX
XX Preparation for diagnosing or treating bipolar affected disorder (BAD)
PT or unipolar depression, or for screening for modulators, comprises a
PT BAD-associated protein isoform -
XX
XX Claim 8; Page 33; 163pp; English.
XX
XX The invention relates to a preparation comprising an isolated Bipolar
CC Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are
CC used to screen, diagnose or prognose of BAD or unipolar depression,
CC determine the stage or severity of BAD or unipolar depression, identify a
CC subject at risk of developing BAD or unipolar depression, or monitor the
CC effect of therapy in a subject. They are also used to screen for or
CC identify agents that interact with a DPI. These agents, antibodies
CC against the DPIs, and nucleic acids encoding the DPIs are used to treat
CC or prevent BAD or unipolar depression. Diseases that can be treated are
CC attention deficient disorder, a schizoaffective disorder, a bipolar or a
CC unipolar affective disorder. The DPIs are used in proteomics. The
CC proteomic approach of using DPIs for screening, diagnosis or prognosis of
CC BAD or unipolar depression overcomes the problems of using gene
CC expression analysis, such as not being able to obtain central nervous
CC system (CNS) tissue from a living patient under normal circumstances.
CC The present sequence is a DIP decreased in the CSF (cerebro-spinal
CC fluid) of subjects having BAD.
XX
XX
SQ Sequence 10 AA;

Query Match 2.9%; Score 10; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 DQDGEILLPR 302
| | | | |
| | | | |
Db 1 DQDGEILLPR 10

RESULT 47
AAU26213
ID AAU26213 standard; Peptide; 10 AA.
XX
XX AAU26213;
XX
DT 18-DEC-2001 (first entry)
XX
XX Depression-Associated Protein Isoform DPI-192 #1.
XX
XX Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;
KM DF; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;
KM CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic;
KM attention deficient disorder; schizoaffective disorder;
KM unipolar affective disorder.
XX
XX Homo sapiens.
XX
XX WO200163294-A2.
XX
XX 30-AUG-2001.
XX
XX 23-FEB-2001; 2001WO-GB00791.
XX
XX 24-FEB-2000; 2000GB-0004412.
PR 08-DEC-2000; 2000GB-0030050.
PR 12-DEC-2000; 2000US-0254830.
XX
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
XX Herath HMAC, Parekh RB, Rohlf C;
PI WPI; 2001-582081/65.
XX
XX Preparation for diagnosing or treating bipolar affected disorder (BAD)
PT or unipolar depression, or for screening for modulators, comprises a
PT BAD-associated protein isoform -
XX
XX Claim 8; Page 34; 163pp; English.
XX
XX The invention relates to a preparation comprising an isolated Bipolar
CC Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are
CC used to screen, diagnose or prognose of BAD or unipolar depression,
CC determine the stage or severity of BAD or unipolar depression, identify a
CC subject at risk of developing BAD or unipolar depression, or monitor the
CC effect of therapy in a subject. They are also used to screen for or
CC identify agents that interact with a DPI. These agents, antibodies
CC against the DPIs, and nucleic acids encoding the DPIs are used to treat
CC or prevent BAD or unipolar depression. Diseases that can be treated are
CC attention deficient disorder, a schizoaffective disorder, a bipolar or a
CC unipolar affective disorder. The DPIs are used in proteomics. The
CC proteomic approach of using DPIs for screening, diagnosis or prognosis of
CC BAD or unipolar depression overcomes the problems of using gene
CC expression analysis, such as not being able to obtain central nervous
CC system (CNS) tissue from a living patient under normal circumstances.
CC The present sequence is a DIP decreased in the CSF (cerebro-spinal
CC fluid) of subjects having BAD.
XX
XX
SQ Sequence 10 AA;

Query Match 2.9%; Score 10; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 48
AAU15120
ID AAU15120 standard; Peptide: 10 AA.
XX
AC AAU15120;
XX
DT 24-OCT-2001 (first entry)
XX
DE Schizophrenia-associated isoform peptide #5.
XX Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;
KW neurological disorder; neuropathy.
XX
OS Homo sapiens.
XX MO200163293-A2.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-GB00783.
XX
PR 24-FEB-2000; 2000GB-0004415.
PR 28-NOV-2000; 2000US-0750395.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PI Herath HMC, Parekh RB, Rohlf C;
XX WPI; 2001-502868/55.
XX
PT Diagnosing and monitoring Schizophrenia by detecting the presence of
PT Schizophrenia Associated Features and Schizophrenia Associated Protein
XX Isoforms in samples of cerebrospinal fluid -
XX
PS Claim 6; Page 29; 160pp; English.
XX
CC The invention relates to methods and compositions for screening,
CC diagnosis and prognosis of Schizophrenia. The method involves detecting
CC the presence of Schizophrenia (SCH) Associated Features (SFS) and SCH
CC Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis,
CC immunoblotting or hybridisation assay, for diagnosing and monitoring SCH,
CC studying the effectiveness of treatments and for identifying potential
CC therapeutic agents. The method is used for (1) screening or diagnosis of
CC SCH and the relative abundance of at least 1 chosen feature correlates
CC with the presence or absence of SCH; and (2) monitoring the effect of
CC therapy administered to a subject with SCH and the relative abundance of
CC at least 1 chosen feature which correlates with the severity of SCH.
CC The expression and activity of the SFS, SPIs and related molecules
CC (e.g. secondary messengers) are studied to diagnose SCH, monitor the
CC progress of the disorder and the effectiveness of treatment and as
CC targets to identify and produce potential therapeutic agents for the
CC treatment of SCH. The paucity of detectable neurologic defects
CC distinguishes neuropsychiatric disorders such as SCH from neurological
CC disorders, where manifestations of anatomical and biochemical changes
CC have been identified in many cases. Consequently the identification and
CC characterisation of cellular and/or molecular causative defects and
CC neuropathies are necessary for improved treatment of neuropsychiatric
CC disorders. AAU15114-AAU15762 represent the amino acid sequences of
CC schizophrenia-associated isoforms used in the method of the invention.
XX
SQ Sequence 10 AA;
XX
Query Match 2.9%; Score 10; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 49
AAU15554
ID AAU15554 standard; Peptide: 10 AA.
XX
AC AAU15554;
XX
DT 24-OCT-2001 (first entry)
XX
DE Schizophrenia-associated isoform peptide #439.
XX Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;
KW neurological disorder; neuropathy.
XX
OS Homo sapiens.
XX MO200163293-A2.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-GB00783.
XX
PR 24-FEB-2000; 2000GB-0004415.
PR 28-NOV-2000; 2000US-0750395.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PI Herath HMC, Parekh RB, Rohlf C;
XX WPI; 2001-502868/55.
XX
PT Diagnosing and monitoring Schizophrenia by detecting the presence of
PT Schizophrenia Associated Features and Schizophrenia Associated Protein
XX Isoforms in samples of cerebrospinal fluid -
XX
PS Claim 6; Page 38; 160pp; English.
XX
CC The invention relates to methods and compositions for screening,
CC diagnosis and prognosis of Schizophrenia. The method involves detecting
CC the presence of Schizophrenia (SCH) Associated Features (SFS) and SCH
CC Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis,
CC immunoblotting or hybridisation assay, for diagnosing and monitoring SCH,
CC studying the effectiveness of treatments and for identifying potential
CC therapeutic agents. The method is used for (1) screening or diagnosis of
CC SCH and the relative abundance of at least 1 chosen feature correlates
CC with the presence or absence of SCH; and (2) monitoring the effect of
CC therapy administered to a subject with SCH and the relative abundance of
CC at least 1 chosen feature which correlates with the severity of SCH.
CC The expression and activity of the SFS, SPIs and related molecules
CC (e.g. secondary messengers) are studied to diagnose SCH, monitor the
CC progress of the disorder and the effectiveness of treatment and as
CC targets to identify and produce potential therapeutic agents for the
CC treatment of SCH. The paucity of detectable neurologic defects
CC distinguishes neuropsychiatric disorders such as SCH from neurological
CC disorders, where manifestations of anatomical and biochemical changes
CC have been identified in many cases. Consequently the identification and
CC characterisation of cellular and/or molecular causative defects and
CC neuropathies are necessary for improved treatment of neuropsychiatric
CC disorders. AAU15114-AAU15762 represent the amino acid sequences of
CC schizophrenia-associated isoforms used in the method of the invention.
XX
SQ Sequence 10 AA;
XX
Query Match 2.9%; Score 10; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID AAU15721 standard; Peptide, 10 AA.
 AC AAU15721;
 DT 24-OCT-2001 (First entry)
 DE Schizophrenia-associated isoform peptide #606.
 KW Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;
 neuroleptic disorder; neuropathy.
 OS Homo sapiens.
 PN WO200163293-A2.
 PD 30-AUG-2001.
 PF 23-FEB-2001; 2001WO-GB00783.
 PR 24-FEB-2000; 2000GB-0004415.
 PR 28-NOV-2000; 2000US-0750395.
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PI Herach HMC, Parekh RB, Rohlf C;
 DR WPI; 2001-502868/55.
 PT Diagnosing and monitoring Schizophrenia by detecting the presence of
 PT Schizophrenia Associated Features and Schizophrenia Associated Protein
 PT Isoforms in samples of cerebrospinal fluid -
 PS Claim 6; Page 41; 160pp; English.
 CC The invention relates to methods and compositions for screening,
 CC diagnosis and prognosis of Schizophrenia. The method involves detecting
 CC the presence of Schizophrenia (SCH) Associated Features (SfAs) and SCH
 CC Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis,
 CC immunoblotting or hybridisation assay, for diagnosing and monitoring SCH,
 CC studying the effectiveness of treatments and for identifying potential
 CC therapeutic agents. The method is used for (1) screening or diagnosis of
 CC SCH and the relative abundance of at least 1 chosen feature correlates
 CC with the presence or absence of SCH; and (2) monitoring the effect of
 CC therapy administered to a subject with SCH and the relative abundance of
 CC at least 1 chosen feature which correlates with the severity of SCH.
 CC (e.g. expression and activity of the SfA, SPIs and related molecules
 CC (e.g. secondary messengers) are studied to diagnose SCH, monitor the
 CC progress of the disorder and the effectiveness of treatment and as
 CC targets to identify and produce potential therapeutic agents for the
 CC treatment of SCH. The paucity of detectable neural defects
 CC distinguishes neuropsychiatric disorders such as SCH from neurological
 CC disorders, where manifestations of anatomical and biochemical changes
 CC have been identified in many cases. Consequently the identification and
 CC characterisation of cellular and/or molecular causative defects and
 CC neuropathies are necessary for improved treatment of neuropsychiatric
 CC disorders. AAU1514-AAU15762 represent the amino acid sequences of
 CC schizophrenia-associated isoforms used in the method of the invention.
 CC
 SQ Sequence 10 AA;
 QY 293 DQDGEILPR 302 2.9%; Score 10; DB 22; Length 10;
 DB 1 DQDGEILPR 10 Best Local Similarity 100.0%; Pred. No. 0.02;
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Search completed: February 21, 2004, 01:47:04
 Job time : 95 secs

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OM protein - protein search, using sw model

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(without alignments)
528.886 Million cell updates/sec

Title: US-10-063-671-8

Perfect score: 350

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Searched: 328717 segs, 42310858 residues

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Total number of hits satisfying chosen parameters: 2194

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Post-processing: Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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423 6 1.7 33 2 US-08-511-872-5 Sequence 5, Appl
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425 6 1.7 33 2 US-08-511-872-8 Sequence 8, Appl
426 6 1.7 33 2 US-08-317-844B-7 Sequence 9, Appl
427 6 1.7 33 3 US-07-927-391-9 Sequence 9, Appl
428 6 1.7 33 3 US-08-190-802A-262 Sequence 262, App
429 6 1.7 34 1 US-08-425-069-42 Sequence 54, Appl
430 6 1.7 34 1 US-08-425-069-54 Sequence 54, Appl
431 6 1.7 34 1 US-08-460-874A-8 Sequence 8, Appl
432 6 1.7 34 2 US-08-388-883B-8 Sequence 42, Appl
433 6 1.7 34 2 US-08-317-844B-42 Sequence 42, Appl
434 6 1.7 34 2 US-08-317-844B-54 Sequence 54, Appl
435 6 1.7 34 3 US-08-462-211A-8 Sequence 8, Appl
436 6 1.7 34 3 US-08-477-346-262 Sequence 262, App
437 6 1.7 34 3 US-08-473-089-262 Sequence 1, Appl
438 6 1.7 34 3 US-08-473-089-262 Sequence 262, App
439 6 1.7 34 4 US-08-487-072A-262 Sequence 262, App
440 6 1.7 35 1 US-08-560-727-1 Sequence 1, Appl
441 6 1.7 35 1 US-08-309-747-52 Sequence 52, Appl
442 6 1.7 35 1 US-08-458-298-52 Sequence 52, Appl
443 6 1.7 35 2 US-08-468-220-40 Sequence 40, Appl
444 6 1.7 35 2 US-08-468-220-40 Sequence 40, Appl
445 6 1.7 35 2 US-08-468-698-40 Sequence 40, Appl
446 6 1.7 35 2 US-08-388-883B-7 Sequence 7, Appl
447 6 1.7 35 2 US-08-700-442A-20 Sequence 20, Appl
448 6 1.7 35 2 US-08-938-975-3 Sequence 3, Appl
449 6 1.7 35 3 US-08-831-028-20 Sequence 20, Appl
450 6 1.7 35 3 US-09-001-984C-11 Sequence 11, Appl
451 6 1.7 35 3 US-09-001-984C-42 Sequence 42, Appl
452 6 1.7 35 3 US-08-194-664A-40 Sequence 40, Appl
453 6 1.7 35 4 US-09-321-399-3 Sequence 3, Appl
454 6 1.7 35 4 US-09-396-347F-11 Sequence 11, Appl
455 6 1.7 35 4 US-09-396-347F-42 Sequence 42, Appl
456 6 1.7 35 5 US-09-322-379-3 Sequence 3, Appl
457 6 1.7 35 5 PCT-US94-01553A-40 Sequence 40, Appl
458 6 1.7 35 5 PCT-US95-10426-40 Sequence 40, Appl
459 6 1.7 36 1 US-08-425-069-32 Sequence 32, Appl
460 6 1.7 36 1 US-08-425-069-37 Sequence 37, Appl
461 6 1.7 36 1 US-08-209-747-43 Sequence 43, Appl
462 6 1.7 36 1 US-08-209-747-48 Sequence 48, Appl
463 6 1.7 36 1 US-08-458-298-43 Sequence 43, Appl
464 6 1.7 36 1 US-08-458-298-48 Sequence 48, Appl
465 6 1.7 36 2 US-08-317-844B-32 Sequence 32, Appl
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466 6 1.7 36 2 US-08-317-844B-37 Sequence 37, Appl
467 6 1.7 36 4 US-09-149-476-400 Sequence 400, Appl
468 6 1.7 37 1 US-08-425-069-35 Sequence 35, Appl
469 6 1.7 37 1 US-08-425-069-36 Sequence 36, Appl
470 6 1.7 37 1 US-08-209-747-46 Sequence 46, Appl
471 6 1.7 37 1 US-08-209-747-47 Sequence 47, Appl
472 6 1.7 37 1 US-08-209-747-49 Sequence 49, Appl
473 6 1.7 37 1 US-08-458-298-46 Sequence 46, Appl
474 6 1.7 37 1 US-08-458-298-47 Sequence 47, Appl
475 6 1.7 37 1 US-08-458-298-49 Sequence 49, Appl
476 6 1.7 37 2 US-08-180-524-10 Sequence 10, Appl
477 6 1.7 37 2 US-08-975-166-10 Sequence 10, Appl
478 6 1.7 37 2 US-08-317-844B-35 Sequence 35, Appl
479 6 1.7 37 2 US-08-317-844B-36 Sequence 36, Appl
480 6 1.7 37 3 US-08-462-211A-8 Sequence 7, Appl
481 6 1.7 38 1 US-08-425-069-27 Sequence 27, Appl
482 6 1.7 38 1 US-08-209-747-38 Sequence 38, Appl
483 6 1.7 38 1 US-08-460-874A-7 Sequence 7, Appl
484 6 1.7 38 1 US-08-458-298-38 Sequence 38, Appl
485 6 1.7 38 2 US-08-317-844B-27 Sequence 27, Appl
486 6 1.7 39 1 US-08-425-069-33 Sequence 33, Appl
487 6 1.7 39 1 US-08-209-747-44 Sequence 44, Appl
488 6 1.7 39 1 US-08-458-298-44 Sequence 44, Appl
489 6 1.7 39 2 US-08-317-844B-33 Sequence 33, Appl
490 6 1.7 39 4 US-09-315-304B-1455 Sequence 1455, Ap
491 6 1.7 39 4 US-08-469-260A-380 Sequence 380, App
492 6 1.7 39 4 US-08-467-344A-380 Sequence 380, App
493 6 1.7 40 1 US-08-425-069-30 Sequence 30, Appl
494 6 1.7 40 1 US-08-209-747-40 Sequence 40, Appl
495 6 1.7 40 1 US-08-458-298-40 Sequence 40, Appl
496 6 1.7 40 1 US-08-458-298-40 Sequence 40, Appl
497 6 1.7 40 2 US-08-317-844B-30 Sequence 30, Appl
498 6 1.7 40 3 US-08-776-971-113 Sequence 113, App
499 6 1.7 40 4 US-03-271-438A-5 Sequence 5, Appl
500 6 1.7 41 1 US-08-425-069-29 Sequence 29, Appl

US-09-161-241-9
Sequence 9, Application US/09161241
Patent No. 6344541
GENERAL INFORMATION:
APPLICANT: Bass, Michael B
APPLICANT: Sullivan, John K
APPLICANT: Theill, Lars E
APPLICANT: Wang, Daquan
TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
FILE REFERENCE: A-548
CURRENT APPLICATION NUMBER: US/09/161,241
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 350
TYPE: PRT
ORGANISM: Human
US-09-161-241-9

Query Match 100.0%; Score 350; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORGATLTCGILAAVPTAPAPATATSAFVKGPAALSTYPOEATINEMFREVEELMED 60
DB 1 MORGATLTCGILAAVPTAPAPATATSAFVKGPAALSTYPOEATINEMFREVEELMED 60
QY 61 TQHKLRSAVEMEAEEAAKASSEVNLANLPSSYHNETNTDTKYGNNTIHVREIRIKITN 120
DB 61 TQHKLRSAVEMEAEEAAKASSEVNLANLPSSYHNETNTDTKYGNNTIHVREIRIKITN 120

QY 121 NOTGQVVFSEVTITTSVGDSEGRSHCIIIDDCGSPMYQFASFQYTCQPCGQRLCTR 180
DB 121 NOTGQVVFSEVTITTSVGDSEGRSHCIIIDDCGSPMYQFASFQYTCQPCGQRLCTR 180
QY 181 DSBCCDQOLCVMGCHCTKMATRGSGNGTICDNQDCCQGLCCAFQGLLPVCTPLPVEGEL 240
DB 181 DSBCCDQOLCVMGCHCTKMATRGSGNGTICDNQDCCQGLCCAFQGLLPVCTPLPVEGEL 240
QY 241 CHDPAARLDLITWELPDPALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQGEILL 300
DB 241 CHDPAARLDLITWELPDPALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQGEILL 300
QY 301 PREVPDEYEGSMEEYRQELDLERSLTFEEMALGSPAAAAALLGGEI 350
DB 301 PREVPDEYEGSMEEYRQELDLERSLTFEEMALGSPAAAAALLGGEI 350
RESULT 2
US-09-161-241-8
; Sequence 8, Application US/09161241
; Patent No. 6344541
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Daquan
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/161,241
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Mouse
US-09-161-241-8
Query Match 11.7%; Score 41; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.7e-31;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 40 YPOEATINEMPREVEIMEDTQHKLSAAYEMEAEEBAAK 80
DB 40 YPOEATINEMPREVEIMEDTQHKLSAAYEMEAEEBAAK 80
RESULT 3
US-09-325-932A-144
; Sequence 144, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flamm, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant develo
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 144
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-325-932A-144
Query Match 2.6%; Score 9; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 337 PAAAAAALL 345
|||||

DB 17 PAAAAAALL 25
RESULT 4
US-09-252-991A-19907
; Sequence 19907, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc U. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; NUMBER OF SEQ ID NOS: 33142
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19907
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19907
Query Match 2.6%; Score 9; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 336 EPPAAAAALL 344
|||||
DB 53 EPPAAAAALL 61
RESULT 5
US-08-460-874A-46
; Sequence 46, Application US/08460874A
; Patent No. 5744298
; GENERAL INFORMATION:
; APPLICANT: Stuber, Werner
; APPLICANT: Mieczorek, Leszek
; APPLICANT: Ziegelmaler, Robert
; TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner.
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington,
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,874A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/936,219
; FILING DATE: 27-AUG-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P4128684.7
; FILING DATE: 29-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Forman, David S.
; REGISTRATION NUMBER: 33,694
; REFERENCE/DOCKET NUMBER: 05552-1210-04000

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-874A-46

Query Match 2.3%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26
DB 5 TAPAPAPT 12

RESULT 6
US-08-388-883B-46
Sequence 46, Application US/08388883B
Patent No. 585185
GENERAL INFORMATION:
APPLICANT: ST BER, Werner
APPLICANT: WIECZOREK, Leszek
APPLICANT: ZIEGELMAIER, Robert
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
TITLE OF INVENTION: and the Use Thereof
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner L.L.P.
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington,
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,883B
FILING DATE: 13-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,305
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA: US 07/936,219
FILING DATE: 27-AUG-1992
APPLICATION NUMBER: DE P4128684.7
FILING DATE: 29-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 5552-1210-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-388-883B-46
Query Match 2.3%; Score 8; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26
DB 5 TAPAPAPT 12

RESULT 7
US-08-462-211A-46
Sequence 46, Application US/08462211A
Patent No. 614393
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: WIECZOREK, Leszek
APPLICANT: ZIEGELMAIER, Robert
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
TITLE OF INVENTION: and the Use Thereof
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner L.L.P.
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington,
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,211A
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/388,883
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA: US 08/300,305
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA: US 07/936,219
FILING DATE: 27-AUG-1992
APPLICATION NUMBER: DE P4128684.7
FILING DATE: 29-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 5552.1210-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-462-211A-46

Query Match 2.3%; Score 8; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26
DB 5 TAPAPAPT 12

RESULT 8
US-08-935-009A-5

Sequence 5, Application US/08935009A
Patent No. 6177241
GENERAL INFORMATION:
APPLICANT: Maine, Gregory T.
TITLE OF INVENTION: USE OF PEPTIDES TO IMPROVE
SPECIFICITY OF AN ENZYME IMMUNOASSAY FOR
THE DETECTION OF HERPESVIRUS SPECIFIC IGM ANTIBODY
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,009A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Weinstein, David L.
REGISTRATION NUMBER: 28,128
REFERENCE/DOCKET NUMBER: 6186-US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-6182
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6177241e
US-08-935-009A-5

Query Match 2.3%; Score 8; DB 3; Length 20;
Best Local Similarity 100.0%; Fred. No. 0.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 19 TABAPAPT 26
DB 9 TABAPAPT 16

RESULT 9
US-08-460-874A-12
Sequence 12, Application US/08460874A
Patent No. 5744298
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Mieczorek, Leszek
APPLICANT: Ziegelmaler, Robert
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
TITLE OF INVENTION: and the Use Thereof
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington,
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,874A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/936,219
FILING DATE: 27-AUG-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 05552-1210-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-874A-12

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,874A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/936,219
FILING DATE: 27-AUG-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 05552-1210-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-874A-12

Query Match 2.3%; Score 8; DB 1; Length 31;
Best Local Similarity 100.0%; Fred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 19 TABAPAPT 26
DB 21 TABAPAPT 28

RESULT 10
US-08-460-874A-13
Sequence 13, Application US/08460874A
Patent No. 5744298
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Mieczorek, Leszek
APPLICANT: Ziegelmaler, Robert
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
TITLE OF INVENTION: and the Use Thereof
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington,
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,874A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/936,219
FILING DATE: 27-AUG-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 05552-1210-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-874A-12

FILING DATE: 29-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 05552-1210-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-874A-13

Query Match 2.3%; Score 8; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26
18 TAPAPAPT 25

Db

RESULT 11
US-08-388-883B-12
Sequence 12, Application US/08388883B
Patent No. 5859185
GENERAL INFORMATION:
APPLICANT: ST BER, Werner
APPLICANT: WIECZOREK, Leszek
APPLICANT: ZIEGELMAIER, Robert
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner L.L.P.
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington,
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,883B
FILING DATE: 13-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,305
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/936,219
FILING DATE: 27-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4128684.7
FILING DATE: 29-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 5552-1210-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-388-883B-12

Query Match 2.3%; Score 8; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26
21 TAPAPAPT 28

Db

RESULT 12
US-08-388-883B-13
Sequence 13, Application US/08388883B
Patent No. 5859185
GENERAL INFORMATION:
APPLICANT: ST BER, Werner
APPLICANT: WIECZOREK, Leszek
APPLICANT: ZIEGELMAIER, Robert
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner L.L.P.
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington,
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,883B
FILING DATE: 13-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,305
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/936,219
FILING DATE: 27-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4128684.7
FILING DATE: 29-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 5552-1210-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-388-883B-13

Query Match 2.3%; Score 8; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26
18 TAPAPAPT 25

Db

RESULT 13
US-08-462-211A-12
; Sequence 12, Application US/08462211A
; Patent No. 6143493
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Mieczorek, Leszek
APPLICANT: Ziegelmaier, Robert
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
TITLE OF INVENTION: and the Use Thereof
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &
ADDRESSEE: Dunner L.L.P.
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington,
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,211A
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/388,883
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,305
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/936,219
FILING DATE: 27-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4128684.7
FILING DATE: 29-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Foreman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 5552.1210-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-462-211A-12

Query Match 2.3%; Score 8; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26
Db 21 TAPAPAPT 28

RESULT 14
US-08-462-211A-13
; Sequence 13, Application US/08462211A
; Patent No. 6143493
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Mieczorek, Leszek
APPLICANT: Ziegelmaier, Robert
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor

TITLE OF INVENTION: and the Use Thereof
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &
ADDRESSEE: Dunner L.L.P.
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington,
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,211A
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/388,883
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,305
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/936,219
FILING DATE: 27-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4128684.7
FILING DATE: 29-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Foreman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 5552.1210-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-462-211A-13

Query Match 2.3%; Score 8; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26
Db 18 TAPAPAPT 25

RESULT 15
US-08-460-874A-15
; Sequence 15, Application US/08460874A
; Patent No. 5744298
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Mieczorek, Leszek
APPLICANT: Ziegelmaier, Robert
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
TITLE OF INVENTION: and the Use Thereof
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington,
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,874A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/936,219
FILING DATE: 27-AUG-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4128684.7
FILING DATE: 29-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fortman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 05552-1210-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-874A-15

Query Match 2.3%; Score 8; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 TAPAPAPT 26
Db 16 TAPAPAPT 23

RESULT 16
US-08-388-883B-15
Sequence 15, Application US/0838883B
Patent No. 5859185
GENERAL INFORMATION:
APPLICANT: ST BER, Werner
APPLICANT: WIECZOREK, Leszek
APPLICANT: ZIEGELMAIER, Robert
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
TITLE OF INVENTION: and the Use Thereof
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner L.L.P.
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington,
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,883B
FILING DATE: 13-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,305
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/936,219

FILING DATE: 27-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4128684.7
FILING DATE: 29-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fortman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 5552-1210-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-388-883B-15

Query Match 2.3%; Score 8; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 TAPAPAPT 26
Db 16 TAPAPAPT 23

RESULT 17
US-08-462-211A-15
Sequence 15, Application US/08462211A
Patent No. 6143493
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: WIECZOREK, Leszek
APPLICANT: ZIEGELMAIER, Robert
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
TITLE OF INVENTION: and the Use Thereof
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner L.L.P.
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington,
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,211A
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/388,883
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,305
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/936,219
FILING DATE: 27-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4128684.7
FILING DATE: 29-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fortman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 5552-1210-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-462-211A-15

Query Match
Best Local Similarity 100.0%; Score 8; DB 3; Length 32;
Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26
Db 16 TAPAPAPT 23

RESULT 18
US-08-388-883B-1
Sequence 1, Application US/0838883B
Patent No. 5859185
GENERAL INFORMATION:
APPLICANT: ST BER, Werner
APPLICANT: WIECZOREK, Leszek
APPLICANT: ZIEGELMAIER, Robert
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
TITLE OF INVENTION: and the Use Thereof
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner L.L.P.
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington,
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,883B
FILING DATE: 13-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,305
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/936,219
FILING DATE: 27-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4128684.7
FILING DATE: 29-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 5552-1210-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1
OTHER INFORMATION: /note= "Some or all amino acids in

OTHER INFORMATION: the regions spanning 0-14 may be absent"
FEATURE:
NAME/KEY: Region
LOCATION: 22
OTHER INFORMATION: /note= "Some or all amino acids in
OTHER INFORMATION: the regions 22-40 may be absent."
US-08-388-883B-1

Query Match
Best Local Similarity 100.0%; Score 8; DB 2; Length 40;
Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26
Db 30 TAPAPAPT 37

RESULT 19
US-08-460-874A-17
Sequence 17, Application US/08460874A
Patent No. 5744298
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: WIECZOREK, Leszek
APPLICANT: ZIEGELMAIER, Robert
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
TITLE OF INVENTION: and the Use Thereof
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington,
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,874A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/936,219
FILING DATE: 27-AUG-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4128684.7
FILING DATE: 29-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 05552-1210-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-874A-17

Query Match
Best Local Similarity 100.0%; Score 8; DB 1; Length 51;
Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26
Db 11 TAPAPAPT 26

Db 35 TAPAPAPT 42

RESULT 20

US-08-388-883B-17
Sequence 17, Application US/0838883B
Patent No. 585185
GENERAL INFORMATION:
APPLICANT: ST BER, Werner
APPLICANT: WIEGZOREK, Leszek
APPLICANT: ZIEGELMAIER, Robert
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
TITLE OF INVENTION: and the Use Thereof
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner L.L.P.
STREET: 1300 I Street, N.W., Suite 700
City: Washington,
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,883B
FILING DATE: 13-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,305
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/936,219
FILING DATE: 27-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4128684.7
FILING DATE: 29-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Foreman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 5552-1210-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-388-883B-17

Query Match 2.3%; Score 8; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26
Db 35 TAPAPAPT 42

RESULT 21
US-08-462-211A-17
Sequence 17, Application US/08462211A
Patent No. 6143493
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Wiegzoer, Leszek
APPLICANT: Ziegelemaier, Robert
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor

TITLE OF INVENTION: and the Use Thereof
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner L.L.P.
STREET: 1300 I Street, N.W., Suite 700
City: Washington,
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,211A
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/388,883
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,305
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/936,219
FILING DATE: 27-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4128684.7
FILING DATE: 29-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Foreman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 5552-1210-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-462-211A-17

US-08-462-211A-17

Query Match

Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26

Db 35 TAPAPAPT 42

RESULT 22

US-09-366-887A-14
Sequence 14, Application US/09366887A
Patent No. 6403782
GENERAL INFORMATION:
APPLICANT: LUSTER, ANDREW D.
APPLICANT: LEDER, PHILIP
APPLICANT: ROTHENBERG, MARC
APPLICANT: GARCIA, EDUARDO
TITLE OF INVENTION: EOTAXIN: AN EOSINOPHIL CHEMOATTRACTANT
FILE REFERENCE: 00383/025002
CURRENT APPLICATION NUMBER: US/09/366,887A
PRIOR FILING DATE: 1999-08-04
PRIOR APPLICATION NUMBER: 60/000,449
PRIOR FILING DATE: 1995-06-22
PRIOR APPLICATION NUMBER: 08/522,713
PRIOR FILING DATE: 1995-09-01
PRIOR APPLICATION NUMBER: 08/522,713
PRIOR FILING DATE: 1998-06-16

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; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-366-887A-14

Query Match
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTLCCLL 13
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Db 5 ATTLCCLL 12

RESULT 23
US-09-886-319A-21
; Sequence 21, Application US/09886319A
; Patent No. 6586185
; GENERAL INFORMATION:
; APPLICANT: Wolf, Eckard
; APPLICANT: Werner, Sabine
; APPLICANT: Halte, Jörn-Peter
; APPLICANT: Regendogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
; TITLE OF INVENTION: the diagnosis or treatment of skin disorders and wound
; TITLE OF INVENTION: Healing and for the identification of pharmacologically
; TITLE OF INVENTION: Active Substances
; FILE REFERENCE: 50125/014002
; CURRENT APPLICATION NUMBER: US/09/886,319A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/222,081
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: DE 10030149.5
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-886-319A-21

Query Match
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTLCCLL 13
   |||||
Db 5 ATTLCCLL 12

RESULT 24
US-09-646-028-4
; Sequence 4, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Bitagyn, Alva
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 156
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-4

Query Match
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTLCCLL 13
   |||||
Db 5 ATTLCCLL 12

RESULT 25
US-08-460-874A-33
; Sequence 33, Application US/08460874A
; Patent No. 5744298
; GENERAL INFORMATION:
; APPLICANT: Stuber, Werner
; APPLICANT: Mieczorek, Leszek
; APPLICANT: Ziegelmayer, Robert
; TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
; TITLE OF INVENTION: and the Use Thereof
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington,
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,874A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/936,219
; FILING DATE: 27-AUG-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P4128684.7
; FILING DATE: 29-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Forman, David S.
; REGISTRATION NUMBER: 33,694
; REFERENCE/DOCKET NUMBER: 05552-1210-04000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-460-874A-33

Query Match
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26
   |||||
Db 59 TAPAPAPT 66
```

RESULT 26
US-08-388-883B-33
Sequence 33, Application US/0838883B
Patent No. 5859185
GENERAL INFORMATION:
APPLICANT: ST BER, Werner
APPLICANT: WIECZOREK, Leszek
APPLICANT: ZIEGELMAIER, Robert
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
TITLE OF INVENTION: and the Use Thereof
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner L.L.P.
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington,
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,883B
FILING DATE: 13-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,305
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/936,219
FILING DATE: 27-AUG-1992
PRIOR APPLICATION DATA: DE P4128684.7
APPLICATION NUMBER: DE P4128684.7
FILING DATE: 29-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 5552-1210-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-388-883B-33

Query Match 2.3%; Score 8; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26
DB 59 TAPAPAPT 66

RESULT 27
US-08-462-211A-33
Sequence 33, Application US/08462211A
Patent No. 6143493
GENERAL INFORMATION:
APPLICANT: Studer, Werner
APPLICANT: WIECZOREK, Leszek
APPLICANT: ZIEGELMAIER, Robert
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
TITLE OF INVENTION: and the Use Thereof
NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner L.L.P.
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington,
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,211A
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/388,883
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,305
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/936,219
FILING DATE: 27-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4128684.7
FILING DATE: 29-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 5552-1210-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-462-211A-33

Query Match 2.3%; Score 8; DB 3; Length 162;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26
DB 59 TAPAPAPT 66

RESULT 28
US-09-433-241A-4
Sequence 4, Application US/09433241A
Patent No. 6525244
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Ralfaleki, Antoni
APPLICANT: Falco, Carl
TITLE OF INVENTION: Plant Histidinol-Phosphate Amino transferase Homologs
FILE REFERENCE: B01256 US NA
CURRENT APPLICATION NUMBER: US/09/433,241A
CURRENT FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: 60/107,273
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Microsoft Office 97
SEQ ID NO 4
LENGTH: 162
TYPE: PRT
ORGANISM: Oryza sp.
FEATURE:

NAME/KEY: UNSURE
LOCATION: (88)
OTHER INFORMATION: Xaa = ANY AMINO ACID
FEATURE:
NAME/KEY: UNSURE
LOCATION: (136)
OTHER INFORMATION: Xaa = ANY AMINO ACID
FEATURE:
NAME/KEY: UNSURE
LOCATION: (137)
OTHER INFORMATION: Xaa = ANY AMINO ACID
FEATURE:
NAME/KEY: UNSURE
LOCATION: (138)
OTHER INFORMATION: Xaa = ANY AMINO ACID
US-09-433-241A-4

Query Match 2.3%; Score 8; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 EPAAAAA 343
DB 55 EPAAAAA 62

RESULT 29
US-09-646-028-9
Sequence 9, Application US/09646028
Patent No. 6562347
GENERAL INFORMATION:
APPLICANT: Kwak, Larry
APPLICANT: Birsayn, Arya
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
FILE REFERENCE: 14014.0316/P
CURRENT APPLICATION NUMBER: US/09/646,028
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 171
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-9

Query Match 2.3%; Score 8; DB 4; Length 171;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTLCULL 13
DB 5 ATTLCULL 12

RESULT 30
US-08-765-856-2
Sequence 2, Application US/08765856
Patent No. 6074817
GENERAL INFORMATION:
APPLICANT: Landini, Maria P.
APPLICANT: Ripalti, Alessandro
APPLICANT: Maine, Gregory T.
APPLICANT: Flanders, Richard T.
TITLE OF INVENTION: RECOMBINANT MONO AND POLY ANTIGENS TO DETECT CYTOMEGALOVIRUS-9
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road

CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,856
FILING DATE: 27-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IT95/00073
FILING DATE: 15-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Weinstein, David L.
REGISTRATION NUMBER: 28,128
REFERENCE/DOCKET NUMBER: 5750.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 937-6182
TELEFAX: (847) 938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 300 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-765-856-2

Query Match 2.3%; Score 8; DB 3; Length 300;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26
DB 241 TAPAPAPT 248

RESULT 31
US-08-935-009A-2
Sequence 2, Application US/08935009A
Patent No. 6177241
GENERAL INFORMATION:
APPLICANT: Maine, Gregory T.
TITLE OF INVENTION: USE OF PEPTIDES TO IMPROVE
TITLE OF INVENTION: SPECIFICITY OF AN ENZYME IMMUNOASSAY FOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,009A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Weinstein, David L.
REGISTRATION NUMBER: 28,128

REFERENCE/DOCKET NUMBER: 6186.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-6182
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 300 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-935-009A-2

Query Match 2.3%; Score 8; DB 3; Length 300;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26
Db 241 TAPAPAPT 248

RESULT 32
US-08-765-856-4
Sequence 4, Application US/08765856
Patent No. 6074817
GENERAL INFORMATION:
APPLICANT: Landini, Maria P.
APPLICANT: Ripalti, Alessandro
APPLICANT: Maine, Gregory T.
APPLICANT: Flanders, Richard T.
TITLE OF INVENTION: RECOMBINANT MONO AND POLY ANTIGENS TO DETECT CYTOMEGALOVIRUS-8
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,856
FILING DATE: 27-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IT95/00073
FILING DATE: 15-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Weinstein, David L.
REGISTRATION NUMBER: 28,128
REFERENCE/DOCKET NUMBER: 5750.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 937-6182
TELEFAX: (847) 938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 302 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-765-856-4

Query Match 2.3%; Score 8; DB 3; Length 302;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26

Db 9 TAPAPAPT 16

RESULT 33
US-08-935-009A-4
Sequence 4, Application US/08935009A
Patent No. 6177241
GENERAL INFORMATION:
APPLICANT: Maine, Gregory T.
TITLE OF INVENTION: USE OF PEPTIDES TO IMPROVE
SPECIFICITY OF AN ENZYME IMMUNOASSAY FOR
THE DETECTION OF HERPESVIRUS SPECIFIC IGM ANTIBODY
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,009A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Weinstein, David L.
REGISTRATION NUMBER: 28,128
REFERENCE/DOCKET NUMBER: 6186.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-6182
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 302 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-935-009A-4

Query Match 2.3%; Score 8; DB 3; Length 302;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26
Db 9 TAPAPAPT 16

RESULT 34
US-09-252-991A-27884
Sequence 27884, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27884
LENGTH: 303
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27884

Query Match 2.3%; Score 8; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 PTAPAP 25
Db 156 PTAPAP 163

RESULT 35
US-08-405-175A-5
Sequence 5, Application US/08405175A

GENERAL INFORMATION:
PATENT NO. 5885772
APPLICANT: Aderem, Alan A.
APPLICANT: Cher, Jiamin
APPLICANT: Chang, Sandy
TITLE OF INVENTION: METHOD FOR THE DETECTION OF ANENCEPHALY
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405.175A
FILING DATE: 16-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-121A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 467-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Predicted primary structure of human MARCKS
HYPOTHETICAL: NO
US-08-405-175A-5

Query Match 2.3%; Score 8; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 GEPAAAA 342
Db 88 GEPAAAA 95

RESULT 36
US-09-110-116-4
Sequence 4, Application US/09110116

PATENT NO. 6013479
GENERAL INFORMATION:
APPLICANT: Xu, Hong
APPLICANT: Cohan, Victoria L.
APPLICANT: Stuart, Susan G.
TITLE OF INVENTION: HUMAN EMRI-LIKE G PROTEIN COUPLED
FILE REFERENCE: PF-0550 US
CURRENT APPLICATION NUMBER: US/09/110.116
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 344
TYPE: PRT
ORGANISM: HOMO SAPIENS
FEATURE:
OTHER INFORMATION: 2935597, GenBank
US-09-110-116-4

Query Match 2.3%; Score 8; DB 3; Length 344;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LUCILAA 15
Db 69 LUCILAA 76

RESULT 37
US-09-032-523-2
Sequence 2, Application US/09032523
PATENT NO. 6232454
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl
APPLICANT: Baugh, Mariah
TITLE OF INVENTION: HUMAN PROTEINASE MOLECULES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032.523
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0479 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: RATEROT02
CLONE: 947429
US-09-032-523-2

Query Match 2.3%; Score 8; DB 3; Length 415;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LCLTAA 16
10 LCLTAA 17

RESULT 38
US-09-252-991A-27213
Sequence 27213, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27213
LENGTH: 417
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27213

Query Match 2.3%; Score 8; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 AAAAALL 345
308 AAAAALL 315

RESULT 39
US-09-252-991A-30846
Sequence 30846, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30846
LENGTH: 428
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30846

Query Match 2.3%; Score 8; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LLLAAVP 18

DB 184 LLLAAVP 191

RESULT 40
US-09-433-241A-12
Sequence 12, Application US/09433241A
Patent No. 6525244
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Falco, Steve
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Plant Histidinol-Phosphate Aminotransferase Homologs
FILE REFERENCE: Bb1256 US NA
CURRENT APPLICATION NUMBER: US/09/433,241A
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: 60/107,273
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Microsoft Office 97
SEQ ID NO 12
LENGTH: 435
TYPE: PRT
ORGANISM: Oryza sativa
US-09-433-241A-12

Query Match 2.3%; Score 8; DB 4; Length 435;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 EPAAAAA 343
57 EPAAAAA 64

RESULT 41
US-09-382-256-10
Sequence 10, Application US/09382256A
Patent No. 6207814
GENERAL INFORMATION:
APPLICANT: MIYAZONO, Kohel
TEN DIKE, Peter
FRANZEN, Petra
YAMASHITA, Hidetoshi
HELDIN, Carl-Henrik
TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS
AND THEIR USE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/382,256A
FILING DATE: 24-Aug-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: No. 6207814ember 17, 1993
APPLICATION NUMBER: GB 9224057.1
FILING DATE: No. 6207814ember 17, 1992
APPLICATION NUMBER: GB 9304677.9
FILING DATE: March 8, 1993
APPLICATION NUMBER: GB 9304680.3

FILED DATE: March 8, 1993
APPLICATION NUMBER: 9311047.6
FILING DATE: May 28, 1993
APPLICATION NUMBER: 9313763.6
FILING DATE: July 2, 1993
APPLICATION NUMBER: 9316099.2
FILING DATE: August 3, 1993
APPLICATION NUMBER: 321344.5
FILING DATE: October 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6207814man D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5298.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-382-256-10

Query Match 2.3%; Score 8; DB 3; Length 503;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 AAAAAALL 345
Db 21 AAAAAALL 28

RESULT 42
US-09-395-115-10
Sequence 10, Application US/09395115
Patent No. 6271365
GENERAL INFORMATION:
APPLICANT: Miyazono, Kohel; DiJke, Peter Ten;
APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felife & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/395,115
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6271365ember-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6271365ember-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304680.3
FILING DATE: 8-March-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9311047.6
FILING DATE: 28-May-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9136099.2
FILING DATE: 3-August-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-October-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-395-115-10

Query Match 2.3%; Score 8; DB 3; Length 503;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 AAAAAALL 345
Db 21 AAAAAALL 28

RESULT 43
US-08-436-265-10
Sequence 10, Application US/08436265
Patent No. 6316217
GENERAL INFORMATION:
APPLICANT: Miyazono, Kohel; DiJke, Peter Ten;
APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felife & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6316217ember-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6316217ember-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304680.3
FILING DATE: 8-March-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9311047.6
FILING DATE: 28-May-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9136099.2
FILING DATE: 3-August-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-October-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-265-10

Query Match 2.3%; Score 8; DB 4; Length 503;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 AAAAAALL 345
Db 21 AAAAAALL 28

RESULT 44
US-09-679-187-10
Sequence 10, Application US/09679187
Patent No. 6331621
GENERAL INFORMATION:
APPLICANT: Miyazono, Kohel; Dijke, Peter Ten;
APPLICANT: Frazer, Peter; Yamashita, Hideoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Palfé & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/679,187
FILING DATE: 03-OCT-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6331621member-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6331621member-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 9304680.3
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9311047.6
FILING DATE: 28-May-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9136099.2
FILING DATE: 3-August-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-October-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-679-187-10

Query Match 2.3%; Score 8; DB 4; Length 503;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 AAAAAALL 345
Db 21 AAAAAALL 28

RESULT 45
US-08-999-689A-6
Sequence 6, Application US/08999689A
Patent No. 6541615
GENERAL INFORMATION:
APPLICANT: ULARICH, AXEL
APPLICANT: KHATTONENKOV, ALEXEI
APPLICANT: CHEN, ZHENGJUN
TITLE OF INVENTION: SIRP PROTEINS AND USES THEREOF
FILE REFERENCE: 038602/0548
CURRENT APPLICATION NUMBER: US/08/999,689A
CURRENT FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 60/030,964
PRIOR FILING DATE: 1996-11-15
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 6
TYPE: PRT
LENGTH: 503
ORGANISM: Homo sapiens
US-08-999-689A-6

Query Match 2.3%; Score 8; DB 4; Length 503;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LUCILIAA 15
Db 14 LUCILIAA 21

RESULT 46
US-08-956-322-4
Sequence 4, Application US/08956322
Patent No. 6277977

```

GENERAL INFORMATION:
APPLICANT: SATHE, GANESH
APPLICANT: MAO, JOYCE
TITLE OF INVENTION: CDNA CLONE HAP0167 THAT ENCODES
TITLE OF INVENTION: A HUMAN 7-TRANSMEMBRANE RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,322
FILING DATE: 23-OCT-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/049,329
FILING DATE: 11-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70075
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 521 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-956-322-4

Query Match      2.3%; Score 8; DB 3; Length 521;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 LILCLILAA 15
Db      237 LILCLILAA 244

RESULT 47
US-09-252-991A-30878
; Sequence 30878, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30878
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30878

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Query Match      2.3%; Score 8; DB 4; Length 607;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      333 ALGEPAA 340
Db      279 ALGEPAA 286

RESULT 48
US-09-110-116-1
; Sequence 1, Application US/09110116
; Patent No. 6013479
; GENERAL INFORMATION:
; APPLICANT: Xu, Hong
; APPLICANT: Cohan, Victoria L.
; APPLICANT: Stuart, Susan G.
; TITLE OF INVENTION: HUMAN EMER1-LIKE G PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: PR-0550 US
; CURRENT APPLICATION NUMBER: US/09/110,116
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 652
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; FEATURE:
; OTHER INFORMATION: 429905, EOSINOT03
US-09-110-116-1

Query Match      2.3%; Score 8; DB 3; Length 652;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 LILCLILAA 15
Db      368 LILCLILAA 375

RESULT 49
US-08-956-322-2
; Sequence 2, Application US/08956322
; Patent No. 6277977
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: MAO, JOYCE
; TITLE OF INVENTION: CDNA CLONE HAP0167 THAT ENCODES
; TITLE OF INVENTION: A HUMAN 7-TRANSMEMBRANE RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,322
; FILING DATE: 23-OCT-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/049,329
; FILING DATE: 11-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031

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REFERENCE/DOCKET NUMBER: GH-70075
TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 652 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-956-322-2

Query Match 2.3%; Score 8; DB 3; Length 652;

Best Local Similarity 100.0%; Pred. No. 25;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LIGLILAA 15

Db 368 LIGLILAA 375

RESULT 50

US-09-413-814-5

Sequence 5, Application US/09413814

Patent No. 6225064

GENERAL INFORMATION:

APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH

APPLICANT: Bristol-Myers Squibb, Co.

APPLICANT: Beyer, Stefan

APPLICANT: Bloeker, Heilmut

APPLICANT: Brandt, Petra

APPLICANT: Cino, Paul M

APPLICANT: Dougherty, Brian A

APPLICANT: Goldberg, Steven L

APPLICANT: Hofle, Gerhard

APPLICANT: Mueller, Joachim

APPLICANT: Reichenbach, Hans

TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polypeptide or

TITLE OF INVENTION: heteropolypeptide compounds

FILE REFERENCE: PCT/US 99/23535

CURRENT APPLICATION NUMBER: US/09/413,814

CURRENT FILING DATE: 1999-10-07

EARLIER APPLICATION NUMBER: DE 198 46 493.2

EARLIER FILING DATE: 1998-10-09

NUMBER OF SEQ ID NOS: 107

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 5

LENGTH: 899

TYPE: PRT

ORGANISM: Sorangium cellulosum

US-09-413-814-5

Query Match 2.3%; Score 8; DB 3; Length 899;

Best Local Similarity 100.0%; Pred. No. 34;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 EPPAAAAA 343

Db 882 EPPAAAAA 889

Search completed: February 21, 2004, 01:52:15

Job time : 39 secs